

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
9 August 2001 (09.08.2001)

PCT

(10) International Publication Number  
**WO 01/57272 A2**

(51) International Patent Classification<sup>7</sup>: **C12Q 1/68**

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(21) International Application Number: **PCT/US01/00663**

(22) International Filing Date: 30 January 2001 (30.01.2001)

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(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/180,312	4 February 2000 (04.02.2000)	US
60/207,456	26 May 2000 (26.05.2000)	US
09/608,408	30 June 2000 (30.06.2000)	US
09/632,366	3 August 2000 (03.08.2000)	US
60/234,687	21 September 2000 (21.09.2000)	US
60/236,359	27 September 2000 (27.09.2000)	US
0024263.6	4 October 2000 (04.10.2000)	GB

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

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**Published:**

— *without international search report and to be republished upon receipt of that report*

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*



**WO 01/57272 A2**

(54) Title: **HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA**

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta is described. Also described are single exon nucleic acid probes expressed in the placenta and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL  
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA

CROSS REFERENCE TO RELATED APPLICATIONS

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The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S. provisional patent application serial nos. 60/236,359, filed September 27, 10 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of UK patent application no. 0024263.6, filed October 4, 2000, 15 the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY  
REFERENCE THEREOF

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The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file pto\_PLACENTA.txt, created 24 25 January 2001, having 26,548,337 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genome- 35 derived single exon nucleic acid probes expressed in human



placenta and single exon nucleic acid microarrays that include such probes.

#### Background of the Invention

5           For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to  
10 further the understanding of proteins – known or suspected – about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent  
15 biological understanding.

          For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via  
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

          More recently, however, the development of high  
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein  
30 product.

          One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences – that is, those accessible through isolation of mRNA – are of greatest initial interest. This "expressed  
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams *et al.*,  
*Science* 252:1651 (1991); Williamson, *Drug Discov. Today*  
4:115 (1999)). For nucleic acids sequenced by this  
approach, often the only biological information that is  
5 known *a priori* with any certainty is the likelihood of  
biologic expression itself. By virtue of the species and  
tissue from which the mRNA had originally been obtained,  
most such sequences are also annotated with the identity of  
the species and at least one tissue in which expression  
10 appears likely.

More recently, the pace of genomic sequencing has  
accelerated dramatically. When genomic DNA serves as the  
initial substrate for sequencing efforts, expression cannot  
be presumed; often the only *a priori* biological information  
15 about the sequence includes the species and chromosome (and  
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence  
accumulation by directed, EST, and genomic sequencing  
approaches – and in particular, with the accumulation of  
20 sequence information from multiple genera, from multiple  
species within genera, and from multiple individuals within  
a species – there is an increasing need for methods that  
rapidly and effectively permit the functions of nucleic  
sequences to be elucidated. And as such functional  
25 information accumulates, there is a further need for  
methods of storing such functional information in  
meaningful and useful relationship to the sequence itself;  
that is, there is an increasing need for means and  
apparatus for annotating raw sequence data with known or  
30 predicted functional information.

Although the increase in the pace of genomic  
sequencing is due in large part to technological changes in  
sequencing strategies and instrumentation, Service, *Science*  
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),  
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of  
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,  
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the  
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many  
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that  
25 function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting  
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al.,  
35 *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

*Ismb* 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al.,  
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic  
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*  
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically – and specifically, that permit the expression of regions predicted to encode protein – readily  
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach  
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries  
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5           The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single  
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex  
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

          Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the  
20 predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

25           Recently, techniques have been developed that permit direct sampling of placenta earlier in pregnancy. There is a need for methods and apparatus that permit analysis of placenta samples for the prediction and diagnosis of diseases caused by genetic defect,  
30 particularly those with polygenic etiology.

#### Summary of the Invention

35           The present invention solves these and other

problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the  
5 expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified  
10 within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon  
15 microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta, comprising a plurality  
20 of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 13,232 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at  
25 least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

30 In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.  
35 Preferably, each of said plurality of probes is amplifiable

using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

5 Suitably, said set of single exon nucleic acid probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 26,232 or a complimentary sequence, or a portion of such a sequence.

10 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

15 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said  
20 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most  
25 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single  
30 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The  
35 nylon may preferably, be positively-charged. Other suitable

substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, 5 polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable 10 set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or 15 more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome- 20 derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of 25 SEQ ID Nos. 13,233 - 26,232, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 13,232.

Accordingly, in a third aspect of the invention, 30 there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 13,232 or a complementary sequence or a fragment thereof 35 wherein said probe hybridizes at high stringency to a



nucleic acid expressed in the human placenta.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.:

5 13,233 - 26,232 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule having a sequence  
10 encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 26,233 - 38,837 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed  
15 in the human placenta.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the  
20 single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon  
25 nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably,  
30 no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

35 In another embodiment of either the third or

fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human placenta, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human placenta; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

5 wherein said detectably labeled nucleic acids are derived from mRNA from the placenta of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon  
10 microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene,  
15 comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in  
20 a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types  
25 indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 26,232 wherein said sequence encodes a peptide.

30 In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 13,233 - 26,232, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be  
35 encoded by a sequence comprising a sequence set out in any

of SEQ ID NOS.: 1 -13,232 .

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ  
5 ID NOS.: 26,233 - 38,837.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 26,233 - 38,837, or fragment thereof.

10 In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for  
15 electronic search, query, and analysis of such annotated sequence.

### Detailed Description of the Invention

20

#### Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each  
25 of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called  
30 in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books  
35 Division (2000) (ISBN: 1881299376). As so defined, the

term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a  
5 natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a  
10 portion thereof set out in exon SEQ ID NOS.: The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a  
15 combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF  
20 present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another  
25 of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit  
30 specific binding when they exhibit avidity of at least  $10^7$ , preferably at least  $10^8$ , more preferably at least  $10^9$  liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

35 As used herein with respect to the visual display

of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional information.

#### Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color

hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed  
5 in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by  
10 microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for  
15 scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the  
20 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than  $1e^{-30}$  ( $1 \times 10^{-30}$ ) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than  $1e^{-30}$  ( $1 \times 10^{-30}$ ) ("known");

25 FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

30

Methods and Apparatus for Predicting, Confirming,  
Annotating, and Displaying Functional Regions From Genomic  
Sequence Data

35 FIG. 1 is a flow chart illustrating in broad



outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained  
5 in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence  
10 is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A  
15 finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

20 Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can  
25 contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part  
30 through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100  
35 in the present invention include GenBank, and particularly

include several divisions thereof, including the  
htgs(draft), NT (nucleotide, command line), and NR  
(nonredundant) divisions. GenBank is produced by the  
National Institutes of Health and is maintained by the  
5 National Center for Biotechnology Information (NCBI).  
Databases of genomic sequence from species other than  
human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*  
*briggsii*, *Drosophila*, zebra fish, and other higher  
eukaryotic organisms will also prove useful as genomic  
10 sequence database 100.

Genomic sequence obtained by query of genomic  
sequence database 100 is then input into one or more  
processes 200 for identification of regions therein that  
are predicted to have a biological function as specified by  
15 the user. Such functions include, but are not limited to,  
encoding protein, regulating transcription, regulating  
message transport after transcription into mRNA, regulating  
message splicing after transcription into mRNA, of  
regulating message degradation after transcription into  
20 mRNA, and the like. Other functions include directing  
somatic recombination events, contributing to chromosomal  
stability or movement, contributing to allelic exclusion or  
X chromosome inactivation, and the like.

The particular genomic sequence to be input into  
25 process 200 will depend upon the function for which  
relevant sequence is to be identified as well as upon the  
approach chosen for such identification. Process step 200  
can be iterated to identify different functions within a  
given genomic region. In such case, the input often will  
30 be different for the several iterations.

Sequences predicted to have the requisite  
function by process 200 are then input into process 300,  
where a subset of the input sequences suitable for  
experimental confirmation is identified. Experimental  
35 confirmation can involve physical and/or bioinformatic

assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the  
5 entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often  
10 will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the  
15 functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within  
20 the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.  
25

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and  
35 facilitating creation of physical and/or informational

substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried for genomic sequence.

The sequence required to be returned by query will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the

sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in  
5 addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100  
10 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a  
15 required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome  
20 ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown  
25 that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer  
30 than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of  
35 sequence accession. Although the process has been

described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, 5 as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the 10 process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously 15 identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily 20 identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other 25 than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity 30 of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) 35 ended 23, as shown. Alternatively, or in addition to

report and termination of the initial inquiry, a new query  
20 can be generated that takes into account the initial  
negative result.

When query 20 returns sequence meeting the query  
5 criteria, the returned sequence is then passed to optional  
preprocessing 24, suitable and specific for the desired  
analytical approach and the particular analytical methods  
thereof to be used in process 25.

Preprocessing 24 can include processes suitable  
10 for many approaches and methods thereof, as well as  
processes specifically suited for the intended subsequent  
analysis.

Preprocessing 24 suitable for most approaches and  
methods will include elimination of sequence irrelevant to,  
15 or that would interfere with, the subsequent analysis.  
Such sequence includes repetitive sequence, such as Alu  
repeats and LINE elements, vector sequence, artificial  
sequence, such as artificial polylinkers, and the like.  
Such removal can readily be performed by identification and  
20 subsequent masking of the undesired sequence.

Identification can be effected by comparing the  
genomic sequence returned by query 20 with public or  
private databases containing known repetitive sequence,  
vector sequence, artificial sequence, and other artifactual  
25 sequence. Such comparison can readily be done using  
programs well known in the art, such as CROSS\_MATCH, or by  
proprietary sequence comparison programs the engineering of  
which is well within the skill in the art.

Alternatively, or in addition, undesirable,  
30 including artifactual, sequence can be identified  
algorithmically without comparison to external databases  
and thereafter removed. For example, synthetic polylinker  
sequence can be identified by an algorithm that identifies  
a significantly higher than average density of known  
35 restriction sites. As another example, vector sequence can

be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25,



where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include, but are not limited to, encoding protein, regulating  
5 transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability  
10 or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function  
15 to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as  
20 further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for  
25 identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs)  
30 using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

As further described in Example 1, below, gene  
35 finding software programs yield a range of results. For

the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%;  
5 and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although discussed herein particularly with respect to exon calling,  
10 consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such  
15 iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored  
20 in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further  
25 described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27  
30 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three  
35 of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In

particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon  
5 nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the  
10 polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with  
15 minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

20 However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer  
25 amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify  
30 regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

35 Conversely, somewhat fewer than 10% of ORFs

predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300,400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

10           The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/> ), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

20           Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

30           Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not

exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for  
5 amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the  
10 organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4<sup>th</sup> edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual,  
15 2<sup>nd</sup> edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

20 Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather,  
25 the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes  
30 not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single  
35 exon probe) is disposed in an array upon a support

substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see  
5 above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene,  
10 polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular,  
15 although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

20 The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination  
25 thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or  
30 can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

35 As is well known in the art, microarrays



typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can  
5 readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified  
product disposed in arrays on a support substrate to create  
10 a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization.  
15 If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using  
20 high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on  
25 nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes.  
30 Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads  
35 provides in aggregate a higher density of nucleic acid

probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high  
5 throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will  
10 depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one  
15 predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

20 The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created  
25 by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or  
30 indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific"  
35 libraries targeted at a particular biological question,

R.S. Thomas *et al.*, *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure  
5 expression only of those genes found in EST libraries,  
shown herein to represent only a fraction of expressed  
genes. Furthermore, such libraries – and thus microarrays  
based thereupon – are biased by the tissue or cell type of  
message origin, by the expression levels of the respective  
10 genes within the tissues, and by the ability of the message  
successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the  
methods of the present invention enable sequences that do  
not appear in EST or other expression databases to be  
15 determined – subsequently arrayed for expression  
measurements could not, therefore, have been represented as  
probes on an EST microarray. And as further demonstrated  
in the examples, *infra*, the remaining population of genes  
identified from genomic sequence by the methods of the  
20 present invention – that is, the one third of sequences  
that had previously been accessioned in EST or other  
expression databases – are biased toward genes with higher  
expression levels.

Representation of a message in an EST and/or cDNA  
25 library depends upon the successful reverse transcription,  
optionally but typically with subsequent successful  
cloning, of the message. This introduces substantial bias  
into the population of probes available for arraying in EST  
microarrays.

30 In contrast, neither reverse transcription nor  
cloning is required to produce the probes arrayed on the  
genome-derived single exon microarrays of the present  
invention. And although the ultimate deposition of a probe  
on the genome-derived single exon microarray of the present  
35 invention depends upon a successful amplification from

genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse  
5 transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias,  
10 than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric  
15 stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present  
25 invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically  
35 include a fair amount of vector sequence, more so when the

probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the

genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without  
5 such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such  
10 microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present  
15 invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual  
20 probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be  
25 designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often  
30 include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized  
35 probes. For human genes, the near-complete sequence of

human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

5 In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70,  
10 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single  
15 exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression  
20 patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such  
25 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention  
30 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon  
35 microarrays of the present invention include sequence drawn

from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay prespliced RNA, and  
5 thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic  
10 synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to  
15 achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (i.e., mismatched) sequence.

20 In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present  
25 invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved  
30 for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention  
35 typically are, but need not necessarily be, bound



noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari *et al.*, *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez *et al.*, *Nucl. Acids Res.* 28:85-86 (2000); Spingola *et al.*, *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm

expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence  
5 drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which  
10 the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is performed.

15 In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization  
20 experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the  
25 expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can  
30 be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see  
35 Ausubel et al. and Maniatis et al., or purchased

commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of  
5 nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As  
10 further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

15 After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are  
20 related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain  
25 sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for  
30 further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived  
35 single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate  
5 can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions (wells) are conveniently used, any device that permits  
10 addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-  
15 derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3'  
20 primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

25 Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

30 In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered  
35 set of amplifiable probes is packaged separately from the

genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences,

SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local  
5 alignment search tool"). The results of such query – including information on identical sequences and information on nonidentical sequences that have diffuse or focal regions of sequence homology to the query sequence – can then be passed directly to process 500, or used to  
10 inform analyses subsequently undertaken in process 200, process 300, or process 400.

Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process  
500 where it is usefully related to the sequence data  
15 itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or  
20 relational database, by linking to external databases, or by a combination thereof. Such database techniques are well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or  
25 displayed 800.

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence  
30 annotation produces a need for methods of displaying the information in meaningful ways.

FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic  
35 works of Piet Mondrian, visual display 80 is alternatively

described herein as a "Mondrian".

Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given  
5 the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left  
10 border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

15 As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides  
20 can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other  
25 pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed.  
30 Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or  
35 fulcrum point about which a chosen range of sequence is

anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or



approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

- 5 For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

- 10 Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

- Alternatively, or in addition, the color, hue, 15 density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be 20 indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 25 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

- As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, 30 field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

- Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 35 can include as few as one such series of rectangles and as

many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show  
5 predictions of a plurality of different functions.  
However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as a graphical user interface for computer query and analysis,  
10 such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the  
15 portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional  
20 inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an  
25 increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

30 Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84  
35 identifies the sequence included within the probe

immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of

rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity  
5 has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links  
10 directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be  
15 resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical  
20 assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of  
25 rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of  
30 hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to  
35 depict expression less than control, corresponding to the

spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 13,232 of these ORFs in placenta.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in placenta is currently available for use in measuring the level of its ORF's expression in placenta.

Given the substantial impact on human morbidity and mortality of diseases directly caused by genetic defect, and given the profound influence of genetic factors on the predisposition, onset, and/or aggressiveness of most, if not all human diseases, there has long been

interest in efficient and safe means for early detection of gene defects and polymorphisms that cause, are associated with, or are implicated in development of disease.

Classically, such antenatal diagnosis was  
5 effected during second trimester by metaphase karyotyping of fetal cells that had shed spontaneously into amniotic fluid.

More recently, techniques have been developed that permit direct sampling of placenta earlier in  
10 pregnancy.

One technique in current clinical practice is chorionic villus sampling, which can be used to detect gene defects or polymorphisms in cells from the developing fetus, usually between 10 and 12 weeks of pregnancy. In  
15 chorionic villus sampling, a small sample of chorionic villi, which are tiny projections that make up part of the placenta, a fetal-derived tissue, is removed through the mother's cervix or the abdominal wall. Placental chromosomal DNA is then isolated from the chorionic villus  
20 cells and analyzed to detect a small number of known genetic defects. Such defects range from gross karyotypic changes, such as triploidy, to discrete point mutations known to cause diseases having significant morbidity or mortality.

25 Although only a few diseases are at present diagnosed by antenatal analysis of human placenta, a far higher number of human diseases and disorders have been catalogued in which dysfunction or misregulation of one or more genes contributes to the disease phenotype. At one  
30 end of the spectrum of genetic diseases are those, such as sickle cell trait, in which a single point mutation is responsible for the disease phenotype. At the other end of the spectrum lie disorders such as Down syndrome wherein the presence of a supernumerary chromosome manifests itself  
35 in variety of phenotypic defects that vary in severity

among affected individuals. For most, possibly all genetic diseases, the precise phenotypic manifestation and its severity is a function of a complex interaction between the definable genetic lesion and the action of many other genes  
5 and environmental factors.

Although the incidence of many genetic diseases is low, a sufficient number of such genetic diseases affect a sufficiently large population that they impact the national health economy. For example, cystic fibrosis,  
10 caused by mutations in a gene encoding a chloride ion channel and resulting in lung and other disorders, occurs at a rate of about 1 in 3000 births among Caucasians and costs over \$1 billion annually for direct medical treatment in the U.S. alone. Furthermore, it is increasingly thought  
15 that for many diseases where no clear-cut genetic lesion appears responsible, possession by individuals of particular gene alleles naturally occurring within certain populations places such individuals at increased risk for developing those diseases. Examples include heart disease,  
20 neurodegenerative disorders, diabetes, cancer and autoimmune disorders. For yet other diseases, especially cancer, the etiology is truly polygenic in that defects in multiple genes must coincide in the same individual or even the same cell for the disease to develop and/or progress.

25 A large number of human genetic diseases and disorders are known, as are the gene or genes implicated in the etiology of the disease. Although in some cases single gene defects are known to be responsible for the etiology of a genetic disease, it is believed that for most or all  
30 such diseases, penetrance of the disease is affected by interaction with other genes. For other diseases or disorders, it is believed that their mechanism is explained by the interaction of multiple genes, or by mutations or other defects in multiple genes. Such diseases and disorders may  
35 be detected in placenta.



The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for antenatal diagnosis of human genetic disorders. With each of the single exon probes described herein shown to be  
5 expressed at detectable levels in human placenta, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

For example, antenatal diagnosis can be based  
10 upon the quantitative relatedness of a placental gene expression profile to one or more reference expression profiles known to be characteristic of a given disease, or to specific grades or stages thereof.

In one embodiment, the gene expression profile is  
15 generated by hybridizing nucleic acids obtained directly or indirectly from placenta, typically through chorionic villus sampling, to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids from  
20 individuals with known disease.

Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

25 In another approach, the genome-derived single exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits presence and/or predisposition to disease to be assessed through the  
30 massively parallel determination of altered copy number, deletion, or mutation of exons known to be expressed in human placenta. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated  
35 gene.

The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art – see Ausubel et al. and Maniatis et al. – each probe reports the level of  
5 expression of message specifically containing that ORF.

It should be appreciated, however, that the probes of the present invention, for which expression in the placenta has been demonstrated are useful for both measurement in the placenta and for survey of expression in  
10 other tissues.

Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which  
15 are not present in existing expression databases to be identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was  
20 measurable in only a single of the tested tissues were represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten  
25 tested tissues were present in existing expressed sequence databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have  
30 significant advantages over the cDNA or EST-based probes that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon  
35 microarrays, in turn, are useful devices for measuring and

for surveying gene expression in the human.

Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell

Carcinoma Using Combination of cDNA Subtraction and  
Microarray Analysis," *Oncogene* 19(12):1519-28 (2000);  
Whitney et al., "Analysis of Gene Expression in Multiple  
Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.*  
5 46(3):425-8 (1999)), in drug discovery screens (see, for  
example, Scherf et al., "A Gene Expression Database for the  
Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44  
(2000)) and in diagnosis to determine appropriate treatment  
strategies (see, for example, Sgroi et al., "In vivo Gene  
10 Expression Profile Analysis of Human Breast Cancer  
Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of  
pharmacological drug candidates upon cells, each probe  
provides specific useful data. In particular, it should be  
15 appreciated that even those probes that show no change in  
expression are as informative as those that do change,  
serving, in essence, as negative controls.

For example, where gene expression analysis is  
used to assess toxicity of chemical agents on cells, the  
20 failure of the agent to change a gene's expression level is  
evidence that the drug likely does not affect the pathway  
of which the gene's expressed protein is a part.  
Analogously, where gene expression analysis is used to  
assess side effects of pharmacological agents - whether in  
25 lead compound discovery or in subsequent screening of lead  
compound derivatives - the inability of the agent to alter  
a gene's expression level is evidence that the drug does  
not affect the pathway of which the gene's expressed  
protein is a part.

30 WO 99/58720 provides methods for quantifying the  
relatedness of a first and second gene expression profile  
and for ordering the relatedness of a plurality of gene  
expression profiles. The methods so described permit  
useful information to be extracted from a greater  
35 percentage of the individual gene expression measurements

from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999);

5 Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in placenta. The individual single exon probes can be provided in the form of substantially isolated and purified  
10 nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA  
15 complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as  
20 complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

25 Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity  
30 suitable for amplification by PCR or by other well known amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and  
35 WO 00/15779. As is well understood, where the probes are

to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

5           Where the probe is to be provided in form suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or  
10 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged  
15 therefrom. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting,  
20 in this embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a  
25 genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF.  
30 Furthermore, when intended for use on a genome-derived single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase  
35 hybridization, however — that is, for use in a

hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 13,233 - 26,232, respectively, for probe SEQ ID NOS. 1 - 13,232. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 13,233 - 26,232 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c<sub>ot</sub>1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high

stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as  
5 the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes  
10 of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one  
15 expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more  
20 usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand  
25 of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art  
30 to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to  
35 provide single-stranded nucleic acid probes that have



sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic  
5 and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

10 And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as  $^3\text{H}$ ,  $^{32}\text{P}$ ,  $^{33}\text{P}$ ,  $^{35}\text{S}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ; fluorescent  
15 labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR<sup>®</sup>

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates  
20 thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

25 The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived  
30 single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96  
35 well microtiter plate can be used, greater efficiency is

obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human placenta.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human placenta. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group

consisting of SEQ ID NOS.: 1 - 13,232.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 13,232 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 13,233 - 26,232, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 13,232 can be used, or that portion thereof in SEQ ID NOS. 13,233 - 26,232 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT<sup>™</sup> Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA;

Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverly, MA)

Furthermore, shorter peptides can be chemically  
5 synthesized using commercial peptide synthesizing equipment  
and well known techniques. Procedures are described, *inter*  
*alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide  
Synthesis: A Practical Approach (Practical Approach Series,  
(Paper)), Oxford Univ. Press (March 2000) (ISBN:  
10 0199637245); Jones, Amino Acid and Peptide Synthesis  
(Oxford Chemistry Primers, No 7) , Oxford Univ. Press  
(August 1992) (ISBN: 0198556683); and Bodanszky, Principles  
of Peptide Synthesis (Springer Laboratory), Springer Verlag  
(December 1993) (ISBN: 0387564314).

15 It is, therefore, another aspect of the invention  
to provide peptides comprising an amino acid sequence  
translated from SEQ ID NOS.: 13,233 - 26,232. Such amino  
acid sequences are set out in SEQ ID NOS: 26,233 - 38,837.  
Any such recombinantly-expressed or synthesized peptide of  
20 at least 8, and preferably at least about 15, amino acids,  
can be conjugated to a carrier protein and used to generate  
antibody that recognizes the peptide. Thus, it is a  
further aspect of the invention to provide peptides that  
have at least 8, preferably at least 15, consecutive amino  
25 acids.

The following examples are offered by way of  
illustration and not by way of limitation.

### 30 EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted  
in Human Genomic Sequence

#### Bioinformatics Results

35 All human BAC sequences in fewer than 10 pieces

that had been accessioned in a five month period immediately preceding this study were downloaded from GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

5           After masking repetitive elements using the program CROSS\_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets:  
10 GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic  
15 DNA.

          The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION  
20 yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

          The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three  
25 programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

          ORFs predicted by any two of the three programs  
30 ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single  
35 gene if fewer than 7 exons were found within the 25 kb

window.

### PCR

The largest ORF from each gene bin that did not  
5 span repetitive sequence was then chosen for amplification,  
as were all consensus ORFs longer than 500 bp. This method  
approximated one exon per gene; however, a number of genes  
were found to be represented by multiple elements.

Previously, we had determined that DNA fragments  
10 fewer than 250 bp in length do not bind well to the amino-  
modified glass surface of the slides used as support  
substrate for construction of microarrays; therefore,  
amplicons were designed in the present experiments to  
approximate 500 bp in length.

15 Accordingly, after selecting the largest ORF per  
gene bin, a 500 bp fragment of sequence centered on the ORF  
was passed to the primer picking software, PRIMER3  
(available online for use at  
<http://www-genome.wi.mit.edu/cgi-bin/primer/> ). A first  
20 additional sequence was commonly added to each ORF-unique  
5' primer, and a second, different, additional sequence was  
commonly added to each ORF-unique 3' primer, to permit  
subsequent reamplification of the amplicon using a single  
set of "universal" 5' and 3' primers, thus immortalizing  
25 the amplicon. The addition of universal priming sequences  
also facilitates sequence verification, and can be used to  
add a cloning site should some ORFs be found to warrant  
further study.

The ORFs were then PCR amplified from genomic  
30 DNA, verified on agarose gels, and sequenced using the  
universal primers to validate the identity of the amplicon  
to be spotted in the microarray.

Primers were supplied by Operon Technologies  
(Alameda, CA). PCR amplification was performed by standard  
35 techniques using human genomic DNA (Clontech, Palo Alto,

CA) as template. Each PCR product was verified by SYBR<sup>®</sup> green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR  
5 amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon)  
10 length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median  
15 size of 150 bp (n=9498). With an average amplicon size of  $475 \pm 25$  bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

20 Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of  
25 successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were  
30 sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR  
35 and sequencing results. The reasons for this are unclear,

but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material  
5 flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was  
10 similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-  
15 described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally  
20 included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt  
25 GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than  $1 \text{ e}^{-100}$ ) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe  
30 sequences showed some homology to a known EST or mRNA (BLAST E values from  $1 \text{ e}^{-5}$  to  $1 \text{ e}^{-99}$ ). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

35 All of the probe sequences (as amplified) were



then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

#### EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single

## Exon Microarrays

The two genome-derived single exon microarrays  
5 prepared according to Example 1 were hybridized in a series  
of simultaneous two-color fluorescence experiments to (1)  
Cy3-labeled cDNA synthesized from message drawn  
individually from each of brain, heart, liver, fetal liver,  
placenta, lung, bone marrow, HeLa, BT 474, or HBL 100  
10 cells, and (2) Cy5-labeled cDNA prepared from message  
pooled from all ten tissues and cell types, as a control in  
each of the measurements. Hybridization and scanning were  
carried out using standard protocols and Molecular Dynamics  
equipment.

15 Briefly, mRNA samples were bought from commercial  
sources (Clontech, Palo Alto, CA and Amersham Pharmacia  
Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were  
incorporated during separate reverse transcriptions of 1 µg  
of polyA<sup>+</sup> mRNA performed using 1 µg oligo(dT)12-18 primer  
20 and 2 µg random 9mer primers as follows. After heating to  
70°C, the RNA:primer mixture was snap cooled on ice. After  
snap cooling on ice, added to the RNA to the stated final  
concentration was: 1X Superscript II buffer, 0.01 M DTT,  
100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM  
25 Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II  
enzyme. The reaction was incubated for 2 hours at 42°C.  
After 2 hours, the first strand cDNA was isolated by adding  
1 U Ribonuclease H, and incubating for 30 minutes at 37°C.  
The reaction was then purified using a Qiagen PCR cleanup  
30 column, increasing the number of ethanol washes to 5.  
Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured  
for dye incorporation. Volumes of both Cy3 and Cy5 cDNA  
corresponding to 50 pmoles of each dye were then dried in a  
35 Speedvac, resuspended in 30 µl hybridization solution

containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c<sub>0</sub>t1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all

tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal — where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) — 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data — that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective

tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; 5 HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose 10 expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, 15 fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

20

#### Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those 25 genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than  $1e-30$  (designated "unknown") 30 upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than  $1e-30$  ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 35 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

#### Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300\_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734\_1 was shown by microarray experiment to be present

in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue  
5 type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However,  
10 in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-  
15 derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the  
20 microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further  
25 studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

30

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain
--

Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca <sup>2+</sup> binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin
AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates



				activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be  
 5 important in the central nervous system or brain. The exon giving the highest signal (AP00217-1) was found to be the gene encoding an S100B  $\text{Ca}^{2+}$  binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097

(1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to  
5 rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being  
10 absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the  
15 highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20  
20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L,  
25 AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in  
30 the literature to be found in brain and liver (Joshi et al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 $\alpha$  (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-  
35 chromosome RNA-binding motif (Chai et al., *Genomics*

49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature  
 5 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process.  
 10 The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average  
 15 expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 ± 0.11	-1.85 ± 0.08
Brain	-1.41 ± 0.11	-1.17 ± 0.05
BT474	1.85 ± 0.09	1.66 ± 0.12
Fetal Liver	-1.62 ± 0.07	-1.41 ± 0.05
HBL100	1.32 ± 0.05	2.64 ± 0.12
Heart	1.16 ± 0.09	1.56 ± 0.10
HeLa	1.11 ± 0.06	1.30 ± 0.15
Liver	-1.62 ± 0.22	-2.07 ±
Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability  
5 of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

### 10 EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

For each genomic clone processed for microarray  
15 as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for  
20 multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the  
25 paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate  
30 synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully  
35 identified 37 of the known exons (100%), while DICTION

identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be  
5 from the same gene, the carbamyl phosphate synthetase gene (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show  
10 identical expression patterns, elegantly demonstrating the reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes.  
15 Interestingly, 4 of the genes on this BAC are protease inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very  
20 good. A novel gene is also found from 86.6 kb to 88.6 kb, upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following  
25 colors indicate a known gene (top to bottom):  
red = kallistatin protease inhibitor (P29622);  
purple = plasma serine protease inhibitor (P05154);  
turquoise =  $\alpha$ 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and  
30 12 did not sequence verify.

#### EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring  
35 Human Gene Expression

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique  
5 exons in the human genome that could be shown to be expressed at significant levels in placenta tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon  
10 microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the  
15 single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 13,232 single exon probes, each fragment corresponding to an extension product from one of  
20 the two amplification primers.)

The structures of the 13,232 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 13,232. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not  
25 included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 13,233 - 26,232, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than  
30 one amplicon.

As detailed in Example 2, expression was demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant  
35 expression is based on a statistical confidence that the

signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give  
5 a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the  
10 population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining  
15 control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations)  
20 are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean +  
25 (3\*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any  
30 signal exceeding the threshold is significant.

The probes and their expression data are presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human placenta and thus  
35 presents the subset of probes that was recognized to be

useful for measuring expression of their cognate genes in human placenta tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 13,233 - 26,232 was individually  
5 used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were  
10 scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted  
15 in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective  
20 probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:" ) from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be  
25 expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the  
30 name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS. corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide  
35 sequences. These are set out as PEPTIDE SEQ ID NOS.:. The



peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs  
5 are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the  
10 exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all  
15 of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion  
20 of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about  $1e-05$  and  $1e-100$ ), the descriptor reveals the likely function of the  
25 protein encoded by the probe's ORF.

Using BLAST E value cutoffs of  $1e-05$  (i.e.,  $1 \times 10^{-5}$ ) and  $1e-100$  (i.e.,  $1 \times 10^{-100}$ ) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of  $1e-30$  was used as  
30 the boundary when only two classes were to be defined for analysis (unknown,  $>1e-30$ ; known  $<1e-30$ ) (see also FIG. 8). Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about  $1e-100$  - which is probative evidence that the query sequence has previously  
35 been shown to be expressed - the top hit is highly unlikely

exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even  
5 the ORF itself is unlikely in such cases to be present identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent  
10 a proper subset of the data present within the attached sequence listing. For each amplicon probe (SEQ ID NOS.: 1 - 13,232) and probe exon (SEQ ID NOS.: 13,233 - 26,232, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

15 (a) the accession number of the BAC from which the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST  
20 query of the EST database, with accession number and BLAST E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

25 (d) the most similar sequence provided by BLASTX query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

#### 30 EXAMPLE 5

Genome-Derived Single Exon Probes Useful For Measuring  
Expression of Genes in Human Placenta

Table 4 (550 pages) presents expression, homology, and  
35 functional information for the genome-derived single exon

probes that are expressed significantly in human placenta.

Page 1 of 550  
Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
463	13658	26695	6				
912	14087	27152	9.68				
1070	14230		3.01				
1330	14487	27555	10.9				
1645	14797	27882	1.92				
1666	14818	27901	4.94				
1784	14913	28008	1.03				
1788	14937	28030	1.87				
1784	14943	28036	8.53				
1939	15082	28183	1.57				
2034	15175	28285	2.66				
2234	15398	28497	3.39				
2353	16484	28616	2.53				
3255	16428	28447	3.75				
3637	16702	28713	1.48				
3604	16788	29783	10.5				
3651	16814		0.84				
3747	16908	28812	0.88				
4057	17213		0.94				
4314	17457	30445	1.55				
4377	17520	30500	6.88				
4396	17639	30519	0.87				
4398	17639	30520	0.87				
4437	17597		1.69				
4512	17651	30639	0.61				
4938	18088	31084	1.86				
6002	18131		0.6				
6157	18278	31244	5.14				
5168	18280	31255	1.24				
5371	18574	31442	1.76				
5371	18574	31443	1.78				
5538	18735		4.12				
5714	18907		7.28				
5798	18735		3.31				

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Table 4  
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5658	18048	32354	4.22				
6148	25820	32688	1.61				
6174	18350	32896	1.92				
6548	19708		1.01				
6678	19838	33226	1.25				
6679	19838	33227	1.25				
7275	20358	33812	1.42				
7275	20358	33813	1.42				
7569	20641	34117	1.18				
7569	20641	34118	1.18				
8251	21333	34851	1.44				
8682	21762	35298	1.14				
9081	22140	35684	0.76				
9061	22140	35685	0.76				
9734	22789	36373	3.82				
9868	23007	36802	0.56				
10086	23124	36725	1.51				
10229	23284	36853	0.88				
10643	23677	37286	0.74				
10643	23677	37287	0.74				
10922	24005		2.32				
11280	24346		1.76				
11348	24410	38083	2.78				
11641	24721	38414	1.73				
11749	23935	37581	1.36				
11749	23935	37582	1.36				
11782	24782		2.09				
12057	25038	38746	1.58				
12623	25419		2.06				
12667	25628	31980	1.5				
6177	18353	32700	16.82	9.8E+00 AJ238028.1	NT		Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
8195	21277	34800	1.5	9.8E+00 U32716.1	NT		Haemophilus influenzae Rd section 31 of 163 of the complete genome
9844	22983	35576	0.48	9.8E+00 Y18930.1	NT		Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
8944	22983	35576	0.48	9.8E+00 Y18930.1	NT		Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7139	20274	33714	0.82	9.8E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
7139	20274	33715	0.82	9.8E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10636	23670	37279	0.83	9.8E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIF polypeptide 2 (Gif2h2) genes, complete cds
10636	23670	37280	0.83	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor IIF polypeptide 2 (Gif2h2) genes, complete cds
2731	15849	28959	0.97	8.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2731	15849	28960	0.97	8.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2890	16166	29182	3.08	9.4E+00	AB043765.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
8290	21372	34893	1.08	9.3E+00	AF130380.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
9204	22282	35822	3.03	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
7625	20695	34171	0.8	9.2E+00	Q61767	SWISSPROT	3 BETA-HYDROXYSTEROID DEHYDROGENASE TYPE IV (3BETA-HSD IV) (3-BETA-HYDROXY-DELTA(6)-STEROID DEHYDROGENASE) (3-BETA-HYDROXY-S-ENE STEROID DEHYDROGENASE) (PROGESTERONE REDUCTASE)
5411	18613	31586	2.59	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5411	18613	31587	2.59	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9630	22685		1	9.0E+00	P09241	SWISSPROT	RHODOPSIN
6160	18336	32681	5.15	8.9E+00	BE971806.1	EST_HUMAN	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3834592 3'
6510	18675	33044	2.03	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cp Tbx3 premature mRNA, partial cds
6510	18675	33045	2.03	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cp Tbx3 premature mRNA, partial cds
453	13649	26683	1.79	8.4E+00	6031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
6654	21097	34611	2.09	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11443	24504		1.96	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8345	21425		0.98	7.8E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7601	20576		1.85	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/3
8566	21637	36174	1.42	7.6E+00	P36441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8566	21637	36175	1.42	7.5E+00	P36441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5921	19108	32421	3.6	7.4E+00	BF700317.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285506 5'
8953	22032	35673	3	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
8953	22032	35674	3	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3042	16218	29238	3.41	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
3042	16218	29239	3.41	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
7174	20307	33760	1.07	7.2E+00	BE178090.1	EST_HUMAN	RCO-HT0813-200300-031-407 HT0813 Homo sapiens cDNA
7289	20381	33838	1.22	7.1E+00	P28109	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7289	20381	33839	1.22	7.1E+00	P28109	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
9768	22388					NT	
11688	24745	38437	8.23	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
10187	23224	38818	2.44	7.1E+00	P05950	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
11528	24584	38281	2.76	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
8478	21559	35093	1.52	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
10559	23594	37200	3.17	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10570	23614	37219	1.12	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
8092	21174	34698	0.6	6.9E+00	P34228	SWISSPROT	SKT5 PROTEIN
8092	21174	34699	1.64	6.8E+00	W03412.1	EST_HUMAN	zaf07c1.1 Scars melanocyte 2N1bHM Homo sapiens cDNA clone IMAGE:291860 5'
			1.84	6.8E+00	W03412.1	EST_HUMAN	zaf07c1.1 Scars melanocyte 2N1bHM Homo sapiens cDNA clone IMAGE:291860 5'
8333	22409		1.82	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS:
10413	23448	37053	3.6	6.8E+00	Q03570	SWISSPROT	OUTER CAPSID PROTEIN VP8
6398	18600		0.86	6.6E+00	Q98028	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
6675	19834	33223	0.86	6.6E+00	BF672121.1	EST_HUMAN	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
9234	26226		0.55	6.6E+00	P51825	SWISSPROT	602162573F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293427 5'
10279	23314	36912	2.14	6.6E+00	Q9ZE07	SWISSPROT	AF-4 PROTEIN (FEL PROTEIN)
10279	23314	36913	2.14	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
10843	23876	37498	0.47	6.6E+00	H26330.1	EST_HUMAN	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
11395	24454		1.48	6.6E+00	Q10309	SWISSPROT	ym60f06.6 Scars infant brain TN1B Homo sapiens cDNA clone IMAGE:52737 3'
9382	22457	36020	7	6.5E+00	P03374	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
10512	23547	37158	0.52	6.5E+00	BE866001.1	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP32; COAT PROTEIN GP36]
9943	22992	36574	1.34	6.2E+00	AY010601.1	EST_HUMAN	601678435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3960969 5'
10787	23820	37444	0.7	6.2E+00	6754621	NT	Schizosaccharomyces commune unknown mRNA
7181	20313	33756	1.6	6.0E+00	BE780163.1	EST_HUMAN	Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA
10021	23059	36655	0.49	6.0E+00	AF000006.1	NT	601468031F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871303 5'
10732	23765	37373	0.82	6.0E+00	AE001862.1	NT	Pyrococcus horikoshii OT3 genome DNA, 1166001-148500 nt, position (87)
10732	23765	37374	0.82	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
						NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
6650	19808	33197	7.14	5.9E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11833	24919		3.02	5.8E+00	BE98630.1	EST_HUMAN	601845279F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930451 6'
3613	18777		1.15	5.8E+00	7661537	NT	Homo sapiens DESC1 protein (DESC1), mRNA
7312	20394	33855	0.74	6.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7312	20394	33856	0.74	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7742	20803		1.34	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11289	24355	37886	2.03	5.6E+00	AB027305.1	NT	Cyprinus carpio mRNA for lysozyme C, complete cds
11289	24355	37897	2.03	5.6E+00	AB027305.1	NT	Cyprinus carpio mRNA for lysozyme C, complete cds
11765	23951	37581	2.62	6.0E+00	Q56276	SWISSPROT	LYCOPENE BETA CYCLASE
6381	19550	32808	0.74	5.8E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HIRA
8982	23021		0.66	5.6E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
11018	24097		1.46	5.3E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11763	23949	37578	2.32	5.6E+00	P11980	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
7069	20122	33536	1.11	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7069	20122	33537	1.11	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7484	20559		1.04	5.4E+00	Q89435	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
8013	21063	34575	0.74	5.4E+00	P50391	SWISSPROT	NEUROPEPTIDE Y RECEPTOR TYPE 4 (NPY4-R) (PANCREATIC POLYPEPTIDE RECEPTOR 1) (PP1)
8054	21137		1.62	5.4E+00	Q91082	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C;
8989	22078	35618	0.93	5.4E+00	P40379	SWISSPROT	LIPOVITELLIN LV-2]
8989	22078	35619	0.93	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
10242	23277	35870	1.45	5.4E+00	Q17094	SWISSPROT	REP1 PROTEIN
10242	23277	35871	1.45	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4908	18038	31024	1.47	5.3E+00	L43126.1	NT	RHODOPSIN
6617	19777		0.7	5.3E+00	P41779	SWISSPROT	Bovine immunodeficiency-like virus surface envelope gene; 5' end of cds
8270	21352		3.39	6.3E+00	P84098	SWISSPROT	HOMEOBOX PROTEIN CEH-20
9184	22292		0.72	5.3E+00	AB034890.1	NT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
11928	24914	36816	1.51	6.3E+00	Q27806	SWISSPROT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
5590	18775		1.16	5.2E+00	BE184840.1	EST_HUMAN	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR
10583	23618		0.98	6.2E+00	AF248070.1	NT	QV4-HT0691-270400-186-009 HT0691 Homo sapiens cDNA
11470	24520		1.93	6.2E+00	Q10136	SWISSPROT	Drosophila orientacea R18 retrotransposable element reverse transcriptase gene, partial cds
9162	22240	35784	0.94	5.1E+00	Q16005	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME 1
10030	23098	36567	1.33	5.1E+00	P08182	SWISSPROT	RHODOPSIN
6416	19584	32946	0.74	6.0E+00	BF310443.1	EST_HUMAN	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
10397	23432		0.7	5.0E+00	BF308561.1	EST_HUMAN	601834910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
							601850420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10645	23679	37289	2.89	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11569	24924	38304	7.24	5.0E+00	Z83860.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 103/162
10437	23472		0.76	4.8E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
4172	17322		12.39	4.8E+00	AF15235.1	NT	
8348	21429	34953	0.6	4.8E+00	BF367909.1	EST_HUMAN	Emutice australis histone H3 (H3) gene, partial cds
8738	21817		4.92	4.8E+00	AW750087.1	EST_HUMAN	RC3-GN0042-100800-011-610 GN0042 Homo sapiens cDNA
300	13517	26550	3.04	4.7E+00	BF240852.1	EST_HUMAN	PW0-BT0547-310100-002-804 BT0547 Homo sapiens cDNA
301	13517	26550	1.85	4.7E+00	BF240852.1	EST_HUMAN	801875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
3347	16520	29534	1.02	4.7E+00	AL163280.2	NT	801875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
7962	21012	34522	0.59	4.6E+00	U87569.1	NT	Homo sapiens chromosome 21 segment HS21C080
8997	22471	38036	1.1	4.6E+00	BE646437.1	EST_HUMAN	Methanococcus jannaschii section 111 of 150 of the complete genome
9397	22471	38037	1.1	4.6E+00	BE646437.1	EST_HUMAN	7e86g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:075140 O75140 KIAA0845 PROTEIN; contains element PTR5 repetitive element
10600	23635		0.63	4.6E+00	AF240786.1	NT	7e86g10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:075140 O75140 KIAA0845 PROTEIN; contains element PTR5 repetitive element
7947	20997		0.7	4.5E+00	AF128177.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11904	24892	38593	1.87	4.5E+00	AE001044.1	NT	Issachienkia orientalis inositolphosphorylceramide synthase (IPC1) gene, complete cds
12058	25039	38747	1.53	4.5E+00	BF688941.1	EST_HUMAN	Archaeoglobus fulgidus section 63 of 172 of the complete genome
3105	16281	29296	0.84	4.4E+00	BF630893.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
3105	16281	29297	0.84	4.4E+00	BF630893.1	EST_HUMAN	602072565F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4215284 5'
6331	19502		1.59	4.4E+00	X13414.1	NT	602072565F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4215284 5'
8245	19419		0.77	4.3E+00	AF058679.1	NT	Murine I gene for MHC class II(a) associated invariant chain
7598	20686	34142	2.53	4.3E+00	Y13402.1	NT	Homo sapiens neutrophil collagenase (CI-GNA) gene, promoter region and 6'UTR
7782	20848	34341	0.88	4.3E+00	AE001222.1	NT	Pleuroidium falciparum R28R+var1 gene, exon 1
11101	24174	37809	14.74	4.3E+00	AF240786.1	NT	Treponema pallidum section 38 of 87 of the complete genome
5634	18823		4.1	4.2E+00	P16444	SWISSPROT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5711	18904	32189	1.07	4.2E+00	P51826	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-1) (RENAL DIPEPTIDASE) (RDP)
5880	19070	027830	0.71	4.2E+00	O27830	SWISSPROT	LA-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
6911	20228	33657	1.87	4.2E+00	P13983	SWISSPROT	PUTATIVE ATP-DEPENDENT HELICASE MTH1802
							EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6911	20226	33658	1.67	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
9160	22238	35783	5.3	4.2E+00	A1809013.1	EST_HUMAN	w87g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360892 3'
10122	23160	36759	1.03	4.2E+00	P31368	SWISSPROT	NUBBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
10352	23397		0.47	4.2E+00	P40886	SWISSPROT	HEXOSE TRANSPORTER HXT6
7261	20344	33780	0.98	4.1E+00	BE253668.1	EST_HUMAN	601110727F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3357534 5'
7839	20894	34396	7.66	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
7860	21010		0.84	4.1E+00	AB041523.1	NT	Palinipeten yessoensis mRNA for calcineurin A, complete cds
7963	21013	34523	3.8	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
7963	21013	34524	3.8	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
8101	21183	34703	2.88	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNUL2 locus
8740	22805	36381	0.61	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
9873	22913	36408	2.25	4.1E+00	BF692425.1	EST_HUMAN	802247838F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'
10370	23405		0.55	4.1E+00	AJ235273.1	NT	Rickettsia prowazekii strain Madrid E. complete genome, segment 4/4
10514	23549		0.52	4.1E+00	P48414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27) (P27KIP1)
11124	24196		2.15	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HYLFI
11214	24283		12.26	4.1E+00	BE886880.1	EST_HUMAN	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909051 5'
3635	16789		0.72	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5576	20130	33546	0.93	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
5575	20130	33547	0.93	4.0E+00	O62663	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7077	20130	33546	0.99	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7077	20130	33547	0.99	4.0E+00	O62663	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7339	20419	33881	1	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
9074	22193	35697	0.49	4.0E+00	Q14167	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0144
10148	23186	36783	0.65	4.0E+00	O61309	SWISSPROT	NITRIC-OXIDE SYNTHASE (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS)
10368	23403	37014	0.8	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
10484	23499	37111	0.45	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
10484	23499	37112	0.45	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11762	23948	37677	1.59	4.0E+00	P14546	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
11843	24832	38524	2.88	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS6)]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11843	24832	38525	2.98	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS6)]
12133	25113	38817	1.34	4.0E+00	P35611	SWISSPROT	ERYTHROCYTE ADDUCIN ALPHA SUBUNIT
3591	16765	29770	6	3.8E+00	XG4518.1	NT	N tabacum chitinase gene 50 for class I chitinase C
4441	17581		0.87	3.9E+00	AF055486.1	NT	Mus musculus seminal vesicle secretory protein 98 (MSV/SP98) gene, promoter region
5775	18957	32270	2.92	3.8E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
5775	18957	32271	2.92	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-h05 BN0070 Homo sapiens cDNA
6772	19927	33322	0.93	3.9E+00	AF298208.1	NT	Dicotyledonous discoidium non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6829	19962	33389	0.7	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
7013	20149	33570	4.43	3.9E+00	P39289	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDS-RPSF INTERGENIC REGION
7519	20562	34068	4.25	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2
8512	21593	35128	2.44	3.9E+00	XG5665.1	NT	Xlaevis mRNA for M4 muscarinic receptor
11874	23902	37624	2.77	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
2693	15813		1.53	3.8E+00	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
6520	19885	33057	1.05	3.8E+00	Q57630	SWISSPROT	HYPOTHETICAL PROTEIN M.0385
8927	21707	35244	1.12	3.8E+00	D44725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
9989	23037		0.6	3.8E+00	AJ390961.1	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7804
12120	25100		11.65	3.8E+00	9631284	NT	Melanoplus sanguinalipes entomopoxvirus, complete genome
4128	17282	30277	12.79	3.7E+00	AL161539.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7316	20398		0.83	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome: segment 3/5
8378	22454	36017	1.04	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11715	24755	38450	2.11	3.7E+00	BF689278.1	EST_HUMAN	602120551F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4277748 5'
11715	24755	38451	2.11	3.7E+00	BF689279.1	EST_HUMAN	602120551F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:4277748 5'
12260	25196		1.87	3.7E+00	AB013748.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
600	13795	28814	3.76	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
5369	18572	31440	0.78	3.6E+00	BF310316.1	EST_HUMAN	601901866F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4131016 5'
8749	21826	35384	0.86	3.6E+00	D12367.1	EST_HUMAN	HUM0007B08 Liver HepG2 cell line, Homo sapiens cDNA clone b08
8749	21826	35365	0.86	3.6E+00	D12367.1	EST_HUMAN	HUM0007B08 Liver HepG2 cell line, Homo sapiens cDNA clone b08
8847	21926	35484	3.87	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PAO1, section 8 of 529 of the complete genome

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8847	21928	35465	3.67	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PAO1, section 8 of 529 of the complete genome
9864	22904	36488	0.51	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
9864	22904	36489	0.51	3.6E+00	U72775.1	NT	Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
11093	24167						Ciconia episcopus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds
3319	16492	28509	3.21	3.6E+00	M98795.1	NT	Escherichia coli glycerophosphate dehydrogenase (gldD) gene, partial cds; and the translation start site has been verified (gldE), the translation start site has been verified (gldG), and repressor protein (gldR) genes, complete cds
6123	19302		1.04	3.5E+00	AF221538.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
8341	19511	32888	0.53	3.5E+00	L42898.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
8681	21781		0.56	3.5E+00	R19745.1	EST_HUMAN	IG40c08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34940 5'
9232	22310	35851	0.99	3.5E+00	P24557	SWISSPROT	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
9232	22310	35851	0.99	3.5E+00	AA190998.1	EST_HUMAN	zps8b04.s1 Stralagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:827055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element
9232	22310	35852	0.99	3.5E+00	AA190998.1	EST_HUMAN	zps8b04.s1 Stralagene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:827055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element
9694	22743	36313	1	3.6E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53
10739	23772	37363	0.58	3.5E+00	AJ133723.1	NT	Bos taurus mRNA for Ran-binding protein 2, partial
1642	14604	27773	3.81	3.4E+00	AF254577.1	NT	Brassica napus RPB5d mRNA, complete cds
2644	16797	28982	1.07	3.4E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7518	20591	34095	2.33	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7880	20932	34437	0.76	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8876	21955						Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K8 (KCNJ1) gene, complete cds
9274	22380	36901	0.77	3.4E+00	U65406.1	NT	ROM-K8 (KCNJ1) gene, complete cds
9312	22388	35938	0.54	3.4E+00	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
10471	23608	37119	3.35	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
11822	24811	38508	2.08	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
6193	19369	32719	0.97	3.4E+00	L77570.1	NT	Homo sapiens Digeorge syndrome critical region, centromeric end
6193	19369	32720	0.97	3.3E+00	Q08669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
6077	21159	34876	1.03	3.3E+00	AF111168.2	NT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
10681	23715	37321	1.04	3.3E+00	AP001511.1	NT	Homo sapiens carine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10681	23715	37322	1.04	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 6/14
513	13707	26735	1.79	3.2E+00	X98422.1	NT	Bacillus halodurans genomic DNA, section 5/14
							D-retio zp-50 POU gene

Table 4

## Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4138	13707	28735	0.78	3.2E+00	X96422.1	NT	D. rerio zp-50 POU gene
4850	17893	30971	0.95	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5886	18580	32170	1.10	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5886	18580	32170	1.10	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5719	18912	32207	2.49	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5719	18912	32208	2.49	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6436	18603	32966	1.91	3.2E+00	P18531	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6436	18603	32966	1.91	3.2E+00	P18531	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6438	19603	32987	1.91	3.2E+00	P18831	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7781	20837	34330	0.88	3.2E+00	P04275	SWISSPROT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7952	21002	34513	2.41	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7952	21002	34514	2.41	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
9230	22308		5.28	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
9730	22795	36369	1.31	3.2E+00	M36383.1	NT	S. cerevisiae threonine deaminase (LDV) gene, complete cds
10345	23380	36991	2.06	3.2E+00	AB016081.2	NT	Oryzias latipes OIGCB gene for guanylyl cyclase C, complete cds
12219	26169		2.95	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
5996	19181	32503	2.29	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7647	20819	34086	0.91	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (CTPT)
7604	20956		1.09	3.1E+00	AF303225.1	NT	Bacillus alcalophilus pectate lyase (pelE) gene, complete cds
8278	21361	34880	0.51	3.1E+00	P40885	SWISSPROT	PROBABLE UBIQUITIN-PROTEIN LIGASE HUL4
8801	21880	35417	5.14	3.1E+00	P48894	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE 1 5DEIODINASE) (DIO1) (TYPE 1 DIO) (5DI)
8801	21880	35418	5.14	3.1E+00	P48894	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE 1 5DEIODINASE) (DIO1) (TYPE 1 DIO) (5DI)
9459	22975		3.7	3.1E+00	Q14957	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9528	22591	36162	0.55	3.1E+00	Q01149	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
10100	23138	36739	0.76	3.1E+00	7624769	NT	Chlorella vulgaris chloroplast, complete genome
10183	23230		0.58	3.1E+00	Q10125	SWISSPROT	HYPOTHETICAL 66.3 KD PROTEIN F8C9.6 IN CHROMOSOME III
10543	23678	37187	4.09	3.1E+00	P49365	SWISSPROT	DEOXYHYPUISINE SYNTHASE (DHS)
11751	23937		2.45	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN [ENVELOPE PROTEIN M]; MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11771	24783		2.49	3.1E+00	S66680.1	NT	retinotic acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2971 nt]
13018	25870		1.17	3.1E+00	U77668.1	NT	Brassica rapa pollen coat protein homolog (BAN103) gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2889	18078	28095	0.95	3.0E+00	8823984	NT	Homo sapiens hypothetical protein PRO0889 (PRO0889), mRNA
5454	18054	31633	1.29	3.0E+00	X53096.1	NT	S aureus genes encoding S aureus DNA methyltransferase and S aureus restriction endonuclease
6888	18044	33234	0.82	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6886	18044	33235	0.82	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7308	20388		11.21	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7346	20426		0.7	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
9108	22187		1.82	3.0E+00	X67838.1	NT	B napus DNA for myrosinase
10501	23536	37146	0.58	3.0E+00	Q58605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
11259	24328	37067	4.98	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
11259	24328	37068	4.98	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
11885	24873	38570	1.37	3.0E+00	P34194	SWISSPROT	NADH-LUBIQUINONE OXIDOREDUCTASE CHAIN 4
2067	18208	28324	2.69	2.8E+00	AE002225.2	NT	Chlamydomonas reinhardtii AR39, section 53 of 94 of the complete genome
7049	20102	33519	1.85	2.9E+00	Z36879.1	NT	F ringlet gdcSPA gene for P-protein of the glycine cleavage system
7360	20439	33889	4.68	2.8E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7360	20439	33800	4.68	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7614	20884	34160	6.19	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
8052	21135	34655	0.57	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8052	21135	34658	0.57	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8289	21371	34892	0.81	2.9E+00	BF344171.1	EST_HUMAN	602017413F1 NC1 COAP_Bm64 Homo sapiens cDNA clone IMAGE:4193059 5'
9438	22512		0.82	2.9E+00	AJ002153.2	NT	Sagittaria cecidius gene for seminal vesicle secreted protein semenogelin I
1486	14839	27722	4.77	2.8E+00	AF186398.1	NT	Buxus harlandii maturase K (matK) gene, partial cds; chloroplast gene for chloroplast product
1682	14814		3.14	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7460	20535	34010	5.05	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
9813	22853		0.6	2.8E+00	BE585182.1	EST_HUMAN	601342750F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:3684807 5'
10828	20835	34010	1.53	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
240	13462	28480	13.96	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
240	13462	28491	13.98	2.7E+00	6679306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
5669	18653	32148	1.41	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kringle IV gene, exons 1 and 2
8339	21420		0.74	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
9168	22246		2.16	2.7E+00	AL118459.1	NT	Bohrys chireea strain T4 cDNA library under conditions of nitrogen deprivation
9832	21075	34587	0.61	2.7E+00	AW088191.1	EST_HUMAN	xs88e12.x1 NCJ_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:M17733
10718	23751		1.84	2.7E+00	BE083527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4788	17831	30917	5.51	2.6E+00	AF068749.1	NT	QMO-BT0281-031199-087-h04 BT0281 Homo sapiens cDNA
5665	18859	32143	2.04	2.6E+00	675560.1	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5665	18859	32144	2.04	2.6E+00	675560.1	NT	Mus musculus SRY-box containing gene 13 (Ssx13), mRNA
5947	19133		2.55	2.6E+00	Y17082.1	NT	Mus musculus SRY-box containing gene 13 (Ssx13), mRNA
7727	26220		1.16	2.6E+00	AJ224639.1	NT	Mycobacterium fortuitum furA II gene
7879	20931		11.25	2.6E+00	AF236602.1	NT	Homo sapiens Surf-5 and Surf-6 genes
8249	21331	34847	1.17	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Shp) gene, exons 16 through 27, and complete cds
8249	21331	34848	1.17	2.6E+00	AJ132180.1	NT	fabu bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-83
8858	22898	36481	2.85	2.6E+00	AL161540.2	NT	fabu bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-83
10563	23598		1.91	2.6E+00	8055183	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
11281	24347	37984	2.2	2.6E+00	AF143676.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12817	26084		3.3	2.6E+00	11419220	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1492	14849	27728	3.03	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/ITAP), member 4 (ABCB4), mRNA
1492	14849	27727	3.03	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5834	19120	32431	2.24	2.5E+00	P13485	SWISSPROT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5834	19120	32432	2.24	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6566	19120	32431	1.42	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6566	19120	32432	1.42	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6668	20020	33429	0.77	2.5E+00	D30052.1	NT	Vibrio cholerae cbaA gene and cbaB gene for cholera toxins, complete cds
7836	20986	34494	1.19	2.5E+00	AW849158.1	EST_HUMAN	QV4-FT0005-110500-205-g07 FT0005 Homo sapiens cDNA
7985	21034	34547	0.82	2.5E+00		NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1) mRNA
9904	22880	36931	1.55	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
10057	23095	36987	0.71	2.5E+00	BE297758.1	EST_HUMAN	60176778F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631080 6'
11832	24821		1.39	2.5E+00	P40170	SWISSPROT	DNAJ PROTEIN
12216	26167		1.85	2.5E+00	AF288665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3078	16254	28276	0.89	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
5027	18158	31134	4.93	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
6134	18313	32852	4.09	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
7538	20611	34086	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
7538	20611	34086	0.71	2.4E+00	BF667502.1	EST_HUMAN	602120856F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278012 5'
8334	21416	34941	2.06	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8334	21416	34942	2.06	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8406	21487		2.8	2.4E+00	AE001488.1	NT	Haicobacter pyleri, strain J99 section 47 of 132 of the complete genome
8852	21831		1.72	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-405 PT0004 Homo sapiens cDNA
9028	22107	35648	8.89	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
10244	23279	36874	2.26	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10244	23279	36875	2.26	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10313	23348	36954	2.31	2.4E+00	X92511.1	NT	H. sapiens CTGF gene and promoter region
10449	23484		7.28	2.4E+00	P09099	SWISSPROT	XYLULOSE KINASE (XYLULOXINASE)
10528	23563	37169	1.64	2.4E+00	BE328702.1	EST_HUMAN	hr63f06.xt NCJ CGAP_Ki611 Homo sapiens cDNA clone IMAGE:3133187 3'
10528	23563	37170	1.64	2.4E+00	BE328702.1	EST_HUMAN	hr63f06.xt NCJ CGAP_Ki611 Homo sapiens cDNA clone IMAGE:3133187 3'
10818	23851	37474	1.06	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN N1RQ
11335	24398	38047	1.36	2.4E+00	Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPKD operon and downstream
11640	24720	38413	2.44	2.4E+00	AF168652.2	NT	Freigaria x enanassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1282	14438	27507	8.89	2.3E+00	Z48724.1	NT	G.domesticus artificial single chain antibody gene (L3)
4237	17383		1.41	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
5957	10143		0.91	2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to PROLYLCARBOXYPEPTIDASE
7612	20682	34158	2.75	2.3E+00	6978554	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
7771	26221		2.37	2.3E+00	P07169	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENPB)
7958	21008	34518	1.28	2.3E+00	X60265.1	NT	M.mazai dnaK and dnaJ genes homologues/coding for DnaK and DnaJ
8310	22386	35938	0.52	2.3E+00	6835317	NT	Polyturus ornatephini mitochondrion, complete genome
9371	22448	36008	1.66	2.3E+00	Q11127	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE 4 (FUCT-IV)
11041	24120	37763	2.72	2.3E+00	Q07078	SWISSPROT	ANNEXIN VII (SYNEXIN)
12075	25056	38763	2.14	2.3E+00	BF641987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12075	25056	38764	2.14	2.3E+00	BF641987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
12445	25315	32091	7.41	2.3E+00	BE895237.1	EST_HUMAN	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918843 6'
4128	17280	30278	1.06	2.2E+00	AF020528.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4432	17572	30563	4.12	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)



Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4432	17572	30554	4.12	2.2E+00	D87071.1	NT	Rat gene for regucalcin, exon1 (non-coding) (xant)
5458	18658	31636	11.22	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5458	18658	31637	11.22	2.2E+00	O88307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>)
5975	19160	32478	1.93	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
5975	19160	32479	1.93	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e08 CT0254 Homo sapiens cDNA
6187	19363	32711	0.39	2.2E+00	BE250383.1	EST_HUMAN	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2859777 3'
6484	19661	33013	2.87	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN (MVU-2)
6730	19886	33278	3.14	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7097	18524		3.4	2.2E+00	AA594574.1	EST_HUMAN	in95502.s1 NCI CGAP_Cot0 Homo sapiens cDNA clone IMAGE:1058379 3'
7470	20546	34017	0.83	2.2E+00	AA137027.1	EST_HUMAN	z0704.r1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:566143 5'
7783	20839	34332	11.91	2.2E+00	AA449012.1	EST_HUMAN	z050g10.r1 Soares_t0tal_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:785634 5'
7868	20920	34427	0.88	2.2E+00	P64818	SWISSPROT	ALANINE RACEMASE
8294	21376	34898	0.95	2.2E+00	BE301580.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
8294	21376	34897	0.85	2.2E+00	BE301580.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
8542	22607		12.49	2.2E+00	BE741678.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
8768	25860		2.12	2.2E+00	Q04708	SWISSPROT	TRANSPOSIN TY1 PROTEIN A
10269	23294	36890	1.12	2.2E+00	A1290373.1	EST_HUMAN	qm69b03.x1 Soares_placenta_8to9weeks_2N6HP8tc9w Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10259	23294	36891	1.12	2.2E+00	A1290373.1	EST_HUMAN	qm69b03.x1 Soares_placenta_8to9weeks_2N6HP8tc9w Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10301	23336	36941	3.04	2.2E+00	BF248782.1	EST_HUMAN	601835591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
10673	23707	37315	2.6	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein HGR74 homolog mRNA, complete cds
11720	23912	37338	3.3	2.2E+00	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
11915	24902	38605	6.04	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
583	16016	26795	13.2	2.1E+00	AF132812.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3678	16841		1.19	2.1E+00	AW449366.1	EST_HUMAN	UHH-B13-aki-e-08-0-UJ.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6260	19434		0.97	2.1E+00	P75357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6847	20280	33638	3.61	2.1E+00	O70169	SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7169	20302	33745	0.77	2.1E+00	4503430	NT	Homo sapiens dyxerlin, limb girdle muscular dystrophy 2B (autosomal recessive) (DYXF) mRNA, and translated products
7191	20056	33466	5.88	2.1E+00	N28575.1	EST_HUMAN	yy08a10.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M56584
8694	21774		2.43	2.1E+00	AU123630.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TFIID (HUMAN);
1223	14383	27444	1.32	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1223	14383	27445	1.32	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1368	14520	27595	1.37	2.0E+00	AF204927.1	NT	Oncidalegus cuticulus Nat-K*-AT Pase beta 1 subunit mRNA, complete cds
1606	14759		3.09	2.0E+00	P25592	SWISSPROT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2216	16360	28480	7.2	2.0E+00	Z78279.1	NT	R. norvegicus mRNA for collagen alpha1 type I
2216	16350	28481	7.2	2.0E+00	Z78279.1	NT	R. norvegicus mRNA for collagen alpha1 type I
4216	17365	30353	1.71	2.0E+00	AW664496.1	EST_HUMAN	h13c05.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872168 3' similar to gb:X01677
4216	17365	30354	1.71	2.0E+00	AW664496.1	EST_HUMAN	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7722	20786		0.96	2.0E+00	P07566	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
8214	21296	34815	4	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
8214	21296	34816	4	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
8214	21296	34817	4	2.0E+00	AB008676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
9122	22201	35743	3.04	2.0E+00	F31500.1	EST_HUMAN	HSPD22703 HM3 Homo sapiens cDNA clone s4000117808
12815	26022	31670	6.76	2.0E+00	5834843	NT	Gallus gallus mitochondrion, complete genome
5715	18908	32202	4.28	1.9E+00	6754389	NT	Mus musculus Inositol 1,4,5-triphosphate receptor 1 (Itp1r), mRNA
5715	18908	32203	4.28	1.9E+00	6754389	NT	Mus musculus Inositol 1,4,5-triphosphate receptor 1 (Itp1r), mRNA
6225	19400	32760	1.2	1.9E+00	BE069695.1	EST_HUMAN	601679636F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:394881 6'
6792	19847		0.92	1.9E+00	AW845869.1	EST_HUMAN	MRO-C10063-071099-002-g02 CT0063 Homo sapiens cDNA
6888	20040		1.91	1.9E+00	Q68627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8633	21733	35272	2.21	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8653	21733	35273	2.21	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8659	21638		3.32	1.9E+00	BF360206.1	EST_HUMAN	CM3-MT0114-010600-323-h12 MT0114 Homo sapiens cDNA
8085	22174		1.86	1.9E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)

Table 4

## Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9830	22870	36452	0.63	1.9E+00	AA669125.1	EST_HUMAN	ab94a04.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element; contains element L1 L1 repetitive element ;
10780	23823	37447	0.67	1.9E+00	AF248260.1	NT	Homo sapiens gag-pro-pol precursor protein gene, partial cds
3162	16337	28346	1.69	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3190	16365	28370	2.15	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3190	16365	28371	2.16	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
5988	19173		1.63	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6230	19405	32755	2.02	1.8E+00	BF311999.1	EST_HUMAN	601697854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 6'
6528	19692		1.26	1.8E+00	BF683327.1	EST_HUMAN	602139470F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4298272 5'
6879	20031	33441	1.15	1.8E+00	BF305652.1	EST_HUMAN	601693489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 6'
7204	20069	33470	1.22	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
7411	20489		0.8	1.8E+00	P27127	SWISSPROT	LIPOLYSACCHARIDE 1,6-GALACTOSYLTRANSFERASE (UDP-D-GALACTOSE--(GLUCOSYL)LIPOPOLYSACCHARIDE-ALPHA-1,3-D-GALACTOSYLTRANSFERASE)
8508	21390	34913	0.98	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8508	21390	34914	0.98	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
9055	22134	36679	2.28	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9376	22451	36013	0.76	1.8E+00	R31042.1	EST_HUMAN	y72c08.r1 Scaree placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
9462	22519	36081	0.82	1.8E+00	AW860004.1	EST_HUMAN	Q70-OT0030-070300-148-a03 OT0030 Homo sapiens cDNA
9886	23034	36626	0.47	1.8E+00	P08828	SWISSPROT	FUSION GLYCOPROTEIN PRECURSOR [CONTAINS: FUSION GLYCOPROTEIN F2; FUSION GLYCOPROTEIN F1]
10054	23092	36694	0.64	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10460	23525		4.71	1.8E+00	AF111849.1	NT	Homo sapiens PR00530 mRNA, complete cds
10777	23810		0.75	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE [CYTIDINE AMINOHYDROLASE] (CDA)
12575	25994		4.97	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12667	25444		6.01	1.8E+00	9508404	NT	Rattus norvegicus Actin-related protein complex 1b (Arp1b), mRNA
13005	25687	31854	1.45	1.8E+00	BF212412.1	EST_HUMAN	601813714F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048351 5'
1132	14297	27362	1.68	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2345	15476	28609	4.9	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2445	15573	28702	1.49	1.7E+00	AI141087.1	EST_HUMAN	oz43105.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878137 3'
4681	17718	30701	0.98	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5730	18923	32216	1.73	1.7E+00	BE063546.1	EST_HUMAN	CAC-BT0282-171299-127-e06 BT0282 Homo sapiens cDNA
5730	18923	32217	1.73	1.7E+00	BE063546.1	EST_HUMAN	CAC-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
6141	18319	32681	3.02	1.7E+00	Q91TR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF I)
6682	16840	33230	0.67	1.7E+00	P35816	SWISSPROT	[PYRUVATE DEHYDROGENASE (LIPONIC ACID):PHOSPHATASE, MITOCHONDRIAL PRECURSOR (PDP) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDPC)]
7367	20448	33909	1.18	1.7E+00	Q03703	SWISSPROT	HYPOPHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
8038	21121	34641	1.1	1.7E+00	AF021335.1	NT	HYPOPHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
8222	21304	34825	1.08	1.7E+00	6755715	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
8252	21334	34852	0.61	1.7E+00	BF530630.1	EST_HUMAN	Mus musculus T-cell acute lymphocytic leukemia 1 (Tal1), mRNA
8739	21818	35352	0.76	1.7E+00	AF245513.1	NT	602071917F1 NCL CGAP_Brib7 Homo sapiens cDNA clone IMAGE:4214689 5'
8828	21907		1.63	1.7E+00	BF308000.1	EST_HUMAN	Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds
8901	21980	35519	0.68	1.7E+00	X69063.1	NT	601884255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8901	21980	35520	0.68	1.7E+00	X69063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
9014	22093	35633	1.03	1.7E+00	U18832.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
9350	25859	35981	2.44	1.7E+00	O60479	SWISSPROT	Rattus norvegicus SA gene, partial cds
9350	25859	35982	2.44	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9806	22846		1	1.7E+00	AF161380.1	NT	HOMEBOX PROTEIN DLX-3
10378	23410		0.54	1.7E+00	AW853681.1	EST_HUMAN	Homo sapiens HSPC282 mRNA, partial cds
10867	23890	37509	0.47	1.7E+00	BE878260.1	EST_HUMAN	EST3385741 IMAGE sequences, MAGC Homo sapiens cDNA
10867	23890	37610	0.47	1.7E+00	BE878260.1	EST_HUMAN	601488170F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890464 5'
11886	24884	36582	1.67	1.7E+00	W22424.1	EST_HUMAN	601488170F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890464 5'
12523	25356	32066	1.94	1.7E+00	AF678443.1	EST_HUMAN	6787 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA, not directional
2080	15230	28352	18.53	1.8E+00	AF199339.1	NT	tu82d07.x1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.11
2101	15241	28362	4.14	1.6E+00	AF077374.1	NT	MSR1 repetitive element
2107	16246	28387	1.28	1.6E+00	Y11344.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2357	15483		0.97	1.6E+00	X98373.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
3026	16202	28225	1.22	1.6E+00	W58426.1	EST_HUMAN	Mus musculus ST6GalNAcII gene, exon 2
							B.napae gene encoding endo-polygalacturonase
							z235101.J1 Soares_fetal_heart NBH19W Homo sapiens cDNA clone IMAGE:341889 5' similar to
							gb:D28805 N-ACETYLACTOSAMINE SYNTHASE (HUMAN);

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3857	17017		1.08	1.6E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4142	17294		6.05	1.6E+00	BF570077.1	EST_HUMAN	6021860951 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'
4472	17012	30590	1.25	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4472	17012	30591	1.25	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5184	18308	31270	0.59	1.6E+00	AF127897.1	NT	Saimiri boliviensis olfactory receptor (SBO27) gene, partial cds
5184	18318	31284	2.83	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5184	18318	31285	2.83	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5948	18134	32447	2.38	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2*01 gene, 3' end
6035	18218	32540	0.78	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
6589	19759	33147	0.91	1.6E+00	BF380703.1	EST_HUMAN	IL2-UT0073-080900-145-E02 UT0073 Homo sapiens cDNA
6849	20002	33411	1.05	1.6E+00	AW294881.1	EST_HUMAN	U1-H-B12-att-B-04-0-U1s1 NCLCGAP Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7394	20472	33938	2.37	1.6E+00	BE697267.1	EST_HUMAN	RCA-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA
8219	21301		1.3	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8574	21655	35186	3.3	1.6E+00	AJ297131.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
9101	22180	35724	1.07	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9101	22180	35725	1.07	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9272	22348	35888	0.49	1.6E+00	BE388331.1	EST_HUMAN	601283325F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605647 5'
9659	25937	34615	1.05	1.6E+00	X52048.1	NT	M. musculus COL3A1 gene for collagen alpha-1
9659	25937	34616	1.05	1.6E+00	X52048.1	NT	M. musculus COL3A1 gene for collagen alpha-1
9786	22826		0.7	1.6E+00	AF043466.1	NT	Thermotogaobacter ethandicus D-xylose-binding protein (xylF) gene, complete cds
9935	22874	36566	1.49	1.6E+00	T41290.1	EST_HUMAN	ph686_18/1TV Outward Ali-primed hncDNA library Homo sapiens cDNA clone ph686_19/1TV
10388	23423	37029	1.09	1.6E+00	AW835844.1	EST_HUMAN	QV4-LT0016-060200-100-407 LT0016 Homo sapiens cDNA
10388	23423	37030	1.09	1.6E+00	AW835844.1	EST_HUMAN	QV4-LT0016-060200-100-407 LT0016 Homo sapiens cDNA
10552	23587	37195	0.52	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
11010	24089	37728	1.77	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 (CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN)
11082	18218	32540	4.8	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
12006	24991	38695	3.68	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
33	13271	26276	2.95	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
241	13463	26492	2.44	1.5E+00	AE002201.2	NT	Chlamydomonas reinhardtii AR39, section 32 of 84 of the complete genome
636	13821		1.81	1.5E+00	6752861	NT	Mus musculus a disintegrin and metalloprotease domain (ADAM) 15 (metargidin) (Adam15), mRNA
2481	15008	28732	1.58	1.5E+00	AJ131402.1	NT	Poliovirus A RNA complete genome, isolate U
2584	16703	28828	2.02	1.5E+00	6678350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3208	15608	28732	1.75	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3462	16826	29840	0.77	1.6E+00	AE001946.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5846	18036	32342	0.71	1.5E+00	AI655301.1	EST_HUMAN	tt12f10.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 O00237 HKF-1.1
5846	19036	32343	0.71	1.5E+00	AI655301.1	EST_HUMAN	tt12f10.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:000237 O00237 HKF-1.1
6536	18699	33072	2.43	1.5E+00	R17878.1	EST_HUMAN	y910e02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31683 5'
7278	20361	33853	1.68	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
7311	20393	33853	16.24	1.5E+00	P47179	SWISSPROT	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
7311	20393	33854	16.24	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7500	20575	34048	0.61	1.5E+00	AA889259.1	EST_HUMAN	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7769	20926	34317	0.77	1.5E+00	AI003254.1	EST_HUMAN	ak26f10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3'
8313	21385	34920	0.9	1.5E+00	BE87746.1	EST_HUMAN	ar07b11.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684893 3' similar to g6c595936 SEROTRANSFERRIN PRECURSOR (HUMAN);
8367	21448	34971	0.5	1.5E+00	AB040887.1	NT	g6c595936 SEROTRANSFERRIN PRECURSOR (HUMAN);
8846	21925	35483	1.09	1.5E+00	K02138.1	NT	Homo sapiens mRNA for KIAA1454 protein, partial cds
9218	22296	35963	0.48	1.5E+00	AB038516.1	NT	Mouse germline IgM chain gene, nu-delta region
9334	22410	35963	0.51	1.5E+00	BF217818.1	EST_HUMAN	Homo sapiens hGPIb alpha gene for platelet glycoprotein Ib alpha, complete cds
9684	22733	36303	0.85	1.5E+00	R81028.1	EST_HUMAN	601882862F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095135 5'
9835	22875	36459	1.6	1.5E+00	AW375897.1	EST_HUMAN	y03h01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147697 5'
10084	23102	36705	8.49	1.5E+00	BF376754.1	EST_HUMAN	QV3-CT0192-281099-008-009 CT0192 Homo sapiens cDNA
10258	23293	37040	1.85	1.5E+00	BF337844.1	EST_HUMAN	RC0-TN0078-150900-034-006 TN0078 Homo sapiens cDNA
10399	23434	37041	2.26	1.5E+00	AA017689.1	EST_HUMAN	80203577F1 NCL CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4183865 5'
10399	23434	37041	2.26	1.5E+00	AA017689.1	EST_HUMAN	z338g08.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
11684	24683	38373	3.4	1.5E+00	AL134197.1	EST_HUMAN	z338g08.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
11834	24823	38817	7.68	1.5E+00	X07380.1	NT	DKFZp547P243.31 547 (synonym: hbrt) Homo sapiens cDNA clone DKFZp547P243 3'
11929	24915	38817	1.39	1.5E+00	AI400798.1	EST_HUMAN	Maize mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene
11929	24916	38818	1.39	1.5E+00	AI400798.1	EST_HUMAN	g94409.x1 NCL CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
12516	26095	31662	1.61	1.5E+00	D69480.1	NT	g94409.x1 NCL CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2116433 3'
12765	25508		3.92	1.5E+00	AL445065.1	NT	Human mRNA for KIAA0148 gene, partial cds
12888	25589		2.17	1.5E+00	6978492	NT	Thermoplasma acidophilum complete genome; segment 3/5
13220	25794	31888	1.31	1.5E+00	BF223933.1	EST_HUMAN	Rattus norvegicus 5'-Lipoxigenase (ALOX5), tRNA
30	13268	26271	2.27	1.4E+00	7661685	NT	7682b08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3'
30	13268	26272	2.27	1.4E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2351	15482		0.87	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glitA) gene, complete cds
2411	15541		9.39	1.4E+00	U87922.1	NT	Ovis aries prion protein gene, complete cds
2734	15851	28984	1.7	1.4E+00	X74483.1	NT	Human papillomavirus type 7 genomic DNA
2833	15947	29055	3.22	1.4E+00	AF064584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2833	15947	29056	3.22	1.4E+00	AF084584.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3414	16553		0.79	1.4E+00	5453733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4370	17513	30483	1.13	1.4E+00	AW900455.1	EST_HUMAN	CMO-NN1005-140300-286-H08 NN1005 Homo sapiens cDNA
4370	17513	30484	1.13	1.4E+00	AW900455.1	EST_HUMAN	CMO-NN1005-140300-286-H08 NN1005 Homo sapiens cDNA
4708	17843		1.51	1.4E+00	BF881547.1	EST_HUMAN	60215687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
5317	18434		0.94	1.4E+00	Q07869	SWISSPROT	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)
5489	18687	31706	1.73	1.4E+00	AW054976.1	EST_HUMAN	W4597.X1 NCI_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2510480 3'
5645	18839		6.04	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6409	19578	32839	3.07	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6424	26214		3.83	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
6542	19705	33078	2.8	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6542	19705	33079	2.8	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6961	20189	33814	0.8	1.4E+00	AW893057.1	EST_HUMAN	CM3-NN0008-300300-132-b12 NN0008 Homo sapiens cDNA
7438	20515	33988	1.99	1.4E+00	AJ133249.1	NT	Homo sapiens cavedin-1/2 locus, Contig1, D7S622, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7454	20631	34005	1.14	1.4E+00	AW467760.1	EST_HUMAN	h23705.X1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918873 3' similar to contains Alu repetitive element
7614	20588	34082	0.7	1.4E+00	P55288	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ)
7514	20588	34083	0.7	1.4E+00	P55288	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ)
8530	21611		0.72	1.4E+00	P07683	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8894	22073		6.4	1.4E+00	AJ271735.1	NT	Homo sapiens Xa pseudotubercular region, segment 1/2
9285	22371	35920	1.65	1.4E+00	R20459.1	EST_HUMAN	y33312.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5'
9398	22472	36038	3.83	1.4E+00	BE084687.1	EST_HUMAN	RC1-BT0313-301299-012-05 BT0313 Homo sapiens cDNA
9432	22506	36072	0.65	1.4E+00	AF134944.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
10412	23447	37052	0.88	1.4E+00	BF675545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4286137 5'
10457	23482	37102	0.88	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10457	23482	37103	0.88	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10744	23777	37390	0.88	1.4E+00	D63441.1	NT	Pandorina clemenciae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10744	23777	37391	0.86	1.4E+00	D63441.1	NT	Pandorina clemenciae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10852	23885	37504	1.15	1.4E+00	Q07283	SWISSPROT	TRICHOHYALIN
11499	24557	38232	4.52	1.4E+00	AB006882.1	NT	Homo sapiens APECD mRNA for AIRE-1, complete cds
11691	24689	38379	3.46	1.4E+00	BE982107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11691	24689	38380	3.46	1.4E+00	BE982107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11711	24751	38444	2.3	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11711	24751	38445	2.3	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12359	26012		2.01	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12785	26204		2.99	1.4E+00	11545838	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen s970-2 (SE70-2), mRNA
684	13775		1.86	1.3E+00	Z73640.1	NT	M.musculo gene encoding 4-Dihydroxyethyltrispurate dehydrogenase
925	14100	27164	2.79	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 26S rRNA gene, isolate Tibet
1153	14317		23.81	1.3E+00	Y19213.1	NT	Homo sapiens putative palHbA pseudogene for hair keratin, exons 2 to 7
1325	14482	27649	14.36	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1325	14482	27550	14.36	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1387	14842		0.88	1.3E+00	U61730.2	NT	Cdk laryme-fbbi dihydrodipicolinate synthase (dapA) gene, complete cds
1641	14763		2.35	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 68 of 85 of the complete genome
2316	15448		2.38	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASPb genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2615	15739		1.81	1.3E+00	BE966735.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915845 3'
3005	16180	26201	0.86	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Sptn1), mRNA
3686	16949	29857	1.14	1.3E+00	AF016484.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P65), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
5631	18525	31900	1	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
5927	19017	32322	0.58	1.3E+00	M27138.1	NT	Human estradiol 17 beta-dehydrogenase gene, complete cds
6142	19320	32662	7.56	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291199-004-108 C10289 Homo sapiens cDNA
6142	19320	32663	7.56	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291199-004-108 C10289 Homo sapiens cDNA
6547	19709	33085	1.14	1.3E+00	M33498.1	NT	D.melanogaster no-on-transient A gene product, complete cdo
6890	20042		0.71	1.3E+00	Q00156	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
6928	20243		0.58	1.3E+00	P49940	SWISSPROT	SPORE GERMINATION PROTEIN KB
6978	20206	33634	1.04	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds



Table 4

## Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
7092	20186	33610	1.16	1.3E+00	BE538819.1	EST_HUMAN	601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447865 5'
7249	20332	33779	0.98	1.3E+00	BE243571.1	EST_HUMAN	TC8AP1D0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TC8A Homo sapiens cDNA clone TC8AP0959
7616	20686	34182	0.78	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8494	21575	35112	1.78	1.3E+00	AJ009612.1	NT	Sus scrofa p1p gene
8942	21722	35259	2.28	1.3E+00	BE963378.2	EST_HUMAN	601657145R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868193 3'
8758	21837	35378	1.05	1.3E+00	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
8907	21986		1.87	1.3E+00	6910247	NT	Homo sapiens GL004 protein (GL004), mRNA
8990	22059	35609	0.89	1.3E+00	AJ927829.1	EST_HUMAN	w085a07.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9347	22423	35976	0.51	1.3E+00	H42881.1	EST_HUMAN	y068c03.s1 Scores breast 3N1-Hst Homo sapiens cDNA clone IMAGE:183076 3'
9347	22423	35977	0.51	1.3E+00	H42881.1	EST_HUMAN	y068c03.s1 Scores breast 3N1-Hst Homo sapiens cDNA clone IMAGE:183076 3'
9715	22780		5.02	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
9724	22789	36359	2.47	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
9724	22789	36360	2.47	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
9823	22863	36444	1.21	1.3E+00	AF058250.1	NT	Homo sapiens lipoxigenase (ALOX12B) mRNA, complete cds
9847	22887		0.47	1.3E+00	AW024390.1	EST_HUMAN	w03f03.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:2528477 3' similar to gb:M31522
9871	22911	36496	1.65	1.3E+00	O00754	SWISSPROT	TRANSCRIPTION FACTOR ITF-1 (HUMAN);
9952	22991	36584	1.21	1.3E+00	AJ927829.1	EST_HUMAN	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
10031	23069	36668	0.68	1.3E+00	AJ223962.1	NT	w085a07.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
10031	23069	36669	0.68	1.3E+00	AJ223962.1	NT	Lactobacillus lactis cremoris NCDO-inv1 chromosomal inversion function DNA
10070	23103	36711	3.93	1.3E+00	BE963378.2	EST_HUMAN	Lactobacillus lactis cremoris NCDO-inv1 chromosomal inversion function DNA
10130	23168		0.57	1.3E+00	AI559944.1	EST_HUMAN	601657145R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868193 3'
10353	23388	36996	0.5	1.3E+00	AF081251.1	NT	IQ77a12.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2214814 3' similar to gb:X14723
10353	23388	36997	0.5	1.3E+00	AF081251.1	NT	CLUSTERIN PRECURSOR (HUMAN);
10418	23453	37059	1.68	1.3E+00	AE004392.1	NT	Escherichia coli serotype O167:H7 O antigen gene cluster
10435	23470	37076	1.59	1.3E+00	M28953.1	NT	Escherichia coli serotype O167:H7 O antigen gene cluster
10811	23844		0.88	1.3E+00	AL163302.2	NT	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
10838	23871	37493	0.47	1.3E+00	AI990946.1	EST_HUMAN	Campylobacter jejuni keramycin phosphotransferase (ephA-7) gene, complete cds
10851	23884		0.53	1.3E+00	8923637	NT	Homo sapiens chromosome 21 segment H521C102
							w032f10.x1 NCL_CGAP_GC3 Homo sapiens cDNA clone IMAGE:2498922 3' similar to SW:TRXB_HUMAN
							Q16881 THIOREDOXIN REDUCTASE ;
							Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA

Table 4  
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.:	Exon SEQ ID NO.:	ORF SEQ ID NO.:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10854	23887	37506	0.46	1.3E+00	7949159	NT	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10854	23887	37507	0.46	1.3E+00	7949159	NT	Mus musculus vesicle-associated membrane protein 4 (Vamp4), mRNA
10861	23894	37516	0.45	1.3E+00	H42881.1	EST_HUMAN	ye88c03.s1 Soares breast 3Nb-HBst Homo sapiens cDNA clone IMAGE:183076 3'
10861	23894	37516	0.45	1.3E+00	H42881.1	EST_HUMAN	ye88c03.s1 Soares breast 3Nb-HBst Homo sapiens cDNA clone IMAGE:183076 3'
10832	24014		4.05	1.3E+00	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
11145	24217	37844	2.4	1.3E+00	P25289	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
11169	24240	37872	1.77	1.3E+00	Z18892.2	NT	Mus musculus desmin gene
11619	24670		1.43	1.3E+00	AW274791.1	EST_HUMAN	ye08a03.x1 NCI_CGAP_HNG Homo sapiens cDNA clone IMAGE:2739868 3'
11831	24820	38511	2.73	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11823	24809	38610	2.28	1.3E+00	Z98682.1	NT	Bacillus subtilis genomic DNA 23.8kb fragment
11894	24979		1.35	1.3E+00	L31891.1	NT	Arabidopsis thaliana 3'-ketoacyl carrier protein synthase III (KAS III) mRNA, complete cds
12504	25347		3.81	1.3E+00	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds
12698	25465	32022	2.76	1.3E+00	BF348043.1	EST_HUMAN	802023785F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158452 5'
12707	25899		1.98	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12822	25549		1.53	1.3E+00	AF187035.1	NT	Stimula illum cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
13200	25783		1.34	1.3E+00	U36978.1	NT	Naphthalenesulfonate-degrading bacterium BN6 2,3-dihydroxybiphenyl dioxygenase (bphCII) gene, complete cds
13231	26981		1.63	1.3E+00	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
667	13853	26881	8.73	1.2E+00	AA676246.1	EST_HUMAN	Z122d08.a1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
846	14024	27082	1.52	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
846	14024	27083	1.52	1.2E+00	P04328	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
846	14024	27084	1.52	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-II)
801	14078		1.21	1.2E+00	8024234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1187	14349	27407	7.6	1.2E+00	AF080245.2	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1232	14391	27463	1.71	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1232	14391	27464	1.71	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2068	18207	28323	1.02	1.2E+00	AF140831.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3178	16354	28359	1.08	1.2E+00	AB020861.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3234	16408	28421	7.01	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3234	16408	28422	7.01	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3358	16530		3.57	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3437	16605	28625	0.61	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3804	16864	28987	9.16	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4084	17249	30254	1.87	1.2E+00	BF373570.1	EST_HUMAN	MRO-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4413	16605	29825	1.08	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4594	17731		1.91	1.2E+00	M87090.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4645	17781	30763	0.94	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4682	17817	30805	2.03	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4712	17847		6.6	1.2E+00	Y09200.1	NT	T. phnatum chloroplast rbcL gene, partial
5554	18781	31788	1.13	1.2E+00	U20780.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5672	18866	32152	2.34	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
5917	19105		0.65	1.2E+00	X81879.1	NT	Calcivirus cDNA for orf1, orf2 and orf3
5995	19180	32502	0.77	1.2E+00	AF019052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6280	19454	32802	2.45	1.2E+00	X74895.1	NT	D. hydei ey1 repeat cluster DNA, fragment 1D
6342	19512	32868	3.81	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN090-270400-190-e03 BN090 Homo sapiens cDNA
6420	19588	32953	1.28	1.2E+00	X88084.1	NT	C. glutamicum pta gene and ackA gene
6420	19589	32954	1.28	1.2E+00	X88084.1	NT	C. glutamicum pta gene and ackA gene
6463	19630	32991	36.06	1.2E+00	AA759254.1	EST_HUMAN	ch84g12.s1 Scores_testes_NHT Homo sapiens cDNA clone 1322374 3'
							y49b12.s1 Scores melanocyte 2Nbr-HM Homo sapiens cDNA clone IMAGE:273599 3' similar to.
6566	19728	33105	0.73	1.2E+00	N33295.1	EST_HUMAN	gb M87893 HUMAAALU472 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb:J04970 CARBOXYPEPTIDASE M PRECURSOR (HUMAN);
6630	19780	33178	0.62	1.2E+00	P17871	SWISSPROT	ECODYSONE-INDUCIBLE PROTEIN E75-A
6634	19783	33182	1.94	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
7055	20108	33924	1.72	1.2E+00	AB028010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7067	20120	33534	2.81	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
7180	20312	33755	0.68	1.2E+00	AA167810.1	EST_HUMAN	zq38f05.r1 Stratiene hNT neuron (4937233) Homo sapiens cDNA clone IMAGE:632001 5' similar to
7403	20491		0.71	1.2E+00	AJ271736.1	NT	gb D10522 Human mRNA for 80K-L protein, complete cds, (HUMAN);
7542	25847	34092	1.85	1.2E+00	AV734585.1	EST_HUMAN	Homo sapiens Xq pseudosubosomal region, segment 1/2
7828	20893	34385	2.91	1.2E+00	X74207.1	NT	AV734585 cda Homo sapiens cDNA clone cJAAAFH03 5'
7897	21047	34560	0.6	1.2E+00	BE787646.1	EST_HUMAN	L. lactis pyrD and pyrF genes
8787	21846	35387	3.19	1.2E+00	AB033030.1	NT	601481781F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884270 5'
							Homo sapiens mRNA for KIAA1204 protein, partial cds
8883	21942	35477	0.82	1.2E+00	P38427	SWISSPROT	ALPHA-ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE)
9077	22156		0.7	1.2E+00	7708271	NT	GLUCOSYLTRANSFERASE
9228	22304	35847	1.81	1.2E+00	AW377210.1	EST_HUMAN	Homo sapiens CGI-30 protein (LOC51611), mRNA
9440	22514	36078	0.51	1.2E+00	H48599.1	EST_HUMAN	MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA
							yc80a06.r1 Scores fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:202066 5'

Table 4

## Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9598	22653	36224	3.79	1.2E+00	Z32850.1	NT	R communis gene for pyrophosphatase-dependent phosphofructokinase beta subunit
9805	22845	36423	2.13	1.2E+00	D11745.1	EST_HUMAN	HUMHMD1A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
10135	23173	36771	3.6	1.2E+00	X56832.1	NT	H. sapiens ENO3 gene for muscle specific enolase
10332	23587		0.82	1.2E+00	AB009868.1	NT	Homo sapiens klotho gene, exon 1
11432	24493	36156	1.69	1.2E+00	M36886.1	NT	Mus musculus Id gene, exon 1
11627	24707	36400	1.51	1.2E+00	AW817817.1	EST_HUMAN	PIMC-ST0264-161189-001-401 ST0264 Homo sapiens cDNA
11668	24743		7.69	1.2E+00	BE160761.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11744	23930	37556	3.13	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
12101	25031	36788	1.68	1.2E+00	M10408.1	NT	Maize mitochondrial F-D-ATPase protolipid (subunit e) gene
12471	25884	31708	17.76	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
12491	25339		1.74	1.2E+00	AP001915.1	NT	Bacillus halodurans genomic DNA, section 8/14
13218	25793		2.68	1.2E+00	AA077909.1	EST_HUMAN	7H11A06 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H11A06
478	13871	26703	1.11	1.1E+00	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1802	14951	28045	1.23	1.1E+00	AW595393.1	EST_HUMAN	QVO-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1948	15091	28192	1.21	1.1E+00	AW575838.1	EST_HUMAN	UI-HF-BR0p-ajk-f02-0-UI.s1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3074834 3'
2017	15157		2.74	1.1E+00	AF137273.1	NT	Gallus gallus alpha 1 (V) collagen mRNA, complete cds
3409	16579	29594	8.86	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3409	16579	29596	8.86	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3575	16740	29757	1.02	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3670	16833	29844	0.99	1.1E+00	AI808360.1	EST_HUMAN	wf64h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW_P531_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ;
3812	16972	29974	1.16	1.1E+00	AE003886.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3812	16972	29975	1.16	1.1E+00	AE003888.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3920	17079		0.92	1.1E+00	X85374.1	NT	H. parahemolyticus hphIM(A), hphIM(C), hphIR and menB genes
4054	17210	30220	1.03	1.1E+00	8322641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4130	17293	30278	0.72	1.1E+00	8755203	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (PsmB7), mRNA
4331	17474		6.82	1.1E+00	5635331	NT	R. uniconis complete mitochondrial genome
5107	18235	31204	3.45	1.1E+00	U18466.1	NT	African swine fever virus, complete genome
5180	18302	31265	2.06	1.1E+00	X78426.1	NT	E. faecalis ppp5 gene
5422	18623	31599	1.49	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5731	18924	32218	14.33	1.1E+00	BE980184.1	EST_HUMAN	60165276R1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:3825835 3'
5750	18942	32243	1.32	1.1E+00	AI138582.1	EST_HUMAN	q88c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736280 3'
6217	19392	32740	0.9	1.1E+00	11419739	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter), member 14 (SLC6A14), mRNA

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
8404	19573	32936	0.59	1.1E+00	AF197861.1	NT	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6637	19700	33073	0.72	1.1E+00	R08037.1	EST_HUMAN	ye8603.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:124924 5'
6656	20009	33419	0.76	1.1E+00	AL404004.1	NT	Mus musculus mRNA for ER protein 68 (EP68 gene)
7447	20524	33997	0.58	1.1E+00	X55981.1	NT	Maize mRNA for endase (2-phospho-D-glycerate hydrolase)
7632	20701	34179	0.67	1.1E+00	BF68374.1	EST_HUMAN	602139978F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301322 5'
7659	20726	34201	2.23	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7659	20726	34202	2.23	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7680	20745	34226	8.35	1.1E+00	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7754	25853	34305	1.04	1.1E+00	11967880	NT	Mus musculus silent mating type Information regulation 2, (S.cerevisiae, homolog-like (Sir2), mRNA
8325	21407	34934	3.2	1.1E+00	BF60396.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246028 5'
8416	21497	35029	0.91	1.1E+00	AK78339.1	EST_HUMAN	hm39H11x1 NCI_OGAP_Ki6711 Homo sapiens cDNA clone IMAGE:2160549 3'
8935	22014	35554	0.86	1.1E+00	AB003088.1	NT	Acetabularia caliculus mitochondrial COXII-like gene
8015	22094	35634	0.87	1.1E+00	S80750.1	NT	VF-anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 376 nt]
8126	22205	35748	0.53	1.1E+00	A1079946.1	EST_HUMAN	o234f05.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1677249 3'
9637	21080	BE384876.1	0.76	1.1E+00	BE384876.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3817418 5'
9828	22868	36450	0.51	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)
9883	22923		0.81	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9974	23013	36607	1.03	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaeE, psafE, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds
10038	23078	36676	1.85	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0934 protein, partial cds
10141	23179	36777	4.09	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
10202	23239	36829	20.74	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10718	23752	37358	1.21	1.1E+00	P73769	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10831	23864	37486	0.56	1.1E+00	AI878921.1	EST_HUMAN	au51c11.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518282 5' similar to gb:D10522 Human mRNA for 80K-L protein, complete cds. (HUMAN);
10868	23970	37600	1.97	1.1E+00	11067364	NT	Homo sapiens KIAA0626 gene product (KIAA0626), mRNA
10947	24029		3.14	1.1E+00	AF068942.1	NT	Klebsiella pneumoniae cytochrome o oxidase subunit 2 (cox2) gene, mitochondrial gene encoding
11343	24403	38055	3.72	1.1E+00	L16877.1	NT	mitochondrial protein, partial cds
11361	18489		2.74	1.1E+00	8522873	NT	Homo sapiens cytochrome P4502C9 (CYP2C9) gene, 5' flank and exon 1
							Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11368	24427	38083	2.93	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11369	24427	38084	2.93	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11637	24717	39409	3.99	1.1E+00	AI809698.1	EST_HUMAN	wf76e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361548 3'
11870	24858	38552	1.38	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
11870	24858	38553	1.38	1.1E+00	D89501.1	NT	Human PBI gene, complete cds
12441	25312		1.82	1.1E+00	P07866	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12847	26371	32070	3.56	1.1E+00	AF216996.1	NT	Taenia solium immunogenic protein Ts76 mRNA, partial cds
12889	25980		1.86	1.1E+00	AF234169.1	NT	Dictyostelium discoideum isopentenyl pyrophosphate isomerase (Dip) mRNA, complete cds
101	13337		1.84	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
118	13347	26374	2.1	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
431	13626		-2.78	1.0E+00	AB021684.1	NT	Marchantia polymorpha gene for 26S rRNA 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
590	13781	26800	1.44	1.0E+00	AJ251660.1	NT	Girardia tigrina mRNA for homeodomain transcription factor (so gene)
694	13877	26910	7.14	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
696	13879		2.29	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1417	16037		1.35	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1785	14944	28037	1.33	1.0E+00	AB006531.1	NT	Plasmodium falciparum virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2554	16679	28803	1.11	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2554	16679	28804	1.11	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2621	15744		0.85	1.0E+00	AA628453.1	EST_HUMAN	af26g08.s1 Soares_total_fetus_Nb2HF8_0v/Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:CA2D8.3 CE04204, contains element MER22 MER22 repetitive element ;
2940	16117	29129	4.51	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2940	16117	29130	4.51	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
3032	16208		0.95	1.0E+00	O14228	SWISSPROT	HYPOPHOSPHATE 67.9 KD PROTEIN C8F12.08C IN CHROMOSOME 1
3269	16443	29463	1.16	1.0E+00	AA628453.1	EST_HUMAN	af26g08.s1 Soares_total_fetus_Nb2HF8_0v/Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:CA2D8.3 CE04204, contains element MER22 MER22 repetitive element ;
3469	16626		0.73	1.0E+00	AF222761.1	NT	Rattus norvegicus neuroamin U precursor (Nmu) gene, exons 5 and 6
3688	19337		0.76	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3772	16933	29939	1.61	1.0E+00	AJ223816.1	NT	Agaricus bisporus mRNA for tyrosinase

Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4180	17330	30322	1.12	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4390	17633		0.72	1.0E+00	8922245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5396	18598	31588	2.3	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
5971	19157	32472	4.38	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5971	19157	32473	4.38	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6077	19259	32588	1.74	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
6241	19415	32763	4.85	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
6248	19422	32768	1.87	1.0E+00	AW452782.1	EST_HUMAN	U1H-B19-ab-d-09-0-U1 s1 NOI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068989 3'
6818	19778	33187	2.04	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6871	19830	33219	0.83	1.0E+00	AF104669.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
6787	19923		1.07	1.0E+00	P46508	SWISSPROT	SRB-11 PROTEIN
6795	19950	33349	0.82	1.0E+00	BE797716.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6795	19950	33350	0.82	1.0E+00	BE797718.1	EST_HUMAN	601581891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936382 5'
6918	20231	33684	1.27	1.0E+00	Y11204.1	NT	V. carteri gene encoding vulvovoxpsin
7288	20371	33828	1.15	1.0E+00	S52770.1	NT	Insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7647	20716						B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE)
7889	20941	34447	9.68	1.0E+00	P20273	SWISSPROT	(BL-CAM)
7903	20955	34462	1.51	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
8019	21070		6.02	1.0E+00	AA77619.1	EST_HUMAN	ac79b08.s1 Stratagene lung (8337210) Homo sapiens cDNA clone IMAGE:898791 3'
8148	21230	34749	0.72	1.0E+00	BF678213.1	EST_HUMAN	602163792F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4284727 5'
8148	21230	34750	1.65	1.0E+00	BE888267.1	EST_HUMAN	601443950F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3848005 5'
8335	18493		1.65	1.0E+00	BE888267.1	EST_HUMAN	601443950F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3848005 5'
			1.48	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8545	21625	35163	2.59	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8545	21626	35164	2.59	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8872	21752		1.07	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8708	21768	35321	0.54	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8708	21768	35322	0.54	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8735	25858		1.82	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0229-181099-011-e08 HT0229 Homo sapiens cDNA
8776	21855	35397	1.15	1.0E+00	U42720.2	NT	Simian Immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
8922	22001	36540	1.8	1.0E+00	M38427.1	EST_HUMAN	Human immunodeficiency virus type 1 (HIV-1), Isolate SF33,
9471	22528	36091	1.95	1.0E+00	BE807592.1	EST_HUMAN	6071497581F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
9682	22731	36301	1.62	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
9682	22731	36302	1.62	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clcat1), mRNA
9810	22850	36428	1.81	1.0E+00	AV689554.1	EST_HUMAN	AV689554 GKC Homo sapiens cDNA clone GKCCYA11 5'
9816	22855	36434	1.32	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
9816	22855	36435	1.32	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (XZPC) mRNA, complete cds
10318	23353	36901	0.82	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBFB) mRNA
10318	23353	36902	0.82	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBFB) mRNA
10408	23443	37050	0.69	1.0E+00	A1077920.1	EST_HUMAN	cy15d07.s1, Soares, senescent fibroblasts, NbfHSF Homo sapiens cDNA clone IMAGE:1065901 3'
10533	23568	37175	3.99	1.0E+00	AV768825.1	EST_HUMAN	AV768825 BM Homo sapiens cDNA clone BMFAW C04 5'
10694	23727	37333	19.71	1.0E+00	AA004982.1	EST_HUMAN	z94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10694	23727	37334	19.71	1.0E+00	AA004982.1	EST_HUMAN	z194a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10726	23761	37368	1.22	1.0E+00	L11970.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
11216	24285	37824	1.37	1.0E+00	S90825.1	NT	PBR1=proline-rich protein (intcon 3) [human, Genomic, 898 nt]
11342	24405	38054	1.46	1.0E+00	AA701494.1	EST_HUMAN	z163b11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435453 3' similar to contains Alu repetitive element; contains element MER38 repetitive element ;
11825	24814		1.62	1.0E+00	L47613.1	NT	Picea glauca EMB13 mRNA
12329	25238		5.49	1.0E+00	P15308	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)
12876	25451		2.87	1.0E+00	AW976184.1	EST_HUMAN	EST388293 MAGE resequences, MAGN Homo sapiens cDNA
3693	16855		1.04	9.9E-01	AF174685.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5752	18944	32246	8.8	9.9E-01	P49857	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN



Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5990	19176	32488	0.83	9.8E-01	Q0832	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.3 IN CHROMOSOME II
9461	22518		1.88	9.8E-01	U65687.1	NT	Lycopodium esculentum putative Mt1 copy 1 nematode-resistance gene
9755	22893		2.14	9.8E-01	Q28842	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
536	13729	26753	1.17	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2370	15501		1.26	9.8E-01	AJ003108.1	NT	Callithrix jacchus UBE1 gene derived retroposon on the Y chromosome
2882	15976		1.28	9.8E-01	AF174644.1	NT	Xenopus laevis rac GTPase mRNA, complete cds
3803	17092	30061	0.67	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3903	17092	30062	0.67	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
7349	20429	33890	4.42	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7349	20429	33891	4.42	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7823	20878	34378	1.14	9.8E-01	BF034016.1	EST_HUMAN	601458337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'
7823	20878	34378	1.14	9.8E-01	BF034016.1	EST_HUMAN	601458337F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3860049 5'
8916	21895	35534	0.94	9.8E-01	P38832	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10653	23887		1.02	9.8E-01	AA825565.1	EST_HUMAN	cd55804.st NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371847 3'
11242	24311	37948	1.84	9.8E-01	BE268705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
11242	24311	37949	1.84	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
12554	25377		2.43	9.8E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (ORTR), CDM protein (CDM), adrenoleukodystrophy protein >
7308	20391	33851	2.73	9.7E-01	U26716.1	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
8701	21781	35314	1.8	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8707	21787	35320	1.94	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)
9039	22118	35691	0.73	9.7E-01	BE789822.1	EST_HUMAN	601592165F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945904 5'
11444	24505		3.96	9.7E-01	BF511209.1	EST_HUMAN	UH-H-B14-act-07-0-U1.st NCI_CGAP_SubB1 Homo sapiens cDNA clone IMAGE:3085140 3'
13208	25799		3.17	9.7E-01	AL114281.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4558	17698	30676	0.74	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4558	17698	30676	0.74	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4580	17717	30700	1.28	9.6E-01	AF197925.1	EST_HUMAN	PM2-UM0053-240300-005-f12 UM0053 Homo sapiens cDNA
5872	19082	32369	3.61	9.6E-01	AW799874.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
5872	19082	32370	3.61	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
6888	20038	33447	0.6	9.6E-01	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment No. 6

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptbr
7612	20586	34059	0.63	0.6E-01	AF197881.1	NT	Helix lucorum presenilin (PS) mRNA, complete cds
8588	21687		1.52	0.6E-01	X95276.1	NT	P.falciparum complete gene map of plastid-like DNA (IR-A)
9052	22131	35875	0.92	0.6E-01	L81138.1	NT	Rattus norvegicus (strain R21) Rpe2r gene, complete cds
11346	24408	39090	1.42	0.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein s4 Y isoform gene, complete cds
11808	24798	39496	3.91	0.6E-01	AV752605.1	EST_HUMAN	AV752605 NP2 Homo sapiens cDNA clone NPDBAG06 5'
11808	24798	39497	3.91	0.6E-01	AV752605.1	EST_HUMAN	AV752605 NP2 Homo sapiens cDNA clone NPDBAG06 5'
12225	25174		1.31	0.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
12815	26061	31656	1.88	0.6E-01	U91423.1	NT	Sphyma tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2545	15870	28784	1.81	0.5E-01	7705581	NT	Homo sapiens CGI-125 protein (LOC61003), mRNA
3882	17041	30038	2.1	0.5E-01	BE902340.1	EST_HUMAN	601976639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3882	17041	30039	2.1	0.5E-01	BE902340.1	EST_HUMAN	601976639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
9202	22280	35818	0.71	0.5E-01	AI160162.1	EST_HUMAN	q457d07.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9306	22382	35933	1.04	0.5E-01	AW861102.1	EST_HUMAN	RC1-CT0295-241199-011-502 CT0295 Homo sapiens cDNA
11520	24576	38254	1.59	0.5E-01	BF218771.1	EST_HUMAN	601985163F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4103630 5'
11737	23923	37548	1.57	0.5E-01	AW233789.1	EST_HUMAN	UH-HB12-ahp-f03-0-UI.s1 NCL_CGAP_Sut4 Homo sapiens cDNA clone IMAGE:2727677 3'
3271	16446		5.72	0.4E-01	AF165890.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3289	16463		2.17	0.4E-01	AF080605.1	NT	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
8068	22145	35692	0.79	0.4E-01	M90724.1	NT	Human Fo-gamma-receptorIIA (FCGR2A) gene, exon 4
12498	25343		1.86	0.4E-01	BE781251.1	EST_HUMAN	601466703F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868828 5'
12914	25975		1.4	0.4E-01	11419857	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-eib-b) oncogene homolog) (EGFR), mRNA
1769	14918		1.24	0.3E-01	AF242382.1	NT	Homo sapiens phytyl-CoA hydroxylase (PHYH) gene, exon 5
2689	19918	28934	3.62	0.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4146	17288	30289	0.86	0.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4146	17288	30290	0.86	0.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5709	18902	32197	1.6	0.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5795	18985	32289	3.48	0.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
7486	20561		1.08	0.3E-01	AF270948.1	NT	Plasmodium falciparum mature parasite-infected erythrocyte surface antigen (MESA) gene, complete cds
8257	21339	34856	1.99	0.3E-01	AA847040.1	EST_HUMAN	oe09503.s1 NCL_CGAP_OV2 Homo sapiens cDNA clone IMAGE:1385357
8013	22092		1.1	0.3E-01	AF081981.1	NT	Xanopus laevis CCHC zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
9137	22216	35760	0.89	0.3E-01	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13039	25683	31861	2.09	9.3E-01	11440298	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 2 (ITPR2), mRNA
13049	25683		1.22	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rPL34 mRNA, complete cds
3311	16484	28505	3.92	9.2E-01	BE822702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
4999	18128		0.61	9.2E-01	BF128973.1	EST_HUMAN	601817814F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4041363 5'
5835	19025		1.58	9.2E-01	7109410	NT	Mus musculus soluble carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
6109	18289	32824	4.97	9.2E-01	BF037586.1	EST_HUMAN	601461153F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864661 5'
6770	18925	33320	0.85	9.2E-01	M64703.1	NT	N crassa valyl-tRNA synthetase (cys-20/un-3) gene
9860	22803	36484	0.98	9.2E-01	AL161665.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9949	22893	36582	1.31	9.2E-01	6671877	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10472	23507	37120	3.6	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10827	23661	37269	1.84	9.2E-01	BF593251.1	EST_HUMAN	7c58e06.x1 NCL_CGAP_KG11 Homo sapiens cDNA clone IMAGE:3678219 3' similar to SW:NU5M_TRYBB
10883	23667	37696	1.76	9.2E-01	BE563811.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5:
12022	25006	38707	1.5	9.2E-01	BF132402.1	EST_HUMAN	601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3888714 5'
						EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
1654	14807	27892	1.52	9.1E-01	T96875.1	EST_HUMAN	ye52101.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains
2183	15328		1.49	9.1E-01	8623056	NT	Alu repetitive element,
						EST_HUMAN	Homo sapiens hypothetical protein FLJ20043 (FLJ20048), mRNA
3276	18449	29468	1.28	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
3275	18449	29469	1.28	9.1E-01	T26418.1	EST_HUMAN	AB200G8R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
6296	19489	32824	1.54	9.1E-01	L36033.1	NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
6635	19794	33183	3.25	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7750	20810	34300	17.46	9.1E-01	AA806823.1	EST_HUMAN	cb71g08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336862 3'
7916	20967	34473	2.81	9.1E-01	U72885.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
10378	23414	37023	0.6	9.1E-01	P38432	SWISSPROT	P80-COILIN
12595	26054		19.67	9.1E-01	AF080113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3277	18451	29472	0.8	9.0E-01	7661625	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
3439	16507		0.73	9.0E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
4219	17368	30367	0.68	9.0E-01	8622310	NT	Homo sapiens hypothetical protein FLJ10251 (FLJ10251), mRNA
4498	17638	30620	1.43	9.0E-01	AF099810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
5127	18262	31218	13.05	9.0E-01	AF017728.1	NT	Oryctolagus cuniculus Rad51 (RAD51) mRNA, complete cds
7551	20823	34100	0.82	9.0E-01	L42547.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
7578	20651		1.42	9.0E-01	D38921.1	NT	Xeropus laevis gene for aldolase, complete cds

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9549	22814	36183	0.68	9.0E-01	AF086781.1	NT	Danio rerio semaphorin 21a mRNA, complete cds
10035	23073	36673	0.48	9.0E-01	U39702.1	NT	Mycoplasma genitalium section 24 of 51 of the complete genome
12113	25093	38797	1.41	9.0E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (NtU) gene, partial cds; tPhlp (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
5814	18004	32309	2.5	8.9E-01	AF026198.1	NT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
6378	19547		1.28	8.9E-01	X80989.1	NT	Rabbit MHC fragment RLA-DF DNA
6580	26827	33134	0.82	8.9E-01	BF217939.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
6590	26827	33135	0.82	8.9E-01	BF217939.1	EST_HUMAN	601882708F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095216 5'
8621	21701	35237	0.92	8.9E-01	AF269867.1	NT	Oithona nana cytochrome-c oxidase subunit 1 (cox) gene, partial cds; mitochondrial gene for mitochondrial product
12080	25060	38766	2.72	8.9E-01	AE003944.1	NT	Xyella fastidiosa, section 80 of 229 of the complete genome
12423	25300		4.02	8.9E-01	AE002186.2	NT	Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome
4684	17789	30786	2.11	8.8E-01	O28350	SWISSPROT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
6489	18688	31706	0.66	8.8E-01	AF310517.1	NT	Pseudorabies Virus Ea glycoprotein M gene, complete cds
7701	20766	34250	0.69	8.8E-01	M81182.1	NT	Homo sapiens peroxisomal 70 kD membrane protein mRNA, complete cds
10436	23471	37077	1.07	8.8E-01	7656978	NT	Homo sapiens cell death-inducing DFFA-like effector B (CIDEb), mRNA
11337	24400	38049	2.23	8.8E-01	Z28337.1	NT	M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
12092	26072	38776	7.56	8.8E-01	AA808055.1	EST_HUMAN	cc38h11.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1352037 3' similar to contains 'Alu
12240	26153		2.13	8.8E-01	D90911.1	NT	repetitive element; contains element MER22 repetitive element;
477	13672	28704	2	8.7E-01	AF106953.2	NT	Synechocystis sp. PCC6803 complete genome, 13727, 1376993-1719843
2475	15602	28727	0.98	8.7E-01	5901893	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
2838	16115	29127	5.32	8.7E-01	AA595863.1	EST_HUMAN	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
5120	18245		4.12	8.7E-01	AF121970.1	NT	nm05f11.s1 NCL CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1076877
8229	21311	34831	0.66	8.7E-01	AW897395.1	EST_HUMAN	Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put-
9130	22209	35752	0.66	8.7E-01	A1239456.1	EST_HUMAN	RC4-NN0057-120500-013-c07 NN0057 Homo sapiens cDNA
9130	22209	35753	0.66	8.7E-01	A1239456.1	EST_HUMAN	q336e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9309	22978	36569	2.07	8.7E-01	AE004963.1	NT	q336e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846786 3'
10511	23546	37156	1.08	8.7E-01	BF570169.1	EST_HUMAN	Pseudomonas aeruginosa PAO1, section 524 of 529 of the complete genome
							602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309908 3'

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10511	23546	37157	1.08	8.7E-01	BF570189.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4308908 3'
11070	24145	37782	5.87	8.7E-01	BF363970.1	EST_HUMAN	QY0-NN1021-100800-337-503 NN1021 Homo sapiens cDNA
12034	25017	38720	3.32	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043584 3'
12034	25017	38721	3.32	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043584 3'
12652	25940		2.8	8.7E-01	AV661898.1	EST_HUMAN	AV661898 GLC Homo sapiens cDNA clone GLCGY007 3'
487	13681		2.39	8.6E-01	X17012.1	NT	Rat IGF1 gene for insulin-like growth factor II
881	14057	27123	3.14	8.6E-01	W69089.1	EST_HUMAN	z444603.r1 Soares fetal NBHH16W Homo sapiens cDNA clone IMAGE:343518 5'
2344	15475	28608	1.31	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3710	16871	29875	0.85	8.6E-01	AL181585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3801	17060	30059	1.31	8.6E-01	U49724.1	NT	Drosophila melanogaster marlin (Dmrlin) mRNA, complete cds
6019	19202	32521	10.02	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6019	19202	32522	10.02	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6508	25825	33042	0.7	8.6E-01	S76772.1	NT	polyprotein [Coxsackie B4 virus CB4, host-nice, E2, originally derived from Edwards CB4 human strain, Genomic RNA Complete, 7397 nt]
6848	20001	33409	1.96	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6848	20001	33410	1.96	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7698	20781		0.84	8.6E-01	AE000591.1	NT	Helicobacter pylori 26695 section 89 of 134 of the complete genome
8112	21194		1.82	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
8232	21314	34634	0.56	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
9887	22927		0.54	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12656	25883		2.11	8.6E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2509	15895		1.46	8.5E-01	AJ011624.1	NT	Arabidopsis thaliana (ecotype Columbia) sp13 gene, exons 1-5
6866	20018	33427	1.1	8.5E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7894	20759	34243	2.36	8.5E-01	BE42612.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3435505 5'
8180	21282	34784	0.57	8.5E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
8613	21693	35230	0.92	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8613	21693	35231	0.92	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8702	21782	35315	0.66	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10558	23583	37198	1.49	8.5E-01	AB006799.1	NT	Cyranidium caldarium gene for SigC, complete cds
10558	23583	37199	1.48	8.5E-01	AB006799.1	NT	Cyranidium caldarium gene for SigC, complete cds
12577	25056		5.29	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type I enhancer-binding protein 1 (HIVEP1), mRNA
12585	25394		6.39	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4873	18006	30889	0.68	8.4E-01	AF083973.2	NT	Fowl adenovirus 8, complete genome

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5611	25808	31871	2.75	8.4E-01	L78728.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5611	25808	31872	2.75	8.4E-01	L78728.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7991	21041	34553	0.57	8.4E-01	AF051142.1	NT	Manesbra brassicae phenolase binding protein 2 precursor (PBP2) mRNA, complete cds
10163	23200		3.42	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
760	13941	26386	2.17	8.3E-01	M83437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3164	16339	29347	3.45	8.3E-01	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3912	17071	30069	0.69	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4120	17274	30273	3.17	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
6383	18585	31484	2.32	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
9870	22910		4	8.3E-01	AI791852.1	EST_HUMAN	nm011212.6 NCL CGAP_C09 Homo sapiens cDNA clone IMAGE:1078485 5' similar to contains THR.t1 THR repetitive element
10316	23351	36858	1.32	8.3E-01	AF098070.1	NT	Drosophila melanogaster Lis1 hemoglobin mRNA, complete cds
10423	23458	37063	3.9	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10911	23994	37627	2.18	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
10930	24012		1.65	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11584	24637	38317	8.95	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2111	16249	28369	2.72	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2156	15292		1.32	8.2E-01	AF145589.1	NT	Mus musculus trophoblast (Tm) gene, complete cds
2744	15861		0.95	8.2E-01	AW376990.1	EST_HUMAN	IL3-CT0219-181199-031-C08 CT0219 Homo sapiens cDNA
4009	17166	30174	0.68	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
4247	17393	30381	0.7	8.2E-01	Z72584.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL062w
4247	17393	30382	0.7	8.2E-01	Z72584.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
5217	18338	31311	1.19	8.2E-01	AB000489.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL062w
6781	19336	33332	0.69	8.2E-01	X95283.1	NT	G. gallus mRNA for C-Serrate-1 protein
6781	19336	33333	0.69	8.2E-01	X95283.1	NT	G. gallus mRNA for C-Serrate-1 protein
6913	20228	33681	0.76	8.2E-01	AJ010142.1	NT	Amanita muscaria mRNA for SCII25 protein
7037	20173	33595	3.19	8.2E-01	AW376433.1	EST_HUMAN	GMA-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
7419	29844	33980	4.48	8.2E-01	Z12126.1	NT	S. cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
8639	21719	35258	0.55	8.2E-01	BE263145.1	EST_HUMAN	601144885F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160412 5'
10231	23268	36858	0.81	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0830 protein, partial cds
10264	23299	36897	1.51	8.2E-01	AF052658.1	NT	Homo sapiens thioredoxin-related protein mRNA, complete cds

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10428	23463	37070	0.54	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10428	23463	37071	0.54	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10586	23631	37238	3.78	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10586	23631	37240	3.78	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11842	24928	38631	4.72	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
12030	25013	38716	5.12	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
12035	25018	38722	3.97	8.2E-01	H87398.1	EST_HUMAN	yw1402.r1 Soares_placenta_8to8weeks_2/bbHP8to9W Homo sapiens cDNA clone IMAGE:252195.5' similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
12807	25408	32048	3.01	8.2E-01	AJ001281.1	NT	Mus musculus mRNA for NIPSNAP2 protein
2817	15931		1.38	8.1E-01	AF191839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3547	16712	28723	2.77	8.1E-01	AF055068.1	NT	Homo sapiens MHC class 1 region
3547	16712	28724	2.77	8.1E-01	AF055068.1	NT	Homo sapiens MHC class 1 region
4730	17856	30847	0.63	8.1E-01	4806290	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN2) mRNA
5825	18015	32321	0.63	8.1E-01	Q01727	SWISSPROT	MELANOCYTE STIMULATING HORMONE RECEPTOR (MSH-R) (MELANOTROPIN RECEPTOR)
6445	18612	32975	0.89	8.1E-01	U16780.1	NT	(MELANOCORTIN-1 RECEPTOR) (MCL-R)
6759	18915	33309	2.17	8.1E-01	Q13491	SWISSPROT	Mus musculus putative collagen alpha-2 (X1) chain (COL11A2) gene, partial cds
6759	18915	33310	2.17	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
7681	20746	34227	0.7	8.1E-01	Q47477	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
							CYTCHROME B
8095	21177	34693	1.1	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8095	21177	34694					Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cds
8808	21887	35428	0.91	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds
8808	21887	35429	0.91	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
							Bacillus halodurans genomic DNA, section 11/14
8969	22048	35691	1.14	8.1E-01	AW242847.1	EST_HUMAN	XP01H03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2692469.3' similar to SW:LYAR_MOUSE
10330	23385	38974	0.58	8.1E-01	P08425	SWISSPROT	Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN, contains MER22.b1 PTR5 repetitive element
10823	23657	37267	0.52	8.1E-01	N84541.1	EST_HUMAN	PROBABLE E4 PROTEIN
10769	23802		0.54	8.1E-01	AE001226.1	NT	KK9872F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK9872.5' similar to EST(CLONE C-0PE11)
							Treponema pallidum section 42 of 87 of the complete genome

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11772	24784	38459	2.82	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-410 TN0080 Homo sapiens cDNA
11772	24784	38480	2.62	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-410 TN0080 Homo sapiens cDNA
12803	26221	32102	2.22	8.1E-01	AE001711.1	NT	Thermotoga maritima section 23 of 136 of the complete genome
181	13404		2.82	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pla gene for phosphate acyltransferase allele 15
289	13516	26548	10.2	8.0E-01	AJ132772.1	NT	Bos taurus tub and rif genes
2083	18233		1.95	8.0E-01	BF530982.1	EST_HUMAN	802072473F1 NCL CGAP_Bing7 Homo sapiens cDNA clone IMAGE:4215091 5'
3146	16322	29334	1.32	8.0E-01	AF127897.1	NT	Samirali bolivensis olfactory receptor (SBO27) gene, partial cds
3387	16557	29572	1.29	8.0E-01	AB006183.1	NT	Mus musculus gene for ovalucial glycoprotein, complete cds
4655	17791	30775	6.77	8.0E-01	X63739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5096	18224	31186	1	8.0E-01	7657382	NT	Mus musculus myosin IXb (Myo9b), mRNA
8179	21281		2.69	8.0E-01	AW901488.1	EST_HUMAN	RCO-TN1012-270300-021-406 NN1012 Homo sapiens cDNA
8722	21802	35338	1.21	8.0E-01	Y11095.1	NT	Rice stipe virus RNA 3'
10835	23689		0.48	8.0E-01	BE83329.1	EST_HUMAN	QV3-OT0065-280800-250-c08 OT0065 Homo sapiens cDNA
10827	23860	37483	0.48	8.0E-01	AB045597.1	NT	Gallus gallus PPAR gamma mRNA for peroxisome proliferator-activated receptor, complete cds
11188	24287	37802	1.43	8.0E-01	O82793	SWISSPROT	CREB-BINDING PROTEIN
466	13681	28697	0.75	7.9E-01	D11476.1	NT	Lymantia dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
733	13915		0.92	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1836	14787		28.32	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1482 protein, partial cds
1887	14833		1.06	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2337	15469	28603	9.03	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitogenin29, complete cds
2338	15469	28604	4.11	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3605	16769	28784	3.57	7.9E-01	AF228684.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4418	17557		0.87	7.9E-01	BE263812.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4734	17869	30852	0.84	7.9E-01	0753745	NT	Mus musculus embigin (Emb), mRNA
4734	17869	30853	0.84	7.9E-01	0753745	NT	Mus musculus embigin (Emb), mRNA
5210	18331		0.88	7.9E-01	0753753	NT	Mus musculus embigin (Emb), mRNA
5235	18357	31325	0.93	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
5235	18357	31326	0.93	7.9E-01	Z47210.1	NT	S.pneumoniae dexB, cap3A, cap3B and cap3C genes and orfs
5283	18402		0.88	7.9E-01	AF139718.1	NT	Chrysomya bezziana peritrophin-48 precursor, gene, complete cds
6475	19542	33003	0.88	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8300	21382	34903	2.68	7.9E-01	X90986.1	NT	P.sativum GR gene
9747	22811	36390	3.24	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
10255	23280	36887	5.43	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
10286	23331	36934	1.17	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GK Homo sapiens cDNA clone GKCDRE12 3'



Table 4

## Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10729	23762	37369	0.78	7.9E-01	AB000831.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-thiamose reductase, complete cds
10845	23878	37488	0.81	7.9E-01	P16305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
11256	24325		1.75	7.9E-01	7682471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11487	24546	38218	1.84	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
899	14074		1.49	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized Infant brain cDNA Homo sapiens cDNA clone c-1kr04
2349	15480	28812	6.89	7.8E-01	AW859567.1	EST_HUMAN	EST371637 IMAGE resequences, MAGF Homo sapiens cDNA
4823	17859	30842	0.73	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5149	18271		0.89	7.8E-01	AW753353.4	EST_HUMAN	RC3-CT0254-130100-023-c02 CT0254 Homo sapiens cDNA
6194	18370	32721	2.26	7.8E-01	AF116958.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds
6348	19518	32876	2.28	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6691	19761	33136	0.84	7.8E-01	AL445056.1	EST	Thermoplasma acidophilum complete genome; segment 4/5
8688	21768	35299	1.13	7.8E-01	BF108927.1	EST_HUMAN	715405.x1 Scores NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525178 3'
9434	22508	36074	1.53	7.8E-01	Y10199.1	NT	D discoideum recGAP gene
9533	22588	36170	0.56	7.8E-01	Q25452	SWISSPROT	Homo sapiens nucleoporin 214KD (CIN) (NUP214), mRNA
10329	23364		1.28	7.8E-01	L28260.1	NT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12571	26033		1.82	7.8E-01		NT	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS5) gene, complete cds
146	13371	28403	5.78	7.7E-01	AF184345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Iaalpha) and major histocompatibility protein class II beta chain (Ib beta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-II
744	13925		1.72	7.7E-01	AF050157.1	NT	CITRATE SYNTHASE
2778	15892	28003	1.34	7.7E-01	O33916	SWISSPROT	Homo sapiens UDP-N-acetyl-alpha-D-glucosamine:polypeptide N-acetylglucosaminyltransferase 7 (GALNAC-T7) (GALNAC-T7), mRNA
3438	18606		0.89	7.7E-01	8383408	NT	Homo sapiens PRO1875 mRNA, complete cds
3889	18851	28859	3.86	7.7E-01	AF118085.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4518	17855	30843	3.38	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4516	17855	30844	3.38	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5678	18872	32169	1.39	7.7E-01	P16653	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5678	18872	32160	1.39	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6076	19258	32587	1.41	7.7E-01	R08600.1	EST_HUMAN	Y24602.s1 Scores fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:127755 3'
10049	23087	36689	0.68	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
12452	25317		7.14	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6224	19399	32748	5.26	7.9E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6224	19399	32749	5.26	7.9E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6947	19806	33193	0.66	7.9E-01	P37938	SWISSPROT	IMATING-TYPE PROTEIN A-ALPHA Z4
6990	18509	31601	0.74	7.9E-01	A1263399.1	EST_HUMAN	eq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030878
6990	18509	31626	0.74	7.9E-01	A1263399.1	EST_HUMAN	eq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030878
7186	20081	33472	0.84	7.9E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
8255	21337	34855	1.54	7.9E-01	AF149793.2	NT	Mus musculus neuromedin U precursor (Nrlu) gene, partial cds; lPHLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and HSAR (Hsar) gene, complete cds
8318	21400	34924	2.38	7.9E-01	6867752	NT	Mus musculus advillin (Advil-pending), mRNA
8318	21400	34925	2.38	7.9E-01	6867752	NT	Mus musculus advillin (Advil-pending), mRNA
8520	21601	35137	0.53	7.9E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE) RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8520	21601	35138	0.53	7.9E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE) RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9167	22246	36789	1.33	7.9E-01	6753577	NT	Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
9479	22536	36100	5.24	7.9E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9479	22536	36101	5.24	7.9E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11639	24719	38411	2.29	7.9E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11639	24719	38412	2.29	7.9E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
12010	24895		2.78	7.9E-01	AL181692.2	NT	Arabidopsis thaliana DNA chromosome 4, centig fragment No. 88
12203	25157		8.21	7.9E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
526	13719		1.31	7.9E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
597	13787	26807	1.08	7.9E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
7690	20765	34240	0.8	7.9E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
12521	25354		5.2	7.9E-01	AF163161.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
1154	14318	27372	1.01	7.4E-01	A1598146.1	EST_HUMAN	tr14509.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
2419	15548	28676	0.97	7.4E-01	AB011108.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
3820	16980	29983	0.97	7.4E-01	AF112538.1	NT	Maia pusilla actin (Act1) mRNA, complete cds

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Table 4

## Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4010	17167	30176	0.71	7.4E-01	AF133310.1	NT	Vibrio cholerae phage CTX01 Calcutta-rsR-a (rsR-a) and Calcutta-rsR-b (rsR-b) genes, complete cds
4428	17569	30551	8.12	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
8027	21110	34028	1.25	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8027	21110	34629	1.25	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8834	21913	35451	1.01	7.4E-01	BF346266.1	EST_HUMAN	602018456F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4154340 5'
8910	21989		1.45	7.4E-01	U87960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9288	22374	35925	6.86	7.4E-01	BE747603.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9367	22432	36990	1.24	7.4E-01	AA187988.1	EST_HUMAN	z067h01.e1 Stragene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:925297 3' similar to SW:TCPO_MOUSE P42932 T-COMPLEX/PROTEIN 1, THETA SUBUNIT;
10813	23647	37256	0.7	7.4E-01	11424933	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
12170	25133		3.69	7.4E-01	6759217	EST_HUMAN	Mus musculus complement component 1 Inhibitor (C1ih), mRNA
12287	25213		1.7	7.4E-01	AI472841.1	EST_HUMAN	ta13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4083	17238		0.73	7.3E-01	AP000062.1	NT	Aeropyrum pernix genomic DNA, section 57
4738	17873	30856	0.8	7.3E-01	AE001168.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4822	17955	30941	2.38	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
6741	19897	33287	6.6	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6741	19897	33288	6.6	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
7243	26941	33771	0.83	7.3E-01	AJ011418.1	NT	Lycopodium obscurum mRNA for ubiquitin activating enzyme
7817	20987	34163	0.69	7.3E-01	Z14133.1	NT	D.melanogaster Cnc mRNA for clathrin heavy chain
7718	20782	34268	7.25	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
7718	20782	34269	7.25	7.3E-01	M26511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
11714	24754	38449	3.29	7.3E-01	AA878019.1	EST_HUMAN	z25b08.s1 Soares_fetal_liver_spleen_1NF1.S_S1 Homo sapiens cDNA clone IMAGE:431799 3'
11714	24754	38449	3.29	7.3E-01	AA878019.1	EST_HUMAN	z25b08.s1 Soares_fetal_liver_spleen_1NF1.S_S1 Homo sapiens cDNA clone IMAGE:431799 3'
854	14031		1.86	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
2012	15152	28257	3.43	7.2E-01	X79140.1	NT	N.tabacum Nelf-4A13 mRNA
2532	19657	28781	1.98	7.2E-01	AB009805.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3135	16311	28323	1.27	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3341	16705	28717	2.36	7.2E-01	AF085808.1	NT	Giardia intestinalis variant-specific surface protein (vssp417-6) gene, vssp417-6/A-1 ellipsa, complete cds
3702	18863	29866	1.35	7.2E-01	AB002307.1	NT	Human mRNA for KIAA0309 gene, partial cds
3975	17132	30139	1.57	7.2E-01	BF338350.1	EST_HUMAN	602035589F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4183222 5'
4173	17323		0.73	7.2E-01	AF108093.1	NT	Homo sapiens IA-2 gene, intron 18

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4882	18022	31007	2.68	7.2E-01	D90814.1	NT	L mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5225	18347	31317	1.07	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaplophysin genes, complete cds; and L-type calcium channel a>
5225	18347	31318	1.07	7.2E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaplophysin genes, complete cds; and L-type calcium channel a>
5308	18425	31395	0.85	7.2E-01	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
7362	20441	33903	0.59	7.2E-01	U69633.1	NT	Solanum tuberosum cold-stress inducible protein (CIT) gene, complete cds
8048	21728	35265	1.31	7.2E-01	AF236081.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
8163	22241		0.64	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD08 5'
10548	28583	37192	2.25	7.2E-01	BF670061.1	EST_HUMAN	602118381F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4275381 5'
10977	24056	37690	3.26	7.2E-01	U82623.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
12530	18491	31530	1.51	7.2E-01	U02568.1	NT	Diclyocaulus viviparus nematode polypeptide precursor (DvA) mRNA, complete cds
12737	26489		4.37	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 6/7
12784	26075		1.48	7.2E-01	Y10168.1	NT	B. thuringiensis PK1 & cap genes, putative
710	13892	26928	11.37	7.1E-01	D21070.1	NT	Rana oatesbelana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha
3130	16308	28320	16.1	7.1E-01	AJ270777.1	NT	Isoform (RyR1), complete cds
4324	17487	30453	3.07	7.1E-01	7305360	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4324	17487	30454	3.07	7.1E-01	7305360	NT	Mus musculus obogelin (Olog), mRNA
6069	19251	32579	1.73	7.1E-01	BF681034.1	EST_HUMAN	Mus musculus obogelin (Olog), mRNA
6069	19251	32580	1.73	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
7088	20182	33606	6.48	7.1E-01	U36232.1	NT	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
8934	22013	35552	1.12	7.1E-01	BE074185.1	EST_HUMAN	Drosophila melanogaster 8-pyruvyltetrahydropterin synthase (pr) gene, complete cds
8934	22013	35553	1.12	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301289-011-409 BT0567 Homo sapiens cDNA
10059	23097	36700	1.8	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301289-011-409 BT0567 Homo sapiens cDNA
10821	23655	37265	1.1	7.1E-01	M12981.1	NT	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
12503	25958		1.8	7.1E-01	AA421492.1	EST_HUMAN	Human T-cell receptor gamma-chain J2 gene
1257	14415	27479	2.84	7.1E-01	AA421492.1	EST_HUMAN	z08h11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:731109 3'
1257	14415	27480	0.85	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1257	14415	27480	0.95	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2521	16647	28770	1.29	7.0E-01	N62412.1	EST_HUMAN	Homo sapiens multiple_sclerosis_2NHT-HMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2521	15647	29771	1.29	7.0E-01	N62412.1	EST_HUMAN	y73e07.s1 Scores_multiple_sclerosis_2NblMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
5169	18291		2.32	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
6073	19255		0.89	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8573	21654		6.52	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
9517	22592	38150	0.58	7.0E-01	U53868.1	NT	Glostridium acetabutylicum mannitol-specific phosphotransferase system (PTS) system, mifA, mifR, mifF, and mifD genes, complete cds
9517	22592	38151	0.58	7.0E-01	U53868.1	NT	Glostridium acetabutylicum mannitol-specific phosphotransferase system (PTS) system, mifA, mifR, mifF, and mifD genes, complete cds
11382	24443	38102	1.47	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
11382	24443	38103	1.47	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
13133	26997	31772	1.47	7.0E-01	9630464	NT	Bacteriophage N15 virion, complete genome
992	14164	27224	6.3	6.8E-01	U69874.1	NT	Candida albicans equalene epoxide (CAERG1) gene, complete cds and translational regulator gene, partial cds
992	14164	27225	6.3	6.8E-01	U69874.1	NT	Candida albicans squalene epoxide (CAERG1) gene, complete cds and translational regulator gene, partial cds
1338	14495	27565	2.91	8.9E-01	AA593530.1	EST_HUMAN	nm28a09.e1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3291	18465	29484	1.71	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
3531	18698	29707	15.79	6.9E-01	Y17373.1	NT	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2811
5311	18428	31398	97.22	6.9E-01	BE762751.1	EST_HUMAN	601465694F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3668943 5'
5902	18091	32405	0.82	6.8E-01	AB035692.1	NT	Branchiostoma belcheri BbNA3 mRNA for notochord actin, complete cds
6112	18282	32627	0.85	6.9E-01	Y18276.1	NT	Drosophila melanogaster mRNA for A-kinase anchor protein DAKAP550, partial
6500	19666	33029	1.12	6.8E-01	BE298188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
7978	21028	34542	0.58	6.9E-01	AF248863.1	NT	Strongylocentrotus purpuratus myosin V, complete cds
8168	21250	34769	2.94	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8168	21250	34770	2.94	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8572	22447		0.68	6.9E-01	AF118046.1	NT	Entamoeba dispar catlin transporting ATPase (atpase) gene, partial cds
9898	22636	36520	0.56	6.8E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
9898	22636	36521	0.56	6.8E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
10619	23633	37263	0.78	6.9E-01	BF242367.1	EST_HUMAN	601880580F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:4109419 5'
11538	24582	38268	2.11	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11536	24592	38269	2.11	6.8E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
12146	25949		3.77	6.8E-01	Q98958	SWISSPROT	FORHEAD BOX PROTEIN C2 (FORHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)

Table 4

## Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
979	14162	27212	1.84	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
2739	15856		1.41	6.8E-01	D90917.1	NT	Synchoecysis sp. PC6803 complete genome, 27/27, 3418852-3573470
2890	14798	27883	1.43	6.8E-01	AA854473.1	EST_HUMAN	aj75a05.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402258 3' similar to gb:X56411.na1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4694	17828	30815	1.32	6.8E-01	J00762.1	NT	Ra(hooded) prolactin gene : exon III and flanks
4880	15109	31085	0.82	6.8E-01	4758621	NT	Homo sapiens hevlin (HEVIN) mRNA
8838	22878	38460	1.08	6.8E-01	AB037768.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
10567	23602		6.72	6.8E-01	AA887938.1	EST_HUMAN	nv13e07.s1 NCL_CGAP_P122 Homo sapiens cDNA clone IMAGE:1220100 3' similar to gb:X13546.na1
11344	24407	38058	2.4	6.8E-01	AJ276675.1	NT	Human HMG-17 gene for non-histone chromosomal protein (HUMAN);
11344	24407	38057	2.4	6.8E-01	AJ276675.1	NT	Siagonospora avenae bg11 gene for beta-glucosidase, exons 1-4
11378	24487	38006	1.81	6.8E-01	AF038839.1	NT	Siagonospora avenae bg11 gene for beta-glucosidase, exons 1-4
11378	24437	38037	1.91	6.8E-01	AF038839.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11578	24833	38312	1.57	6.8E-01	AF164151.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
							Anopheles gambiae strain M2 translation initiation factor 4C (T4) (eIF-4C) mRNA, complete cds
							Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lapasin; RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11808	24893	38594	1.97	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lapasin; RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11808	24893	38595	1.97	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lapasin; RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
309	13525	28559	30.38	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
349	13580	28588	25.24	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1961	15104		1.14	6.7E-01	M12132.1	NT	Quail fast skeletal muscle troponin I gene, complete cds
2214	15348	28477	1.98	6.7E-01	AA451884.1	EST_HUMAN	zx12g12.s1 Soares_total_fetus_Nb2HF8_giv Homo sapiens cDNA clone IMAGE:786310 3' similar to contains element TAR1 repetitive element ;
2235	16058	28498	6.16	6.7E-01	AF188073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
3060	18236	28258	5.81	6.7E-01	6678580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4575	17712	30636	0.82	6.7E-01	X74421.1	NT	S.tuberosum mRNA for glucose-6-phosphate dehydrogenase
5828	18820	31894	1.44	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5828	18820	31895	1.44	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6083	18286	32594	0.79	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6453	18820	32983	1.3	6.7E-01	9636035	NT	Gallid herpesvirus 2, complete genome
6453	18820	32984	1.3	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6754	18910	33304	0.59	6.7E-01	BE68241.2	EST_HUMAN	001660177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
6754	18910	33305	0.59	6.7E-01	BE68241.2	EST_HUMAN	001660177R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905778 3'
7468	20543		3.87	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 187 of 529 of the complete genome
7495	20570	34042	0.94	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10348	23383		1.01	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
11186	24285	37800	2.06	6.7E-01	BF354648.1	EST_HUMAN	CM3-HIT0769-010600-197-03 HT0769 Homo sapiens cDNA
11746	23932	37598	2.75	6.7E-01	O14357	SWISSPROT	N-ACETYL GLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPII
11659	24044	38649	2.48	6.7E-01	AA342521.1	EST_HUMAN	EST48065 Fetal spleen Homo sapiens cDNA 3' end
2670	16896	28819	0.97	6.8E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2765	15880	26989	1.13	6.8E-01	AF169339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3578	16743	28760	1.16	6.8E-01	4508880	NT	Homo sapiens serpin domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (serpinH9) 5A (SEMASA) mRNA
3748	16909	28913	4.58	6.8E-01	Y07689.1	NT	Callicans random DNA marker, 282bp
4225	17373		2.48	6.8E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6462	18629	32990	3.82	6.8E-01	6880577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7272	20355	33808	0.82	6.8E-01	AE004458.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
7272	20355	33809	0.82	6.8E-01	AE004458.1	NT	Pseudomonas aeruginosa PA01, section 19 of 529 of the complete genome
7882	20916	34421	3.7	6.8E-01	AV680506.1	EST_HUMAN	AV680506 GLC Homo sapiens cDNA clone GLCGLD04 3'
8784	21843	35384	0.58	6.8E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
8885	22805		2.34	6.8E-01	AL183278.2	NT	Homo sapiens chromosome 21 segment HS21C078
10207	23243		0.51	6.8E-01	AU118188.1	EST_HUMAN	AU118188 HEMBA1 Homo sapiens cDNA clone HEMBA1003079 5'
840	13825	26848	2.02	6.8E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
640	13825	26849	2.02	6.8E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3519	16886	28698	5.5	6.8E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4148	17300	30292	1.73	6.8E-01	4504632	NT	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA
4397	17540	30521	7.71	6.8E-01	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
5174	18286	31268	2.88	6.8E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5559	25807	31795	1.88	6.5E-01	P18480	SWISSPROT	TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWISNF COMPLEX COMPONENT SNF5)
6855	20017	33428	1.3	6.9E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanocortin mlttr protein, complete cds
7760	20819	34309	0.74	6.5E-01	X04769.1	NT	Murine Ig-related lambrida (50) gene (exon 1) transcribed selectively in pre-B lymphocytes
7848	20801	34404	0.69	6.5E-01	A1768882.1	EST_HUMAN	wc46a02.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2321842 3'
10042	23080		0.88	6.5E-01	T78804.1	EST_HUMAN	yc21b04.at Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:108847 3'
10542	23577	37186	2.53	6.5E-01	AF118676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10869	23954	37583	2.55	6.5E-01	H67583.1	EST_HUMAN	yt1706.r1 Soares placenta_8to9weeks_2N3HP809W Homo sapiens cDNA clone IMAGE:252515 5'
10926	24008	37843	2.88	6.5E-01	AA601287.1	EST_HUMAN	nc15c07.at NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
11030	24108		3.38	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACET1 Homo sapiens cDNA clone PLACE1007810 5'
11899	24887	38586	6.43	6.5E-01	AF014115.1	NT	Placodium berghali cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12566	25386		8.69	6.5E-01	BE465050.1	EST_HUMAN	hw74a10.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12840	25889		3.83	6.5E-01	Z74145.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL097c
282	13481	26613	8.59	6.4E-01	U48848.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3545	16710	28721	4.42	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3984	17122	30126	1.46	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4614	17751	30731	0.74	6.4E-01	Y12488.1	NT	M.musculus whn gene
4814	17751	30732	0.74	6.4E-01	Y12488.1	NT	M.musculus whn gene
8812	21891	35432	1.58	6.4E-01	AE001247.1	NT	T.reponema pallidum section 63 of 87 of the complete genome
10221	23257		0.5	6.4E-01	11418320	NT	Homo sapiens hypothetical protein FLJ10140 (FLJ10140), mRNA
10294	23328	36933	7.31	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10308	23344	36949	1.31	6.4E-01	BF670405.1	EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281128 6'
12693	25481		19.53	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGCG09 5'
447	13843	26882	3.76	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
548	13741	26765	1.85	6.3E-01	U38889.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2230	15364	28483	3.28	6.3E-01	U81136.1	NT	Shigella flexneri multi-antigen resistance locus
2646	15769	28884	3.65	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2646	15769	28885	3.65	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3081	16257		0.93	6.3E-01	Y17275.1	NT	Lyoparacoon esculentum p89a gene, complete CDS
6189	19385	32713	0.84	6.3E-01	BE063908.1	EST_HUMAN	PX0-B.T0767-010500-002-405 BT0767 Homo sapiens cDNA
6733	19889	33281	1.01	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6733	19889	33282	1.01	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds



Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8718	21788		3.44	6.3E-01	BE02044.1	EST_HUMAN	601678889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5'
9087	22166	35712	0.79	6.3E-01	S62927.1	NT	glycoprotein Ila (Alu 1 and 3 fusion) [human, Genomic Mutant, 300 nt]
9421	22493	36062	0.65	6.3E-01	BF21694.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102596 5'
9820	22675	36245	3.14	6.3E-01	9627521	NT	Varicella virus, complete genome
9820	22675	36246	3.14	6.3E-01	9627521	NT	Varicella virus, complete genome
10142	23180		0.68	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10841	23675	37285	1.59	6.3E-01	Z73003.1	NT	S. cerevisiae chromosome VII reading frame ORF YGR218w
10747	23780	37393	1	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
10781	23814		0.48	6.3E-01	AW785395.1	EST_HUMAN	PIMQ-UM0018-130500-003-g12 UM0018 Homo sapiens cDNA
11315	24379	38024	1.78	6.3E-01	AA877715.1	EST_HUMAN	nc08108.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 002916 HLARK.
11620	24671	38359	6.18	6.3E-01	A1904180.1	EST_HUMAN	CM-BT043-000299-046 BT043 Homo sapiens cDNA
11709	24749	38442	1.55	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INOT-IDS2 INTERGENIC REGION
11888	24876	38573	2.12	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
12086	25068	38772	1.47	6.3E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
12262	26130	31546	15.92	6.3E-01	9910283	NT	Mus musculus keratin complex 2, gene 5g (Krt2-5g), mRNA
12358	26257		1.6	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPS) mRNA, complete cds
12882	26029		4.27	6.3E-01	X89528.1	NT	C. limicola pscD gene
5991	19178	32497	2.15	6.2E-01	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7864	20731		3.59	6.2E-01	AF022253.1	NT	Mus musculus calcium-sensing receptor related protein 4 (CaSR-r4) mRNA, partial cds
7715	25852	34286	1.16	6.2E-01	AL021127.2	NT	Mus musculus chromosome X config; putative Magea9 gene, Cetractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
8487	21578	35114	4.67	6.2E-01	H72255.1	EST_HUMAN	ys01e08.e1 Soares fetal liver spleen 1NELS Homo sapiens cDNA clone IMAGE:213542 3'
9057	22139	35681	0.7	6.2E-01	AF034411.1	NT	Lycopodium obscurum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinase
9848	21091	34606	1.47	6.2E-01	BE562887.1	EST_HUMAN	dehydratase/shikimate:NADP oxidoreductase gene, complete cds
9710	22759		2.58	6.2E-01	M24481.1	NT	601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
10283	23318	35619	6.83	6.2E-01	AL161511.2	NT	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds
10426	23461	37087	0.63	6.2E-01	11420793	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10428	23461	37088	0.63	6.2E-01	11420793	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA
10758	23789	37405	5.75	6.2E-01	P27410	SWISSPROT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1), mRNA NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOLE PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]

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## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10756	23789	37406	5.75	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN (CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOL PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN)
2488	19598		6.27	6.1E-01	6978078	NT	Mus musculus secreted acidic cytolysin rich glycoprotein (Sparc), mRNA
5653	18847	32129	1.33	6.1E-01	M59940.1	NT	Caenorhabditis elegans N2 Cehyod (hlt-1), alternatively spliced genes, complete cds
7009	20745	33564	3.4	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7009	20745	33565	3.4	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
7160	20283	33738	0.87	6.1E-01	AW105653.1	EST_HUMAN	xd50h03.x1 NCI_CGAP_OY23 Homo sapiens cDNA clone IMAGE:2597237 3' similar to gb:X12871_mai HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
7254	20337	33787	0.69	6.1E-01	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8428	21509	35041	3.47	6.1E-01	AF033335.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8995	22074	35612	1.51	6.1E-01	11431085	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8995	22074	35613	1.51	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8615	22670	36239	20.44	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
8615	22670	36240	20.44	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
10047	23085	36888	1.05	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PA01, section 13 of 528 of the complete genome
10252	23287	36883	0.82	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
10833	23855	37489	0.47	6.1E-01	AF026993.1	NT	Sus scrofa neural cell adhesion molecule (NCAM) gene, 3' UTR and microsatellite repeat region
12033	25016	38718	1.77	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12033	25016	38719	1.77	6.1E-01	S83182.1	NT	hyaluronan-binding protein-hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
13062	25895		1.16	6.1E-01	X95287.1	NT	M.mazal orfA, orfB, and orfC of archaeal ABC-transporter system
507	13701	26730	1.79	6.0E-01	D97875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
575	13767		4.74	6.0E-01	5802399	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1393	14547	27623	1.83	6.0E-01	AF085283.1	NT	Human respiratory syncytial virus strain CH93-55b attachment protein (G) gene, complete cds
3917	17078	30073	0.87	6.0E-01	AF233398.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4305	17448		1.28	6.0E-01	AF058895.1	NT	Homo sapiens Nctb3 (NOTCH3) gene, exons 26, 27, and 28
5395	18597	31567	1.96	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5555	18753	31791	2.5	6.0E-01	AW139713.1	EST_HUMAN	UI-HB1-aab-a-10-0-J1.s1 NCI_CGAP_S153 Homo sapiens cDNA clone IMAGE:2718619 3'
6669	18828	33216	2.74	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6800	18965	33385	0.68	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD138 ANTIGEN)

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6955	20288	33705	0.77	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
6955	20288	33706	0.77	6.0E-01	L10234.1	NT	Strongylocentrotus purpuratus kinesin light chain isoform 2 mRNA, complete cds
7509	20593	34056	6.49	6.0E-01	AJ277861.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8315	21397	34922	4.15	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8315	21397	34923	4.15	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
10028	23086	36684	1.57	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds
10480	23516		1.04	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PERO3 (PEROXIN-3)
10594	23629		0.81	6.0E-01	BE837779.1	EST_HUMAN	RC2-FN0084-190700-017-d08 FN0084 Homo sapiens cDNA
11312	24376	38021	1.38	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperton protein, 419 kD isoform
11312	24376	38022	1.38	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperton protein, 419 kD isoform
11848	24835	38529	2.74	6.0E-01	AI420626.1	EST_HUMAN	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12603	25440	32052	2.08	6.0E-01	11421663	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12781	25523		1.46	6.0E-01	AA706087.1	EST_HUMAN	z58g05.s1 Scanes, fetal_liver, spleen, 1NFUS, S1 Homo sapiens cDNA clone IMAGE:462776 3'
12953	25958		1.44	6.0E-01	5903136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
12988	25963	31788	5.48	6.0E-01	9055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
13032	25880		8.12	6.0E-01	BE157617.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
1025	14195	27264	1.09	6.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3343	16518	29530	5.23	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3343	16516	29531	5.23	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3916	17075	30072	0.62	5.9E-01	U74341.1	NT	Pterodroma neglecta cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
4337	17480		3.95	5.9E-01	AF162756.1	NT	Rattus norvegicus cenadin 2 mRNA, partial cds
6289	18407	31374	0.65	5.9E-01	AF026566.1	NT	Ovis aries SRY gene promoter region
6594	18754	33140	1.95	5.9E-01	AF085440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7416	20494	33982	3.08	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7556	20828		0.83	5.9E-01	X68801.1	NT	G. gallus gene for skeletal alpha-actinin, exon EF2
8188	21270	34785	0.48	5.9E-01	D80811.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
8839	21918	35456	0.48	5.9E-01	D12922.1	NT	Legionella pneumophila gene for iron superoxide dismutase, complete cds
9743	22807	36385	1.01	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain K/UW/31/Ox major outer membrane protein (omp1) gene, complete cds
10117	23155		0.84	5.9E-01	P08468	SWISSPROT	E6 PROTEIN
10391	23426	37033	1.28	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10908	23991	37624	2.24	6.9E-01	Q9X013	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
10916	23999	37632	1.71	6.9E-01	AF187944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
11203	24272	37908	2.76	5.9E-01	AW937175.1	EST_HUMAN	PM1-DT0041-190100-002-h03 DT0041 Homo sapiens cDNA
11469	24528	38201	1.98	6.9E-01	AF064626.1	NT	Mus spretus strain SPRET/EI CD48 antigen (Cd48) gene, partial cds
12302	25220	32101	1.78	6.9E-01	L42320.1	NT	Oryzotegus cuticulus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12549	25372		1.82	6.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5'-phosphate decarboxylase, complete cds
12789	25533		4.82	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1958	15101	28201	1.28	5.9E-01	P40472	SWISSPROT	SIM1 PROTEIN
4092	17247	30252	1.11	5.9E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4076131 5'
4637	17773	30753	3.59	5.9E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4917	18047		2.22	6.9E-01	AF110846.1	NT	Megastelia scalaris sex-lethal homolog (Meglsl) gene, partial cds, alternatively spliced products
5490	18689		1.02	5.9E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome
5648	18842	32123	0.81	5.9E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6313	19485	32840	1.69	5.9E-01	D78859.1	EST_HUMAN	HUM500E06B Human placenta polyA+ (TFUJiware) Homo sapiens cDNA clone GEN-500E06 5'
6442	19609	32972	0.58	6.9E-01	D50801.1	NT	Shigella sonnei DNA for 26 ORFs, complete cds
6952	20265		2.37	6.9E-01	S85091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
8071	21153		2.87	6.9E-01	H41671.1	EST_HUMAN	yr91b03 s1 Soares adult brain N2b5HB5Y Homo sapiens cDNA clone IMAGE:175757 3' similar to
8278	21360	34878	0.86	5.9E-01	A1280051.1	EST_HUMAN	gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8278	21360	34879	0.86	5.9E-01	A1280051.1	EST_HUMAN	qhesd10.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8385	21466	34691	2.71	6.9E-01	P14328	SWISSPROT	qhesd10.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8385	21466	34992	2.71	6.9E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP98
9092	22171	35716	10.4	5.9E-01	AJ270774.1	NT	SPORE COAT PROTEIN SP98
9172	22260	36783	1.23	5.9E-01	Q27368	SWISSPROT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
9173	22251	35794	0.57	5.9E-01	Q20471	SWISSPROT	TRANSCRIPTION FACTOR E2F
9705	22835		0.79	5.9E-01	BF031608.1	EST_HUMAN	PUTATIVE CASEIN KINASE I F46F2.2 IN CHROMOSOME X
11237	24306	37843	7.26	6.9E-01	AJ243213.1	NT	60155774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5'
11291	24357		3.36	6.9E-01	BF700092.1	EST_HUMAN	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
11407	24468		1.44	5.9E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284403 5'
3108	16284		0.73	6.7E-01	6755253	NT	602127577F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284403 5'
3295	16469	29488	1.46	5.7E-01	Q9WTJ2	SWISSPROT	Mus musculus plesinacytoma variant translocation 1 (Pvt1), mRNA
3593	16757		2.84	5.7E-01	AB033503.1	NT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1) (MOVO1A)
6485	18652	33014	4.41	5.7E-01	BF035413.1	EST_HUMAN	Populus euramericana peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
							601454982F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3858590 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6850	20003	33412	0.92	5.7E-01	AA194201.1	EST_HUMAN	z38c08.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665674 5'
7000	18519	31512	1.15	5.7E-01	AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7941	20991	34501	1.88	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE)
8157	21239		0.55	5.7E-01	AL251835.1	NT	Mus musculus Kcnq1, Ltpc3, Mash2, Tapa-1, Tesc4 and Tescd genes, alternative transcripts
10004	23042	36634	1.13	5.7E-01	AL161532.2	NT	Arabidopsis thaliana chromosome 4, contig fragment No. 32
10004	23042	36635	1.13	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10803	23836	37481	0.91	5.7E-01	BF540962.1	EST_HUMAN	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066810 5'
12255	25192		1.28	5.7E-01	BE715051.1	EST_HUMAN	MR3-HT0738-180700-003-a02 HT0738 Homo sapiens cDNA
13025	25675		1.31	5.7E-01	BE959722.2	EST_HUMAN	601854814R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839763 3'
3449	16817	29635	1.1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3449	16817	29636	1.1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3989	17148	30152	0.59	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4354	17497	30476	0.77	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
8003	22082	35625	4.11	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
8003	22082	35626	4.11	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF5F05 5'
8575	22717	36285	1.13	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
12153	28123		7.84	5.6E-01	BE888280.1	EST_HUMAN	601614007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
12272	25204	38382	1.39	5.6E-01	AA493535.1	EST_HUMAN	ng75g10.s1 NCL_CGAP_P16 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element:
12851	17145	30152	2.38	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12880	25460		2.56	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
13167	25758		3.64	5.6E-01	BF573929.1	EST_HUMAN	602132026F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1238	14397	27459	6.04	5.5E-01	8383912	NT	Rattus norvegicus Propionyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2768	16881	28990	8.3	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10)
2768	16881	28991	8.3	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10)
2955	16161	28178	1.17	5.5E-01	5902085	NT	Homo sapiens superkiller viralidic activity 2 (S. cervisiae homdog)-like (SKIV2L), mRNA
3134	16310		1.57	5.5E-01	H48219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2b5H555 Homo sapiens cDNA clone IMAGE:178288 3'
3308	16480	29501	2.93	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3783	16944	29651	1.34	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
5249	18370		1	5.5E-01	AF063868.1	NT	Melanoplus sanguinalipes entomopoxvirus, complete genome
5269	18386	31356	1.01	5.5E-01	U69097.1	NT	Bos taurus MHC class II beta-chain Bcl-A-DIB1 gene, partial cds

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7405	20483	33950	0.59	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase- $\alpha$ , palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
7405	20483	33951	0.69	5.5E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region: butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase- $\alpha$ , palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>
7439	20516		0.74	5.5E-01	AB015596.1	NT	Caressius auratus gene for gonadotropin II beta subunit, complete cds
8676	21758	35291	0.47	5.5E-01	BE163243.1	EST_HUMAN	QV3-HT0468-170200-090-105 HT0458 Homo sapiens cDNA
8669	23003		0.56	5.5E-01	U88415.1	NT	Crimean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds
10588	23623	37230	0.83	5.5E-01	T05047.1	EST_HUMAN	EST02935 Fetal brain, Stralagene (cat#838206) Homo sapiens cDNA clone HFBCQ35
11406	24467	38132	1.84	5.5E-01	BF129507.1	EST_HUMAN	601811077R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4054003 3'
147	13372	26404	8.11	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mex2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
147	13372	26405	8.11	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mex2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
598	13788	26808	1.01	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
598	13788	26809	1.01	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
1300	14455	27522	2.21	5.4E-01	AW896087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2173	15308		2.8	5.4E-01	AE002247.2	NT	Chlamydomonas reinhardtii AR39, section 74 of 84 of the complete genome
2328	15461	28594	2.82	5.4E-01	AJ276882.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
5774	18668	32269	0.83	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6320	19492	32850	0.83	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
7170	20303	33746	0.77	5.4E-01	BE066592.2	EST_HUMAN	601660276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906090 3'
7480	20465	34035	1.88	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7480	20565	34036	1.96	5.4E-01	Z21619.1	NT	S. cerevisiae RIB3 gene encoding DBP synthase
7492	20567	34039	1.47	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) (INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE)
10195	23232		2.69	5.4E-01	BF572338.1	EST_HUMAN	602076545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243600 5'
11334	24367	38046	2.68	5.4E-01	P36858	SWISSPROT	NITRATE REDUCTASE (NADPH) (NR)
11920	24906	38607	2.76	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11920	24906	38608	2.76	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)

Table 4

## Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12039	19492	32850	1.3	5.4E-01	AB025017.1	NT	Rattus norvegicus gene for TIS11, complete cds
12217	25168		2.41	5.4E-01	AB58398.1	EST_HUMAN	w37g04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427128 3' similar to gb:M13452 LAMIN A (HUMAN);
529	13722	26748	2.12	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
2843	15957	29065	8.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2843	15957	29068	8.83	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3315	18488	28506	3.8	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSTCL) gene, complete cds
4327	17470		1.2	5.3E-01	U39887.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5574	18770	31813	1.55	5.3E-01	AB20921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5574	18770	31814	1.56	5.3E-01	AB20921.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5671	18865	32150	0.95	5.3E-01	AA193872.1	EST_HUMAN	z42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5671	18865	32151	0.95	5.3E-01	AA193872.1	EST_HUMAN	z42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5762	18954	32257	2.32	5.3E-01	BE645920.1	EST_HUMAN	7a73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
5762	18954	32258	2.32	5.3E-01	BE645920.1	EST_HUMAN	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9105	22184		1.59	5.3E-01	L01950.2	NT	7a73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
9166	22234	35779	0.76	5.3E-01	BF433956.1	EST_HUMAN	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
9166	22234	35780	0.76	5.3E-01	BF433956.1	EST_HUMAN	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
10416	23451	37056	0.65	5.3E-01	AB94210.1	EST_HUMAN	7a71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element ;
11857	24845	38542	5.63	5.3E-01	BE566291.1	EST_HUMAN	7a71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains element MER29 repetitive element ;
12145	26958		1.73	5.3E-01	AA916053.1	EST_HUMAN	wp54b02.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to SW:COXA_HUMAN P20874 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ;
839	14017	27072	20.65	5.2E-01	L20770.1	NT	601339807.F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3682168 5'
1180	14352	27410	7.57	5.2E-01	Q9WV30	SWISSPROT	og30605.s1 NCI_CGAP_B17 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02611
1218	14378	27438	3.05	5.2E-01	AF224492.1	NT	APOLIPOPROTEIN D PRECURSOR (HUMAN);
1635	15078		3.88	5.2E-01	AL183285.2	NT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
							NUCLEAR FACTOR OF ACTIVATED T CELLS 6 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5)
							(REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
							Homo sapiens phospholipid scramblase 1 gene, complete cds
							Homo sapiens chromosome 21 segment H521C085

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2213	15347	28476	2.85	5.2E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3189	18364	29369	2.1	5.2E-01	U65942.1	NT	Chlamydia abortus strain S263 POMP91A and POMP90A precursor, genes, complete cds
3309	18493		1.05	5.2E-01	D73493.1	NT	Azotobacter vinelandii lsd gene for isocitrate dehydrogenase, complete cds
3491	18558		1.61	5.2E-01	AL118780.1	NT	Borlytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3530	18595	29706	2.01	5.2E-01	AA984165.1	EST_HUMAN	am77q03.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1016504 3'
3722	18893		0.77	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
3724	18885	28891	0.87	5.2E-01	U82871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltracrin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1p
4729	17864	30846	0.61	5.2E-01	6752947	NT	Mus musculus acetylcholine receptor beta (Acrb), mRNA
5770	18952	32263	0.92	5.2E-01	AA284281.1	EST_HUMAN	z44d09.T7 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325169 3'
8932	25802	36582	0.87	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9832	25862	36593	0.87	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
10136	23174	36772	0.49	5.2E-01	AA194518.1	EST_HUMAN	zq05b09.r1 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:628783 5'
10233	23288	36856	1.32	5.2E-01	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
13128	25738		4.83	5.2E-01	P16516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
632	13817	26841	2.5	5.1E-01	M58509.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
665	13851	26878	4.57	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
665	13851	26879	4.57	5.1E-01	AJ233944.1	NT	Polyangium vitellinum (strain PI vt1) 16S rRNA gene
1684	14836		1.02	5.1E-01	X87885.1	NT	R.norvegicus mRNA for mammalian fusca protein
4188	17338	30331	3.87	5.1E-01	AB58495.1	EST_HUMAN	w39b12x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427263 3'
4303	17446	30432	2.89	5.1E-01	P86380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5179	18301		0.6	5.1E-01	BE091766.1	EST_HUMAN	IL2-BT0731-250400-077-G08 BT0731 Homo sapiens cDNA
6352	19522	32879	1	5.1E-01	BE541068.1	EST_HUMAN	601063906F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450000 5'
8408	19575		0.9	5.1E-01	AV712328.1	EST_HUMAN	AV712328 DCA Homo sapiens cDNA clone DCAAU07 5'
7057	20110	33526	1.35	5.1E-01	R80873.1	EST_HUMAN	y94a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146872 3'
8770	21849	35389	0.84	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
8770	21849	35390	0.84	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
9888	22628	36510	4.85	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
9889	22628	36513	3.95	5.1E-01	W22302.1	EST_HUMAN	65B1 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
10363	23398	37009	0.99	5.1E-01	M94579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
12368	25874		3.49	5.1E-01	BF030207.1	EST_HUMAN	60156863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828767 5'



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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12834	25427		1.31	5.1E-01	BF439832.1	EST_HUMAN	ncs51110.x1 NCL CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3408218 3' similar to contains element TAR1 repetitive element:
2203	15338	28494	1.95	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2203	15338	28465	1.65	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
							Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (apCDGAH-FEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2211	15345	28472	2.09	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (apCDGAH-FEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2211	15345	28473	2.09	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (apCDGAH-FEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2231	15365		1.56	5.0E-01	AL161533.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 33
3942	17001	30004	0.86	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3934	17093	30091	0.93	5.0E-01	L39483.1	NT	Rattus norvegicus jagged protein mRNA, complete cds
3977	17134	30137	2.87	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
6782	19937		0.82	5.0E-01	BF578189.1	EST_HUMAN	602132642F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271939 5'
7842	20897	34398	0.84	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7842	20897	34398	0.84	5.0E-01	AL161549.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
8727	21807		1.63	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8870	21849	35484	0.86	5.0E-01	BF107848.1	EST_HUMAN	601823860R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
9657	21100	34813	2.13	5.0E-01	BF117212.1	EST_HUMAN	601903871 F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
							GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCAN TRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9824	22864	36446	1.47	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCAN TRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9824	22864	36446	1.47	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCAN TRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10602	23637		1.23	5.0E-01	BE689218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3648436 5'
12307	26226		3.84	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
13093	25713		2.26	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21G102
13109	25724		4.71	5.0E-01	O13991	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
812	13891	27045	1.83	4.9E-01	BF571462.1	EST_HUMAN	602076649F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243860 5'
1692	14844	27828	1.08	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1955	15098	28188	1.34	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5522	18719	31735	1.17	4.9E-01	Q61664	SWISSPROT	FIBRILLIN 1 PRECURSOR

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6161	18337	32682	2.67	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6161	18337	32683	2.67	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7610	20680	34156	1.61	4.8E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
7882	20934	34439	0.86	4.8E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
7882	20934	34440	0.86	4.8E-01	Q10606	SWISSPROT	PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE
9180	22268		1.96	4.9E-01	BF209791.1	EST_HUMAN	601874984F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'
9389	22484	35028	0.96	4.9E-01	AW339905.1	EST_HUMAN	hc80c02.x1 Soares_NFL_T_GBC_31 Homo sapiens cDNA clone IMAGE:2807286 3' similar to TR:095714
9496	26228		2.2	4.9E-01	10948863	NT	Q96714 HERC2 ;
10524	23559	37166	1.05	4.9E-01	AF053980.1	NT	Mus musculus unc13 homolog (C. elegans)1 (Unc13h1), mRNA
12197	25154		2.61	4.9E-01	AF176912.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
13085	26174		4.94	4.9E-01	AA613562.1	EST_HUMAN	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
13084	25714	31839	1.69	4.8E-01	AL163301.2	NT	nq22e11.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1144652 3'
13181	25768		1.27	4.9E-01	11431439	NT	Homo sapiens chromosome 21 segment HS21C101
4452	17592		0.59	4.8E-01	4504850	NT	Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA
5624	18818	31892	9.66	4.8E-01	J02987.1	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK5) mRNA, and translated products
6817	19970	33378	0.69	4.8E-01	U92882.1	NT	Saccharomyces cerevisiae) sporulation protein (SPO11) gene required for meiotic recombination, complete cds
6927	19980		4.18	4.8E-01	AA699878.1	EST_HUMAN	Mus musculus slow skeletal muscle troponin T (Tnni1) gene, complete cds
7469	20544		1.83	4.8E-01	6031650	NT	nu85f09.s1 NCI_CGAP_Av1 Homo sapiens cDNA clone IMAGE:1217513
7845	20900	34403	1.06	4.8E-01	AL163209.2	NT	Homo sapiens reproduction 8 (D6S2298E) mRNA
7938	20989	34497	3.59	4.8E-01	AL161492.2	NT	Homo sapiens chromosome 21 segment HS21C009
7938	20989	34498	3.59	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
8089	21171	34686	1.81	4.8E-01	AB20744.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
9448	22662		1.05	4.8E-01	BE155148.1	EST_HUMAN	Y77110.y5 Soares breast 2NcHBst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MER1 repetitive element ;
10212	23248		0.55	4.8E-01	BF568833.1	EST_HUMAN	PM1-HT0350-201289-004-b04 HT0350 Homo sapiens cDNA
10966	24047		1.9	4.8E-01	X83502.1	NT	602184287F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
12278	25208		1.56	4.8E-01	AL163227.2	NT	S. cerevisiae ORFs from chromosome X
12509	25913		5.78	4.8E-01	AF227668.1	NT	Homo sapiens chromosome 21 segment HS21C027
13142	18318		0.59	4.7E-01	AF192387.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
6844	19803	33190	8.07	4.7E-01	BF217173.1	EST_HUMAN	Felis catus feline leukemia virus subgroup C receptor (FLVCR1) mRNA, complete cds
7186	20051	33461	0.84	4.7E-01	AL204374.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4098387 5'
							qf72a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1765944 3'

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8049	21132	34652	0.75	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
8049	21132	34653	0.75	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
9276	22352	35904	0.81	4.7E-01	6981501	NT	Rattus norvegicus Spermine binding protein (Sbp), mRNA
11084	24158		4.37	4.7E-01	AF102673.1	NT	Influenza A virus isolate tk51697 hemagglutinin (HA) gene, partial cds
11340	24403	38052	1.94	4.7E-01	U41069.1	NT	Human collagen alpha2(XI) (COL11A2) gene, exons 8 through 10, and partial cds
11658	24737	39426	1.45	4.7E-01	AW889448.1	EST_HUMAN	RCE-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
12401	25231		1.84	4.7E-01	BE897763.1	EST_HUMAN	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
12529	25361		1.25	4.7E-01	AW341561.1	EST_HUMAN	hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809188 3'
3837	16997	28899	1.62	4.6E-01	BF683300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3837	16997	30000	1.82	4.6E-01	BF683300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
6535	18732	31747	0.93	4.6E-01	BF313593.1	EST_HUMAN	801900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5535	18732	31748	0.93	4.6E-01	BF313593.1	EST_HUMAN	801900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5588	18783	31828	3.52	4.6E-01	Q90843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5588	18783	31829	3.52	4.6E-01	Q90843	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5653	18857	32140	1.84	4.6E-01	BE734781.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'
5877	18871	32167	3.62	4.6E-01	A1247676.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.
5877	18871	32158	3.62	4.6E-01	A1247676.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.
5885	18879	32169	1.44	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
5763	18655		0.85	4.6E-01	AF212124.1	NT	Anolis schwartzi cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5850	19040		0.9	4.6E-01	BE817247.1	EST_HUMAN	PMO-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
6386	19553	32914	0.82	4.6E-01	AE000894.1	NT	Methanobacterium thermoautotrophicum from bases 1165761 to 1176238 (section 100 of 148) of the complete genome
6908	20221	33649	2.39	4.6E-01	U62332.1	NT	Emmericella nidulans NEMPA (nempa) gene; mitochondrial gene encoding putative mitochondrial protein, complete cds
6906	20221	33650	2.39	4.6E-01	U62332.1	NT	Emmericella nidulans NEMPA (nempa) gene; mitochondrial gene encoding putative mitochondrial protein, complete cds
7379	25943	33920	0.66	4.6E-01	L07320.1	NT	Murine cytomegalovirus e1 protein gene, complete cds
7908	20958	34464	0.78	4.6E-01	AA493577.1	EST_HUMAN	rh04h05.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:843363 similar to contains Alu repetitive element; contains element L1 repetitive element;
8515	21596	35131	14.55	4.6E-01	BF697399.1	EST_HUMAN	602130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287928 5'
8946	22025	35565	0.54	4.6E-01	AA932237.1	EST_HUMAN	0076608.e1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb:M36341 ADP-RIBOSYLATION FACTOR 4 (HUMAN);

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8946	22025	35568	0.54	4.6E-01	AA682237.1	EST_HUMAN	cc76808.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1572087 3' similar to gb1436341 ADP- RIBOSYLATION FACTOR 4 (HUMAN);
9501	22557	36120	0.93	4.6E-01	P65202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9501	22557	36121	0.93	4.6E-01	P65202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9866	22806	36480	0.52	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB:1) gene, complete cds; nuclear gene for chloroplast product
9866	22806	36491	0.52	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB:1) gene, complete cds; nuclear gene for chloroplast product
10181	23218	36809	1.15	4.6E-01	A1915634.1	EST_HUMAN	wg73et12.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
10181	23218	36810	1.15	4.6E-01	A1915634.1	EST_HUMAN	wg73et12.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370766 3'
11238	24307	37856	2.31	4.6E-01	P98163	SWISSPROT	POTATIVE VITELLOGENIN RECEPTOR PRECURSOR (VL)
11248	24317	37857	5.08	4.6E-01	BE165449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11760	23946	37573	4.3	4.6E-01	AF019389.1	NT	Human thiolpurine methyltransferase (TPMT) gene, exon 10 and complete cds
11760	23946	37574	4.3	4.6E-01	AF019389.1	NT	Human thiolpurine methyltransferase (TPMT) gene, exon 10 and complete cds
1960	16103	28203	1.15	4.5E-01	AE001831.1	NT	Delnoccocus radiodurans R1 section 68 of 229 of the complete chromosome 1
1960	15103	28204	1.15	4.5E-01	AE001831.1	NT	Delnoccocus radiodurans R1 section 68 of 229 of the complete chromosome 1
2833	16110	29124	4.83	4.5E-01	AA677085.1	EST_HUMAN	z55502.s1 Soares fetal_liver脾脏 INFIL_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3380	16552	29565	0.68	4.6E-01	AW083761.1	EST_HUMAN	xc25c06.x1 NCL_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2585290 3' similar to gb1407807 DYNAMIN-1 (HUMAN);
3380	16552	29566	0.68	4.6E-01	AW083761.1	EST_HUMAN	xc25c06.x1 NCL_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2585290 3' similar to gb1407807 DYNAMIN-1 (HUMAN);
3393	16563	29578	4.46	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3465	16632	29651	1.51	4.5E-01	AF126378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4139	17261	30329	1.18	4.5E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4166	17356	30329	1.02	4.5E-01	A1708908.1	EST_HUMAN	COLLAGEN ALPHA 5(V) CHAIN
4292	18478	31161	4.71	4.5E-01	AW873495.1	EST_HUMAN	es6608.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2353480 3'
5058	18186	31161	1.18	4.5E-01	BE063445.2	EST_HUMAN	hs60g02.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
5686	18960	32145	1.67	4.5E-01	AW808814.1	EST_HUMAN	601657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868023 3'
6740	18998	34120	1.38	4.5E-01	Q00956	SWISSPROT	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA COAT PROTEIN
7571	20843	34120	0.91	4.5E-01	M37038.1	NT	Rat nuclear proteins B23.1 and B23.2

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7785	20841	34333	2.39	4.5E-01	A1859849.1	EST_HUMAN	w32e02.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
8502	21583		1.11	4.5E-01	M32891.1	NT	SWJ5NF COMPLEX 170 KDA SUBUNIT.
8509	21679	35217	2.87	4.5E-01	A1848596.1	EST_HUMAN	D.melanogaster Shaw2 protein mRNA, complete cds tz50g11.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292844 3'
8768	21835	35378	0.85	4.5E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
8981	22060		2.38	4.5E-01	11444786	NT	Homo sapiens hypothetical protein DKFZp647G183 (DKFZp647G183), mRNA
9200	22278	35817	0.86	4.5E-01	AE000218.1	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
10145	23183		0.96	4.5E-01	9830816	NT	Bornbyx mori nuclear polyhedrosis virus, complete genome
10713	23746	37352	25.59	4.5E-01	M86006.1	EST_HUMAN	EST02531 Fetal brain, Stratagene (cat#5936206) Homo sapiens cDNA clone HFBCY17
10713	23746	37353	25.59	4.5E-01	M86009.1	EST_HUMAN	EST02631 Fetal brain, Stratagene (cat#5936206) Homo sapiens cDNA clone HFBCY17
11104	24176	37812	2.52	4.5E-01	AW591271.1	EST_HUMAN	xc14h01.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
11226	24294	37835	2.16	4.5E-01	11430789	NT	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1]:
11530	24588		1.3	4.5E-01	AV719382.1	EST_HUMAN	Homo sapiens cadherin 3, P-cadherin (placental) (CDH3), mRNA
12164	26162		5.58	4.5E-01	BE871491.1	EST_HUMAN	AV719382 GLC Homo sapiens cDNA clone GLCCED12 5'
12895	25882		1.2	4.5E-01	BF337431.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5'
12970	25830		12.42	4.5E-01	11422069	NT	602035275F1 NCL_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183290 5'
2084	16234		1.11	4.4E-01	8680503	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA Mus musculus Integral membrane-associated protein 1 (linap1), mRNA
2482	15989	28715	4.18	4.4E-01	P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3390	18560	29575	1.54	4.4E-01	AF059780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3390	18560	29576	1.54	4.4E-01	AF059780.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3395	18565	29580	2.12	4.4E-01	BF056726.1	EST_HUMAN	7191d02.y1 NCL_CGAP_Brn10 Homo sapiens cDNA clone IMAGE:3393795 5'
4349	17482		1.35	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608383 5'
5536	18733	31749	1.31	4.4E-01	PO4929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5536	18733	31750	1.31	4.4E-01	PO4929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5805	18995	32300	1.58	4.4E-01	965019.1	NT	mucln [rate, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5823	19013	32318	1.81	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5'
6074	19258	32584	1.12	4.4E-01	A1168413.1	EST_HUMAN	ql62h11.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6074	18256	32585	1.12	4.4E-01	AI198413.1	EST_HUMAN	q82h1.1 x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168 UNKNOWN PROTEIN
6370	19539	32899	1.87	4.4E-01	AW080785.1	EST_HUMAN	xx27608.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:O95154 O95154 AFLATOXIN B1-ALDEHYDE REDUCTASE
8458	19825		1.05	4.4E-01	AA776132.1	EST_HUMAN	ae85d11.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:970965 3' similar to gb:M16038
7657	20629	34104	1.14	4.4E-01	AE000571.1	NT	Helicobacter pylori 26895 section 48 of 134 of the complete genome
8024	21107		12.3	4.4E-01	Z11679.1	NT	S.tuberosum mRNA for induced sclerol tip protein (partial)
8962	22041	35584	1.11	4.4E-01	AA056427.1	EST_HUMAN	Z169a03.a1 Stratiogene colon (H937204) Homo sapiens cDNA clone IMAGE:508836 3'
8952	22427	35985	0.78	4.4E-01	AF112540.1	NT	HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds
9385	22460	36023	0.82	4.4E-01	AW612578.1	EST_HUMAN	h105c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2854222 3' similar to
9490	22547	36110	1.13	4.4E-01	O62836	SWISSPROT	SW_MSH6_HUMAN P52701 DNA MISMATCH REPAIR PROTEIN MSH6
10167	23204	36788	1.95	4.4E-01	A126650.1	EST_HUMAN	ZINC FINGER X-CHROMOSOMAL PROTEIN
10168	23205		2.09	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10302	23337	36942	4.94	4.4E-01	P36590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10585	23820	37226	1.76	4.4E-01	S78404.1	NT	beta-HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10585	23820	37227	1.76	4.4E-01	S78404.1	NT	beta-HKA-H,K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10829	23882	37486	0.46	4.4E-01	P02716	SWISSPROT	ACETYLCHOLINE RECEPTOR PROTEIN, DELTA CHAIN PRECURSOR
11522	24578	38286	1.84	4.4E-01	6691408	NT	Tetrahymena redua mitochondrion, complete genome
12435	25308	32087	4.23	4.4E-01	6677874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
12447	26084		13.47	4.4E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
13051	26689		1.41	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
424	13619	26689	2.42	4.3E-01	AF155218.1	NT	Caillitrix jacchus MW/LW opsin gene, upstream flanking region
424	13619	26689	2.42	4.3E-01	AF155218.1	NT	Caillitrix jacchus MW/LW opsin gene, upstream flanking region
1633	14785	27871	1.11	4.3E-01	AW869550.1	EST_HUMAN	QV4-SN0024-200400-163-501 SN0024 Homo sapiens cDNA
2835	16112		1.34	4.3E-01	AW865289.1	EST_HUMAN	GM2-DT0003-010200-077-c01 DT0003 Homo sapiens cDNA
3127	16303	28316	0.95	4.3E-01	AW999477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4826	13619	26689	1.27	4.3E-01	AF155218.1	NT	Caillitrix jacchus MW/LW opsin gene, upstream flanking region
4528	13619	26689	1.27	4.3E-01	AF155218.1	NT	Caillitrix jacchus MW/LW opsin gene, upstream flanking region
5071	18198		1.04	4.3E-01	AL101502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5220	18342		0.94	4.3E-01	9635250	NT	Xestia c-nigrum granulovirus, complete genome
5480	18679	31693	0.95	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5480	18679	31694	0.95	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)

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6009	19194	32512	1.31	4.3E-01	BE181655.1	EST_HUMAN	QV1-HT0638-070500-191-d08 HT0638 Homo sapiens cDNA
6027	19210	32530	1.89	4.3E-01	AF179825.1	NT	Salmli cellreus difactory receptor (SSC188) gene, partial cds
6847	20000	33408	3.1	4.3E-01	AJ001678.1	NT	Columik columix japonica fnG gene
6825	20240	33675	0.67	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
7005	20141		0.77	4.3E-01	O33367	SWISSPROT	DNA GYRASE SUBUNIT B
7596	20558		1.28	4.3E-01	BF948001.1	EST_HUMAN	602023134F1 NCL_CGAP_Bin87 Homo sapiens cDNA clone IMAGE:4158296 5'
8922	21702		3.15	4.3E-01	U97040.1	NT	Methanococcus voltae flagella-related protein C-1 (flaC-flaI) genes, complete cds
8455	22571	36137	1.02	4.3E-01	Y14604.1	NT	Erwinia amylovora tcsV gene
9928	22988	36559	2.36	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
9928	22988	36557	2.36	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2988554 5'
10433	23468	37075	0.99	4.3E-01	AW170559.1	EST_HUMAN	TRC00189 O00189 MU-ADAPTIN-RELATED PROTEIN 2. ;
11172	20240	33675	2.27	4.3E-01	AF075629.1	NT	Equus caballus microsatellite LEX027
13162	25754		1.66	4.3E-01	AJ003022.1	NT	Streptomyces coelicolor whiH gene
1389	16036	27619	1.17	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
2002	15143		1.02	4.2E-01	AA761653.1	EST_HUMAN	n224e09.s1 NCL_CGAP_GCBT Homo sapiens cDNA clone IMAGE:1288696 3'
3697	16858	29882	4.1	4.2E-01	AE003947.1	NT	Xyella fastidiosa, section 93 of 229 of the complete genome
3727	16888	29892	1.09	4.2E-01	AI280338.1	EST_HUMAN	q64b01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1878945 3'
3803	18477		0.73	4.2E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40493
3984	17141	30146	0.74	4.2E-01	AW835527.1	EST_HUMAN	QV0-LT0015-180200-127-401 LT0015 Homo sapiens cDNA
4819	17952	30937	2.57	4.2E-01	AA634093.1	EST_HUMAN	n59h01.s1 NCL_CGAP_P10 Homo sapiens cDNA clone IMAGE:997777 similar to gb:M33500 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4903	18033	31022	3.8	4.2E-01	R13467.1	EST_HUMAN	Y77e01.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5832	19023	32330	1.42	4.2E-01	BF242055.1	EST_HUMAN	60187921F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
5801	18090	32404	1.83	4.2E-01	AW854162.1	EST_HUMAN	RC3-CT0254-060400-029-g04 CT0254 Homo sapiens cDNA
6334	19505	32863	0.99	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7090	20184	33608	8.72	4.2E-01	AU188472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7090	20184	33608	8.72	4.2E-01	AU188472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7151	25839	33727	3.21	4.2E-01	S82604.1	NT	Breast breast cancer gene [rat, WF, epsee], Genomic, 419 nt, segment 2 of 2]
7242	20323	33770	6.61	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7745	20805	34294	0.81	4.2E-01	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
8182	21284	34786	4.01	4.2E-01	AW957448.1	EST_HUMAN	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA
8182	21284	34787	4.01	4.2E-01	AW957448.1	EST_HUMAN	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA

Table 4

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8401	21482	35010	0.72	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit Vic (COX6C), nuclear gene encoding mitochondrial protein, mRNA
9511	22576	36141	0.51	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
9511	22576	36142	0.51	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
10175	23212		0.81	4.2E-01	AA705007.1	EST_HUMAN	295501.s1 Soares fetal liver spleen_TNFLS_S1 Homo sapiens cDNA clone IMAGE:452649 3'
10714	23747	37354	1.44	4.2E-01	AW868668.1	EST_HUMAN	MR3-SN0010-280300-103-107 SN0010 Homo sapiens cDNA
11288	24384	38005	1.43	4.2E-01	AB023489.1	NT	Oryza latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
11879	24876	38368	1.87	4.2E-01	BE86485.2	EST_HUMAN	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
1118	14283	27338	2.11	4.1E-01	AI905481.1	EST_HUMAN	RC-BT091-210189-142 BT091 Homo sapiens cDNA
1127	14292	27347	1.46	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1127	14292	27348	1.46	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1640	14792	27877	1.77	4.1E-01	AI805949.1	EST_HUMAN	PM-BT103-270486-684 BT103 Homo sapiens cDNA
2775	15890	28001	1.46	4.1E-01	7703263	NT	Homo sapiens anaphase-promoting complex/subunit 7 (APC7), mRNA
3008	16181	29202	2.12	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
3008	16181	29203	2.12	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
3375	16547	29561	0.69	4.1E-01	AA906944.1	EST_HUMAN	q94b08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
3871	17030	30028	0.73	4.1E-01	AW861292.1	EST_HUMAN	EST373364 MAGG resequences, MAGG Homo sapiens cDNA
3871	17030	30029	0.73	4.1E-01	AW861292.1	EST_HUMAN	EST373364 MAGG resequences, MAGG Homo sapiens cDNA
4389	17532	30513	3.78	4.1E-01	AI249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoJ, isoK, isoL and isoF genes
4422	17563		0.99	4.1E-01	AA909257.1	EST_HUMAN	om33402.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4789	17924	30912	1.36	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPC8DF10 5'
6111	19281	32626	4.84	4.1E-01	BF681393.1	EST_HUMAN	602766590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
6857	20010	33420	0.65	4.1E-01	U02298.1	NT	Mus musculus NIH 3T3 chemokine ratites (Soyas) gene, complete cds
7590	20661	34137	2.48	4.1E-01	U67535.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
8226	21307	34827	1.38	4.1E-01	BF574604.1	EST_HUMAN	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'
9292	22368	35918	1.51	4.1E-01	6755521	NT	Mus musculus signaling intermediate in Toll pathway evolutionarily conserved (Sitpece-pending), mRNA
9765	22782		0.75	4.1E-01	AF160597.1	NT	Voa160 gymnocaulus Vgym560 cytochrome b (cyb) gene, complete cds; mitochondrial gene for
10470	23503		1.56	4.1E-01	AL139076.2	NT	mitochondrial product
10822	23656	37286	1.15	4.1E-01	AV649579.1	EST_HUMAN	Campylobacter jejuni NCTC11169 complete genome; segment 318
10725	23758	37365	0.68	4.1E-01	P18584	SWISSPROT	AV649579 GLC Homo sapiens cDNA clone GLOBVD12 3'
10725	23758	37366	0.68	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10806	23839		1.14	4.1E-01	BF349382.1	EST_HUMAN	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)



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11078	24153	37780	40.17	4.1E-01	X68700.1	NT	Zea mays ZMPM52 gene for 19 kDa zain protein
11075	23903	37525	1.83	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
12810	28139		2.33	4.1E-01	D87678.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
13153	26169		1.24	4.1E-01	AJ131016.1	NT	Homo sapiens SCL gene locus
1064	14229	27288	1.49	4.0E-01	8404858	NT	Laqueus rubellus mitochondrion, complete genome
1370	14525	27599	1.21	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
1514	14667		5.48	4.0E-01	6679258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2081	16053	28318	1.08	4.0E-01	Z86933.1	NT	Ascolobus immerus masc2 gene
2081	16063	28317	1.08	4.0E-01	Z96933.1	NT	Ascolobus immerus masc2 gene
2868	13369	28402	1.11	4.0E-01	6678490	NT	Mus musculus ubiquitin-protein ligase e3 component n-recogin (Ubr1), mRNA
3033	16209	29231	1.18	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
3033	16209	29232	1.16	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Streptococcus pneumoniae Y10C (y10C), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (murY) genes, complete cds
3766	16947	29955	1.87	4.0E-01	AF088903.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3932	17091	30088	3.21	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3932	17091	30089	3.21	4.0E-01	AJ277511.1	NT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
4938	18068		8.59	4.0E-01	Q31849	SWISSPROT	EST382691 MAGG resequenced, MAGG Homo sapiens cDNA
6031	19214	32535	1.07	4.0E-01	AW670810.1	EST_HUMAN	STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
6568	19730	33108	0.82	4.0E-01	P27285	SWISSPROT	MR4-TN0110-160900-202-g02 TN0110 Homo sapiens cDNA
8113	21195	34714	0.51	4.0E-01	BF092634.1	EST_HUMAN	Homo sapiens OCTN2 gene, complete cds
8201	21283	34806	0.73	4.0E-01	AB016625.1	NT	EST26068 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
9208	22286	35927	1.11	4.0E-01	AA323289.1	EST_HUMAN	601558283F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3828092 5'
11869	24857		1.67	4.0E-01	BF030262.1	EST_HUMAN	Synechocystis sp. PCC 9413 transposase gene, complete cds
12021	25005		2.38	4.0E-01	L76080.1	NT	Homo sapiens chromosome 21 segment HS21C100
12463	26978		2.5	4.0E-01	AL163300.2	NT	S. cerevisiae chromosome X reading frame ORF YJL026w
13027	26116		1.38	4.0E-01	Z49301.1	NT	rab84c05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3' similar to SW:NTCR_BOVIN_O18875 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 1; S. cerevisiae chromosome X reading frame ORF YJL026w
13168	26036		1.21	4.0E-01	BF432020.1	EST_HUMAN	S. cerevisiae chromosome X reading frame ORF YJL026w
13222	25907		1.28	4.0E-01	Z49301.1	NT	Garilla gorilla carboxy-ester lipase (CEL) gene, complete cds
1409	14563	27638	1.84	3.9E-01	AF206618.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2707	15925	28940	3.34	3.9E-01	AB033019.1	NT	H. sapiens B-myb gene
2770	15885	28994	5.03	3.9E-01	X82032.1	NT	

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2770	15885	28995	5.03	3.9E-01	X82032.1	NT	H.sapiens B-myb gene
3166	16341	26349	4.24	3.9E-01	AJ226996.1	NT	Sinorhizobium meliloti epl. syB2, cys3 genes and of3
4190	17340	30333	1.48	3.9E-01	BF92811.1	EST_HUMAN	7661d01.x1 NCL_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339169 3'
5106	18234	31203	1.47	3.9E-01	BE728667.1	EST_HUMAN	601963949F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833699 5'
6055	19237	32582	4.58	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
6410	19579	32940	0.64	3.9E-01	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8140	21222	34740	0.99	3.9E-01	U79416.1	NT	Homo sapiens prepro dipeptidyl peptidase 1 (DPP-I) gene, complete cde
8062	22141	35686	0.83	3.9E-01	AW177011.1	EST_HUMAN	CM3-CT0105-170869-004-b08 CT0105 Homo sapiens cDNA
9071	22150		0.82	3.9E-01	BF348634.1	EST_HUMAN	802018944F1 NCL_CGAP_Br167 Homo sapiens cDNA clone IMAGE:4155322 5'
9435	22508	36075	1.73	3.9E-01	AW196989.1	EST_HUMAN	xs86d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:094821 O94821 KIAA0713 PROTEIN ;
9746	22809	36387	1.59	3.9E-01	AJ937337.1	EST_HUMAN	wp76d02.x1 NCL_CGAP_Br25 Homo sapiens cDNA clone IMAGE:2467668 3' similar to SW-RFX5_HUMAN P48382 BINDING REGULATORY FACTOR. ;
10082	23120	36722	2.88	3.9E-01	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11; and L1 and Alu repeats
10369	23404	37016	0.68	3.9E-01	D88722.1	NT	Porphyria purpurea mitochondrion, complete genome
10562	23597	37203	0.61	3.9E-01	BF361856.1	EST_HUMAN	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10562	23597	37204	0.61	3.9E-01	BF361856.1	EST_HUMAN	CM2-NN0034-030600-218-h04 NN0034 Homo sapiens cDNA
10836	23869		0.47	3.9E-01	AB037832.1	NT	CM2-NN0034-030600-218-h04 NN0034 Homo sapiens cDNA
11059	24135		1.37	3.9E-01	AV695974.1	EST_HUMAN	Homo sapiens mRNA for KIAA1411 protein, partial cds
12049	25030	38736	1.89	3.9E-01	AV702823.1	EST_HUMAN	AV695974 GK Homo sapiens cDNA clone GKBCGC11 5'
12221	26053		4.03	3.9E-01	AF304354.1	NT	AV702823 ADB Homo sapiens cDNA clone ADBDBE05 5'
12916	26033		1.76	3.9E-01	11433335	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
164	13389		7.58	3.8E-01	7019488	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
518	13711		6.1	3.8E-01	AB029291.1	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1919	15062		1.36	3.8E-01	AE003870.1	NT	Mus musculus pen-1 mRNA for pericentriolar material-1, complete cds
2837	15760	28874	1.84	3.8E-01	AF214117.1	NT	Xylella fastidiosa, section 16 of 229 of the complete genome
2697	16069	28331	5.2	3.8E-01	6678002	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
3066	16242		0.71	3.8E-01	AJ251057.1	NT	Mus musculus colute carrier family 1, member 6 (Slc1a6), mRNA
3113	16289	28905	1.91	3.8E-01	AF043383.1	NT	Human immunodeficiency virus type 1 complete genome (isolet 88SE-MP1213)
3572	16737	29752	8.7	3.8E-01	AL191618.2	NT	Pleuronectes americanus aminopeptidase N (ampN) gene, partial cds
3628	16762		1.09	3.8E-01	AI807219.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
							wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3643	16792		0.97	3.8E-01	AI807219.1	EST_HUMAN	w38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3652	17012	30012	1.07	3.8E-01	BE164080.1	EST_HUMAN	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
4027	17183	30192	0.65	3.8E-01	8754095	NT	Mus musculus general transcription factor III (GTF2), mRNA
5727	18920	32214	1.11	3.8E-01	Q04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
6469	18636		0.63	3.8E-01	S48825.1	NT	p190 protein (Mink, Genomic, 2446 nt)
6781	18917	33312	5.74	3.8E-01	BE072399.1	EST_HUMAN	QV3-BT0537-271299-048-e02 BT0537 Homo sapiens cDNA
6889	20214	33844	4.39	3.8E-01	AI374601.1	EST_HUMAN	ta54f11.x1 Soares_fetal_fetus_Nb2HF8_8w Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element;
7079	20132	33549	1.39	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7689	20750		4.27	3.8E-01	XG1597.1	NT	Mus musculus gene for kallikrein-binding protein
8493	21674	35111	0.54	3.8E-01	M81385.1	NT	Mouse liver receptor homologous protein (LFRH-1) mRNA, complete cds
8764	21833	35373	2.04	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1831 protein, partial cds
8826	21805	35444	1.09	3.8E-01	11441284	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
9017	22096	36636	1.29	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9781	22699		4.35	3.8E-01	T95413.1	EST_HUMAN	ye43H06.11 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains Alu repetitive element; contains PTR5 repetitive element;
11034	24113		1.38	3.8E-01	AV755814.1	EST_HUMAN	AV755814 BM Homo sapiens cDNA clone BMFBC07 5'
11999	24696	36386	1.57	3.8E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
11824	24813		2.87	3.8E-01	BE19219.1	EST_HUMAN	RCO-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
11992	24977	36681	2.6	3.8E-01	R42550.1	EST_HUMAN	y92h11.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
11982	24977	36682	2.5	3.8E-01	R42550.1	EST_HUMAN	y92h11.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
12436	25309		2.61	3.8E-01	AE001124.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12689	25082		2	3.8E-01	U84788.1	NT	Human p53 (TP53) gene, complete cds
12695	25463		1.71	3.8E-01	BE829256.1	EST_HUMAN	QV3-ET0063-190700-271-a06 ET0063 Homo sapiens cDNA
13106	25720		1.48	3.8E-01	U78031.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
13188	25772	31933	1.78	3.8E-01	AF194972.1	NT	Mus musculus developmental control protein mRNA, partial cds
2551	16876	28799	12.91	3.7E-01	AB037831.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3549	16714	29726	10.67	3.7E-01	AF056336.1	NT	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
3974	17131	30135	1.09	3.7E-01	AA319482.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end
4344	17487	30470	9.09	3.7E-01	AI218707.1	EST_HUMAN	cl33c07.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4440	17580	30659	1.31	3.7E-01	AW878037.1	EST_HUMAN	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
4509	17648	30636	2.91	3.7E-01	AE002408.1	NT	Neisseria meningitidis serogroup B strain M/58 section 50 of 206 of the complete genome

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5280	18399	31388	0.74	3.7E-01	T12298.1	EST_HUMAN	A033R Heart Homo sapiens cDNA clone A033
5280	18399	31389	0.74	3.7E-01	T12298.1	EST_HUMAN	A033R Heart Homo sapiens cDNA clone A033
5883	19072	32380	1.27	3.7E-01	AF135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
6071	18253	32582	1.25	3.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment H321C078
6639	18788	33187	0.7	3.7E-01	M10806.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
6660	18919		0.8	3.7E-01	L10353.1	NT	Mus saxicola heptoglobin mRNA, complete cds
7283	20375	33832	3.48	3.7E-01	11525843	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7665	21015	34527	0.69	3.7E-01	T88802.1	EST_HUMAN	yaf50a07.r3 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:68324.5'
8524	21605	35143	1.96	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8524	21605	35144	1.96	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8560	21641	35180	0.68	3.7E-01	AA002912.1	EST_HUMAN	ok43b11.s1 NCI CGAP Lei2 Homo sapiens cDNA clone IMAGE:1516701.3'
9402	22476		1.34	3.7E-01	AJ271386.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bodo gene)
10373	23408		0.5	3.7E-01	K00691.1	NT	mouse lg germline alpha membrane oxo region
10414	23449	37054	4.21	3.7E-01	AJ336411.1	EST_HUMAN	q46b07.x1 Soares fetal lung NHL19W Homo sapiens cDNA clone IMAGE:1960997.3'
10783	23816	37437	0.46	3.7E-01	U08361.1	NT	HIV-1 RU107B from Russia, gp120 V3-V5 region (env) gene, partial cds
10783	23816	37438	0.46	3.7E-01	U08361.1	NT	HIV-1 RU107B from Russia, gp120 V3-V5 region (env) gene, partial cds
11097	24170	37805	1.8	3.7E-01	X05958.1	NT	Rabbit mRNA for fast skeletal muscle myosin heavy chain (MHC)
11285	24351	37889	2.02	3.7E-01	AJ287357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11285	24351	37890	2.02	3.7E-01	AJ287357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11754	23940	37566	2.73	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
12004	24989		1.42	3.7E-01	AA973640.1	EST_HUMAN	cc48d03.s1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1569221.3' similar to qb:M77698
12066	25047		3.5	3.7E-01	6677678	NT	TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN);
12137	25654		1.17	3.7E-01	J04982.1	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
12314	25229		3.94	3.7E-01	AJ243525.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
12410	26289		1.82	3.7E-01	D88978.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
12821	25543		2.84	3.7E-01	AI121154.1	EST_HUMAN	Human mRNA for KIAA0223 gene, partial cds
12902	25697	31971	6.89	3.7E-01	Y18000.1	NT	DKFZp782K075.r1 t82 (synonym: hmel2) Homo sapiens cDNA clone DKFZp782K075.5'
271	13469	26520	0.77	3.6E-01	AJ008609.1	NT	Homo sapiens NF2 gene
1020	14181		9.07	3.6E-01	U89241.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
1342	14498	27570	3.97	3.6E-01	T80255.1	EST_HUMAN	Human mbp gene, partial cds
1342	14498	27571	3.97	3.6E-01	T80255.1	EST_HUMAN	y03a05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443.5'
1968	15109	28209	6.55	3.6E-01	AW590184.1	EST_HUMAN	y03a05.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24443.5'
1968	15109	28210	6.55	3.6E-01	AW590184.1	EST_HUMAN	hg33102.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2947419.3'
1968	15109	28210	6.55	3.6E-01	AW590184.1	EST_HUMAN	hg33102.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2947419.3'

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2007	15147	28263	6.7	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2113	16261		1.15	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2343	15474		2.33	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2463	15690		2.8	3.6E-01	X76725.1	NT	P. irregularis (P3804) gene for acilin
2556	15681	28808	2.66	3.6E-01	AW812033.1	EST_HUMAN	RC8-ST0171-181099-011-q07 ST0171 Homo sapiens cDNA
							PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2694	15814	28929	1.69	3.6E-01	P24206	SWISSPROT	Drosophila melanogaster sugar transporter 3 (suc3) mRNA, complete cds
2864	18475		8.47	3.6E-01	AF189485.1	NT	H. sapiens melanogaster sugar transporter gene, exons 9 and 10
3558	16723	29738	1.98	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3558	16723	29739	1.98	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4528	17686	30652	1.2	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150800-014-b12 HT0545 Homo sapiens cDNA
4863	17698	30981	0.69	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
5123	18249	31215	3.18	3.6E-01	AW338393.1	EST_HUMAN	ha02g04.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5209	18330	31302	0.92	3.6E-01	BE087689.1	EST_HUMAN	MR4-BT0358-270300-005-GT0 BT0358 Homo sapiens cDNA
5498	18697	31713	0.64	3.6E-01	AJ006555.1	NT	Homo sapiens lipo gene intron 5
							FORMAT HYDROGENLYASE SUBUNIT 5 PRECURSOR (PHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)
6211	16388	32735	0.96	3.6E-01	P16431	SWISSPROT	Homo sapiens PHEX gene
6607	19767	33155	1.63	3.6E-01	Y10186.1	NT	Homo sapiens PHEX gene
7298	20380		3.85	3.6E-01	R94080.1	EST_HUMAN	y74a06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:275987 5'
							w72c10.x1 Soares thymus NHFT Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
7435	20512	33985	1.52	3.6E-01	AW027174.1	EST_HUMAN	O15117 FYN BINDING PROTEIN. [1]:
8419	21500	35032	0.75	3.6E-01	P98167	SWISSPROT	SCO-SPONDIN
8474	21555	35087	16.45	3.6E-01	AL161953.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9179	22257	35799	0.48	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9179	22257	35800	0.48	3.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
9203	22281	35820	3.04	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9203	22281	35821	3.04	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA

Table 4  
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8393	22469	36032	1.23	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8599	22654	36225	1.13	3.6E-01	X17650.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
8599	22654	36226	1.13	3.6E-01	X17650.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
8669	22631		0.58	3.6E-01	X62825.1	NT	C. perfringens plc gene for phospholipase C; upstream region containing bent DNA fragment
10067	23105	36708	16.64	3.6E-01	O53194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
11187	24256	37891	2.42	3.6E-01	BE002360.1	EST_HUMAN	60187641BF1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
11370	24431	38088	3.27	3.6E-01	AB004283.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11729	23915		4.44	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
12173	28205	37640	3.16	3.6E-01	Y18210.1	NT	Homo sapiens Hbb5 gene for hair keratin, exons 1 to 9
12261	25197		7.87	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1656 section 225 of 400 of the complete genome
12420	26297		3.63	3.6E-01	U68888.1	NT	Mus musculus Emr1 mRNA, complete cds
12828	25552		1.98	3.6E-01	11432598	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA
13130	26141		1.4	3.6E-01	AW190228.1	EST_HUMAN	X60611.X1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2678116 3' similar to gb:K00556 TUBULIN
13146	25745		1.38	3.6E-01	Z54173.1	NT	ALPHA-1 CHAIN (HUMAN);
214	13437	26467	3.71	3.5E-01	6678933	NT	Pyrococcus sp. pol gene
695	13678	26911	1.03	3.5E-01	AL161581.2	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
743	13824	26985	1.53	3.5E-01	7706136	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
743	13924	26966	1.53	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
801	13981	27033	4.68	3.5E-01	BF128798.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC51306), mRNA
1670	14822	27805	1.28	3.5E-01	U35776.1	NT	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'
2571	16068	28908	1.34	3.6E-01	AA223252.1	EST_HUMAN	Rattus norvegicus ADP-ribosylation factor-1 directed GTPase activating protein mRNA, complete cds
3795	16956		0.73	3.5E-01	BF214381.1	EST_HUMAN	xr08a09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
4378	17521	30501	2.62	3.5E-01	AF071253.1	NT	601845470F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4076680 5'
5048	18176	31163	4.34	3.5E-01	M18349.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
5323	13549	26376	0.6	3.5E-01	AL161636.2	NT	Rat leukocyte common antigen (L-Ca) gene, exons 1 through 5
5449	18649	31627	1.1	3.5E-01	Q96887	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
5449	18649	31628	1.1	3.5E-01	Q96887	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5667	18861	32146	1.29	3.5E-01	D42045.1	NT	EARLY E2A DNA-BINDING PROTEIN
6367	18537		1	3.6E-01	AW863916.1	EST_HUMAN	Human mRNA for KIAA0088 gene, complete cds
							PM4-SN0012-030400-001-a11 SN0012 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6538	19701	33074	0.79	3.5E-01	AA431933.1	EST_HUMAN	zw7903.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR:G1066935 G1066935 F10F2.1;
6580	19742	33124	0.69	3.5E-01	U37150.1	NT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
6803	19958	33358	0.9	3.5E-01	O24357	SWISSPROT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7201	20066		3.38	3.5E-01	X98905.1	NT	S. scrofa mRNA for CD31 protein (PECAM-1)
7713	20778	34264	0.59	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
7713	20778	34265	0.59	3.5E-01	P47281	SWISSPROT	HISTIDYL-TRNA SYNTHETASE (HISTIDINE-TRNA LIGASE) (HISRS)
8262	21344		2.12	3.5E-01	11448042	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8265	21347	34862	0.82	3.5E-01	BF358871.1	EST_HUMAN	RC4-ET0024-260600-014-d07 ET0024 Homo sapiens cDNA
8682	21742		0.77	3.5E-01	AF051561.1	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
9127	22206	35749	1.17	3.5E-01	4507610	NT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
9337	22970	36567	1.75	3.5E-01	Q02294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BII)
10090	23128	36731	4.78	3.5E-01	Z26825.1	NT	Xlaeis gene for albumin including HP1 enhancer
10172	23209	36802	1.12	3.5E-01	BE174764.1	EST_HUMAN	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
10972	24052	37685	2.82	3.5E-01	X81084.1	NT	C. griseus rhodopsin gene for opsh protein
11274	24342	37981	1.97	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11274	24342	37982	1.97	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11810	24800	38499	1.33	3.5E-01	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
11892	24880	38577	1.44	3.5E-01	N77597.1	EST_HUMAN	ys20ht12.r1 Scores_multiple_sclerosis_2Nbl-MSP Homo sapiens cDNA clone IMAGE:290375 5'
11980	24965	38687	1.53	3.5E-01	L05145.1	NT	Human glucokinase (GCK) gene, repeat polymorphism
12271	26209		1.51	3.5E-01	AF297468.1	NT	Schistosoma mansoni strain NIMRI chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
12344	26249		6.66	3.5E-01	X84565.1	NT	B. taurus alpA1 gene for F(O)F(1) ATP synthase alpha-subunit
12507	26348		2.91	3.5E-01	AE001774.1	NT	Thermoboga maritima section 88 of 138 of the complete genome
12710	26472		1.5	3.5E-01	AE001691.1	NT	Thermoboga maritima section 3 of 138 of the complete genome
13196	26025	31673	3.16	3.5E-01	H80814.1	EST_HUMAN	ys64f11.r1 Scores retina N2b4-HR Homo sapiens cDNA clone IMAGE:219597 5'
13196	26025	31674	3.16	3.5E-01	H80814.1	EST_HUMAN	ys64f11.r1 Scores retina N2b4-HR Homo sapiens cDNA clone IMAGE:219597 5'
725	13907		1.78	3.4E-01	AJ242950.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7, and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
998	14169	27230	8.2	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, colS genes, of222 and partial inaA gene
1000	14171	27232	2.06	3.4E-01	AW380120.1	EST_HUMAN	QV3-HT0261-241189-019-g10 HT0261 Homo sapiens cDNA
1357	14912	27585	2.35	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2474	15601	28726	2.54	3.4E-01	D80909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3065	16241	29281	0.87	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3085	16241	29282	0.87	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3218	16392	29403	1.09	3.4E-01	D90908.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3230	16404	29416	6.1	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3424	16593	29808	0.78	3.4E-01	AF034882.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3620	16784	29800	4.47	3.4E-01	AF106835.1	NT	Methyovirus sp. strain SS1 putative GrpE (grpE), and putative DnaJ (dnaJ) genes, complete cds
3890	17049		1.88	3.4E-01	BF446010.1	EST_HUMAN	7n94a01.x1 NCI_CGAP_OY18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9ULJ15
4163	17313		1.48	3.4E-01	AA584196.1	EST_HUMAN	Q9ULJ15.DJ18C8.1;
4767	17802	30884	1.79	3.4E-01	BE069912.1	EST_HUMAN	no11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
5066	18194		4.3	3.4E-01	A1240973.1	EST_HUMAN	MP4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
5802	18992	32295	2.64	3.4E-01	AL161594.2	NT	qj5c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element;
5932	19118		4.92	3.4E-01	AA085313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6130	19309		2.17	3.4E-01	L02871.1	NT	zn12a11.s1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:547221 3'
6154	19330	32876	0.86	3.4E-01	BE748912.1	EST_HUMAN	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds
6234	19409	32757	1.8	3.4E-01	AW204505.1	EST_HUMAN	60167181T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838828 3'
6364	19534	32893	1.71	3.4E-01	AL120544.1	EST_HUMAN	UH-HB1-act-e-12-0-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6882	20034		1.39	3.4E-01	N95225.1	EST_HUMAN	DKFZp761A249_t1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
7086	20180	33604	1.07	3.4E-01	AI468082.1	EST_HUMAN	zb53a12.s1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:307342 3'
7205	20070	33480	0.8	3.4E-01	BF678702.1	EST_HUMAN	hm3g05.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431
8090	21172		0.48	3.4E-01	AE000463.1	NT	LAMININ RECEPTOR (HUMAN);
8432	21513	35044	0.88	3.4E-01	Y14930.1	EST_HUMAN	602085283F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:4249365 5'
8684	21639	35380	0.71	3.4E-01	L04650.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
8953	22132	35676	1.87	3.4E-01	P26013	SWISSPROT	Homo sapiens TCRAY28 gene, allele A4, partial
9413	22487	36051	4.12	3.4E-01	P26013	SWISSPROT	EST141765 Endometrial tumor Homo sapiens cDNA 5' end
9413	22487	36052	4.12	3.4E-01	P26013	SWISSPROT	Orctulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
9921	22678		0.57	3.4E-01	AB017510.1	NT	Bovine enterovirus strain K2577, complete genome
9645	21088	34602	4.68	3.4E-01	U19492.1	NT	INTEGRIN BETA-8 PRECURSOR
							INTEGRIN BETA-8 PRECURSOR
							Ephedra fluviatilis mRNA for PLC-gamma3, complete cds
							Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds



Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9845	21088	34603	4.88	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9897	22937	36522	0.88	3.4E-01	U68763.1	NT	Glycine max putative transcription factor SCOF-1 (scf-1) mRNA, complete cds
10093	23131	36735	2.44	3.4E-01	AJ228084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 19
10695	23728		0.73	3.4E-01	AE004086.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
11287	24338		3.28	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
11307	24372	38014	2.1	3.4E-01	P06925	SWISSPROT	PROBABLE E4 PROTEIN
11350	24412	38086	1.86	3.4E-01	AF045931.1	NT	Rutillus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11561	24616	38295	1.91	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11561	24616	38296	1.91	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11791	24781	38478	1.68	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-galactin/MUC18, complete cds
11817	24808	38502	3.23	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
12078	25058	38765	1.59	3.4E-01	BF081948.1	EST_HUMAN	7k68d12.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:3480646 3'
12110	25090	38793	1.65	3.4E-01	Q27548	SWISSPROT	INOSINE-URIDINE PREFERRING NUCLEOSIDE HYDROLASE (IU-NUCLEOSIDE HYDROLASE)
12150	25120		2.03	3.4E-01	U83604.1	NT	(PURINE NUCLEOSIDASE)
12284	25198		1.55	3.4E-01	Z21621.1	NT	Citrus variegation virus putative replicase gene, partial cds
12387	25912		1.16	3.4E-01	AF254351.1	NT	S. cerevisiae RIB5 gene encoding Riboflavin synthase
12489	25338		10.71	3.4E-01	L26339.1	NT	Schizosaccharomyces pombe Cwi8p (cwi8) gene, complete cds
12517	25944		2.38	3.4E-01	BE218652.1	EST_HUMAN	Human autogenous mRNA, complete cds
12579	26052		1.79	3.4E-01	8838361	NT	h42h08.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13
12700	25466	32023	1.36	3.4E-01	AJ297131.1	NT	PTR5 repetitive element
12954	26160		1.86	3.4E-01	AJ288948.1	NT	Beta vulgaris mitochondrion, complete genome
13055	25691		2.26	3.4E-01	AF019413.1	NT	Mus musculus SIL, MAP_17, CYP_a, SOL, CYP_b genes
15	13253	26253	6.72	3.3E-01	X07990.1	NT	Clostridium cellulolyticum partial spoIVB gene and spoIV gene, strain ATCC 35319
108	13263	26263	3.19	3.3E-01	X07990.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes>
461	13656	26694	1.41	3.3E-01	AL161545.2	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
650	13836	26863	1.97	3.3E-01	7652485	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
1227	14387	27450	2.57	3.3E-01	Q12446	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
1335	14492	27582	3.39	3.3E-01	BF568880.1	EST_HUMAN	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
							PROLINE-RICH PROTEIN LAS17
							80218401811 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1638	14788	27873	1.28	3.3E-01	8753685	NT	Mus musculus disintegrin 5 (Digm5), mRNA
1674	14828		1.43	3.3E-01	6754477	NT	Mus musculus kappa B and Res recognition component (Krc), mRNA
1777	14926		1.02	3.3E-01	AA32734.1	EST_HUMAN	EST36722 Embryo, 8 week Homo sapiens cDNA 5' end
2477	15504		6.23	3.3E-01			Homo sapiens uridine monophosphate synthetase (cotlate phosphoribosyl transferase and orotidine-5'- decarboxylase) (UMPS) mRNA
3014	16180	29215	1.61	3.3E-01	4507834	NT	Bacteriophage phi-Yeo3-12 complete genome
3080	16256		1.09	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3121	16297	29311	0.78	3.3E-01	AJ007932.2	NT	Streptomyces argillaceus mitochondrial biosynthetic genes
3584	16749	29768	1.04	3.3E-01	AB012922.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3911	17070	30088	2.72	3.3E-01	O84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3921	17080	30076	0.82	3.3E-01	P22302	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
4072	17288	30235	1.19	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4108	17282	30282	1.81	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4487	17827		2.37	3.3E-01	D31682.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4812	17845		1.91	3.3E-01	A1539114.1	EST_HUMAN	lp78b12.x1 NCL CGAP U13 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
4843	17876	30806	1.02	3.3E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTP3) mRNA, complete cds
4960	18089	31085	1.14	3.3E-01	D84003.1	NT	Synedochystis sp. PCC6803 complete genome, 22/27, 2755703-2868766
5439	18639	31617	2.55	3.3E-01	X89819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5439	18639	31618	2.55	3.3E-01	X89819.1	NT	R. norvegicus mRNA for 3'UTR of ubiquitin-like protein
5507	19006	32411	0.68	3.3E-01	BF213973.1	EST_HUMAN	601848090F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078823 5'
6057	19249	32578	1.37	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6057	19249	32577	1.37	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6162	19338	32684	1.29	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
6932	20247	33680	0.59	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
6932	20247	33681	0.59	3.3E-01	AB034233.1	NT	Flexibacter littoralis gyrB gene for DNA gyrase B subunit, partial cds
7029	20165	33586	4.63	3.3E-01	A1628131.1	EST_HUMAN	ly84h01.x1 NCL CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
7029	20165	33587	4.63	3.3E-01	A1628131.1	EST_HUMAN	ly84h01.x1 NCL CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
7961	21011	34521	1.9	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8759	21838	35379	23.1	3.3E-01	BF883954.1	EST_HUMAN	802140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
8926	22005	35544	0.73	3.3E-01	BF210322.1	EST_HUMAN	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4087180 5'
9314	22300	35941	0.83	3.3E-01	Q62925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1)(MEK KINASE 1) (MEKK 1)
9578	22720	36288	1.16	3.3E-01	BE828461.1	EST_HUMAN	CM3-E10041-180500-187-d10 ET0041 Homo sapiens cDNA
9578	22720	36288	1.16	3.3E-01	BE828461.1	EST_HUMAN	CM3-E10041-180500-187-d10 ET0041 Homo sapiens cDNA
9711	22760	36330	2.9	3.3E-01	N69866.1	EST_HUMAN	za67h01.s1 Soares_fetal_lung_NBHL19W Homo sapiens cDNA clone IMAGE:287649 3'
9752	22690	36260	2.81	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
10198	23233		2.08	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
10885	23897	37520	0.74	3.3E-01	AE000831.1	NT	Helicobacter pylori 26695 section 109 of 134 of the complete genome
10860	24041	37675	3.35	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10960	24041	37676	3.35	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
11278	24345		2.1	3.3E-01	BF826469.1	EST_HUMAN	602070802F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4213585 5'
11507	24565	38242	9.35	3.3E-01	BE219351.1	EST_HUMAN	hvt51g02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
							GALECTIN-3 (GALECTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (ICE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-2B) (CBP30)
11628	24705	38399	3.7	3.3E-01	P47953	SWISSPROT	cb71g02.s1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:1336850 3'
12018	25002		2.8	3.3E-01	AA806621.1	EST_HUMAN	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
12038	13253	28253	2.33	3.3E-01	X07990.1	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
12250	25190	38357	1.85	3.3E-01	8598319	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-54400C nt, position (217)
13044	25685		22.03	3.3E-01	AP000002.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
469	13664		2.6	3.2E-01	AF018261.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
738	13918		0.76	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1188	14350	27408	23.03	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1311	14457	27535	1.48	3.2E-01	Z60202.1	NT	P.vulgaris arc5-1 gene
1421	14675	27648	6.74	3.2E-01	Q48924	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1683	14815		1	3.2E-01	AF209730.1	NT	Arabidopsis thaliana cultivar Columbia RPP13 (RPP13) gene, complete cds
1815	14864	28057	1.3	3.2E-01	Z6041.1	NT	S.cerevisiae chromosome II reading frame ORF YBR172c
1825	14974	28069	6.42	3.2E-01	AW957194.1	EST_HUMAN	EST1368284 MAGe resequences, MAGD Homo sapiens cDNA
1825	14974	28070	6.42	3.2E-01	AW957194.1	EST_HUMAN	EST1368284 MAGe resequences, MAGD Homo sapiens cDNA
1891	15035	28142	1.25	3.2E-01	AL111655.1	NT	Bdittys chinensis strain T4 cDNA library under conditions of nitrogen deprivation
2227	15361	28480	3.22	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2606	15729		2.83	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pbxox1), mRNA
2774	16889	28000	1.23	3.2E-01	AF080568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3898	16857		0.76	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4081	17217		0.83	3.2E-01	AL161646.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
4614	17653	30641	1.37	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4621	17783	30740	1.35	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4880	17893		0.89	3.2E-01	BF693617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
5386	18598	31560	2.93	3.2E-01	BE173964.1	EST_HUMAN	CMO-HT0569-060300-269-110 HT0569 Homo sapiens cDNA
6078	19260	32589	1.08	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6433	19601	32865	0.73	3.2E-01	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete cds
6729	19886	33277	0.65	3.2E-01	AV718037.1	EST_HUMAN	AV718037 FHIA Homo sapiens cDNA clone FHTAABH01 5'
6872	20024		1.17	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0381 gene, KIAA0381 protein
8040	21123	34843	0.52	3.2E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8365	21446	34969	1.6	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
8461	21542	35072	0.87	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat map NOS-D12W.alpha1
8562	21643	35182	15.01	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8565	21648	35187	14.52	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8656	21736		1.24	3.2E-01	AL161874.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8698	21778	36310	0.69	3.2E-01	BF246771.1	EST_HUMAN	601865580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8698	21778	36311	0.69	3.2E-01	BF246771.1	EST_HUMAN	601865580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8771	21850	35391	1.14	3.2E-01	AE002015.1	NT	Delphococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
8871	21950	35485	0.85	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH8-a2) gene, partial cds
8871	21950	35486	0.88	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH8-a2) gene, partial cds
9267	22344	35895	0.67	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment H521C004
9278	22354		2.64	3.2E-01	M88511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9351	22426	35983	0.61	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9351	22426	35984	0.61	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
10198	23235	36824	4.33	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes
10402	23437	37044	0.62	3.2E-01	BE326230.1	EST_HUMAN	h09005.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181589 3'
10518	23553		3.94	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10905	23988	37620	3.05	3.2E-01	T06813.1	EST_HUMAN	EST04702 Fetal brain, Stragelene (cat#36206) Homo sapiens cDNA clone HFBDDZ21
12289	26083		3.11	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12881	25572		3.26	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12969	25891		2.2	3.2E-01	AF157625.1	NT	Bos taurus inositol 1,4,5-trisphosphate receptor type I mRNA, complete cds
13018	25669		2.07	3.2E-01	L39874.1	NT	Homo sapiens deoxydylate deaminase gene, complete cds
13089	26129	31545	1.24	3.2E-01	BE985776.1	EST_HUMAN	801275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2738	15853	28987	3.39	3.1E-01	R18051.1	EST_HUMAN	ye90h06.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to
2782	16001	28985	3.77	3.1E-01	7681971	NT	gb:M84241 QM PROTEIN (HUMAN);
2782	16001	28986	3.77	3.1E-01	7681971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2920	16098		1.28	3.1E-01	AW629038.1	EST_HUMAN	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
3242	48416		3.61	3.1E-01	AB029069.1	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
4016	17173	30181	0.84	3.1E-01	AJ251589.1	NT	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 6
5077	18205	31177	0.7	3.1E-01	AE003984.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5695	18780	31838	9.24	3.1E-01	AF176111.1	NT	Xyella fastidiosa, section 130 of 228 of the complete genome
5717	18910	32205	0.7	3.1E-01	P44132	SWISSPROT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5718	18911	32208	0.75	3.1E-01	Z74883.1	NT	HYPOTHETICAL PROTEIN HI236
5729	18922		0.83	3.1E-01	Y13278.1	NT	S cerevisiae chromosome XV reading frame, ORF YOL141w
5892	19080	32390	2.65	3.1E-01	AF184122.1	NT	Mus musculus mRNA for polycystin
6595	19755	33141	1.3	3.1E-01	AW983549.1	EST_HUMAN	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6883	19822	33209	0.96	3.1E-01	A1284458.1	EST_HUMAN	RC3-HN0001-310300-011-604 HN0001 Homo sapiens cDNA
6821	19974	33382	0.78	3.1E-01	X71887.1	NT	q138401.x1 NCL CGAP_Co8 Homo sapiens cDNA clone IMAGE:1874693 3'
6905	20220		0.89	3.1E-01	AW37354.1	EST_HUMAN	H. sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
7109	25801	31491	2.32	3.1E-01	BE737392.1	EST_HUMAN	MR2-CT0222-281099-005-H05 CT0222 Homo sapiens cDNA
7856	20911	34416	0.7	3.1E-01	4885380	NT	601308121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
8849	21928	35467	0.84	3.1E-01	R45318.1	EST_HUMAN	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
10108	23144	36742	0.68	3.1E-01	6679322	NT	Yp48701.a1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:35839 3'
10272	23307	36903	1.04	3.1E-01	BF69639.1	EST_HUMAN	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
10272	23307	36904	1.04	3.1E-01	BF69639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10334	23369	36979	1.68	3.1E-01	A1244001.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10510	23545		0.98	3.1E-01	T66325.1	EST_HUMAN	q181e11.x1 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S66700
11076	24151	37789	1.84	3.1E-01	BF216117.1	EST_HUMAN	HYDROXYMETHYL GLUTARYL-COA LYASE PRECURSOR (HUMAN);
							Yp47H08.e1 Stragelene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:74387 3' similar to similar
							to gb:MD91038_ma2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
							601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11474	24533	38203	1.62	3.1E-01	AW074910.1	EST_HUMAN	xs62g09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2571424 3'
11827	24818	38507	2.08	3.1E-01	7682297	NT	Homo sapiens KIA00764 gene product (KIA00764), mRNA
11828	24817	38508	1.67	3.1E-01	R55735.1	EST_HUMAN	y88b05.t1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:40722 5' similar to contains Alu repetitive element
12123	25103		1.3	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12418	25285		1.22	3.1E-01	AF294308.1	NT	Anolis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
12455	25319		1.73	3.1E-01	AF304162.1	NT	Stizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
12813	25412		3.73	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
13028	26877		3.82	3.1E-01	AF196778.1	NT	Homo sapiens transcription factor IGIM enhancer 3, JM11 protein, JM4 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
13068	26123		1.22	3.1E-01	10946823	NT	Mus musculus peptidoglycan recognition protein-like (Pglypr)-pending, mRNA
74	16978	26336	1.65	3.0E-01	6756083	NT	Mus musculus protein kinase C, epsilon (Pkc), mRNA
264	13483	26515	11.52	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1251	14410	27472	2.35	3.0E-01	AW300400.1	EST_HUMAN	xs63f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1537	14690	27769	5.77	3.0E-01	AJ008755.1	NT	Belaeoptera physalus gene encoding atrial natriuretic peptide
1838	14984	28084	1.2	3.0E-01	X90882.1	NT	A. Imnerius putative gene encoding integrase, Mars2 (RP)
3059	16245		0.8	3.0E-01	AB008877.1	NT	Bos taurus mRNA for UDP-glucuronosyltransferase, complete cds
3283	18457		1.33	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alyFG gene for polygluturonate lyase, complete cds
3968	17123	30129	1.58	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0292-261189-001-g01 ST0292 Homo sapiens cDNA
4082	17237	30243	1.16	3.0E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4636	17772	30752	1.79	3.0E-01	AJ006755.1	NT	Belaeoptera physalus gene encoding atrial natriuretic peptide
5258	16949	29685	2.33	3.0E-01	P23825	SWISSPROT	GATA BINDING FACTOR-3 (TRANSCRIPTION FACTOR NF-E1C) (GATA-3)
5487	18687	31646	5.1	3.0E-01	BE741628.1	EST_HUMAN	601594960F1 NIH_MGC_B Homo sapiens cDNA clone IMAGE:3948734 5'
5648	18745		0.64	3.0E-01	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
5552	18749	31785	1	3.0E-01	AF229247.1	NT	Canigato orthopoxvirus hemagglutinin gene, complete cds
5821	18815	31883	4.01	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5621	18815	31884	4.01	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5658	18852	32135	3.87	3.0E-01	U01247.1	NT	Mus musculus 129/ev Clara cell 10 kd protein (mCC10) gene, complete cds
6970	20198	33624	2.82	3.0E-01	D16313.1	NT	Mouse cyclophilin 15 gene, complete cds
6999	18518	31511	0.78	3.0E-01	U02369.1	NT	Strongylocentrotus purpuratus 34/67 kDa laminin-binding protein mRNA, partial cds
7085	20118	33532	1.15	3.0E-01	AF229247.1	NT	Canigato orthopoxvirus hemagglutinin gene, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7270	20353	33808	0.95	3.0E-01	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
7481	20558	34028	4.3	3.0E-01	10947007	NT	Mus musculus midkalin (Midn-pending), mRNA
7670	20739	34214	1.51	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
8111	21103	34713	1.34	3.0E-01	AE001755.1	NT	Thermoplasma maritima section 67 of 139 of the complete genome
8558	21649						Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clactf8), mRNA
8558	21738	35279	0.48	3.0E-01	9910161	NT	H. sapiens gene for U5 snRNP-specific 200KD protein
8671	21751	35288	1.23	3.0E-01	BE586083.1	EST_HUMAN	601339078F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3881594 5'
9029	22108	35649	0.69	3.0E-01	AF141676.1	NT	Streptomyces sulfonolactams isopenicillin N synthase (pcbc) gene, partial cds
9072	22151		0.82	3.0E-01	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
9419	22493	36050	1.09	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dmrB) gene, complete cds; putative antranilate phosphoribosyltransferase gene, partial cds; and unknown gene
9773	22813	36391	0.64	3.0E-01	P76389	SWISSPROT	HYPOPHETICAL 69.5 KO PROTEIN IN WZA-ASMA INTERGENIC REGION
9927	22967		0.46	3.0E-01	D90804.1	NT	Synochocystis sp. PCC6803 complete genome, 6/27, 630555-781448
10173	23210	36803	0.84	3.0E-01	BF574612.1	EST_HUMAN	602133271F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4289336 5'
10346	23381	36992	0.45	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetocorritans TadA (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10346	23381	36993	0.45	3.0E-01	AF152598.3	NT	Actinobacillus actinomycetocorritans TadA (tadA), TadB (tadB), TadC (tadC), TadD (tadD), TadE (tadE), TadF (tadF), and TadG (tadG) genes, complete cds
10606	23640	37248	0.8	3.0E-01	AW18111.1	EST_HUMAN	xe03d10.x1 Soares_NFL_T_GSC_ST Homo sapiens cDNA clone IMAGE:2605035 3'
10608	23642	37250	2.51	3.0E-01	AB030231.1	NT	Aspergillus oryzae bifa gene for ER chaperone BIP, complete cds
10629	23663	37271	0.76	3.0E-01	BF683841.1	EST_HUMAN	602140733F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
10629	23663	37272	0.76	3.0E-01	BF683841.1	EST_HUMAN	602140733F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
12067	25043	38755	2.16	3.0E-01	H51029.1	EST_HUMAN	y984b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12067	25048	38766	2.16	3.0E-01	H51029.1	EST_HUMAN	y984b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
12470	25324		1.3	3.0E-01	P54660	SWISSPROT	PONTICULIN PRECURSOR
12731	26062		1.88	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
13061	26121		4.49	3.0E-01	6677766	NT	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA
1771	14920		0.94	2.9E-01	AJ249695.1	NT	Mus musculus mas proto-oncogene and lgt2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1830	15073	28178	0.94	2.9E-01	5174502	NT	Homo sapiens membrane component, chromosome 11, surface marker 1 (M11S1) mRNA
2080	15220	28340	2.36	2.6E-01	AE000736.1	NT	Aquifex aeolicus section 98 of 109 of the complete genome
2322	16454	28565	1.01	2.9E-01	AF222718.1	NT	Chrysididymus synurideus mitochondrial, complete genome
3253	18427	29445	0.96	2.9E-01	AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3323	18496	29513	2.88	2.9E-01	AW764239.1	EST_HUMAN	PM1-CT0328-171289-001-112 CT0328 Homo sapiens cDNA
3323	18496	29514	2.88	2.9E-01	AW764239.1	EST_HUMAN	PM1-CT0328-171289-001-112 CT0328 Homo sapiens cDNA
4003	17160	30169	1.12	2.9E-01	AI610838.1	EST_HUMAN	lp21a11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;
4045	17201	30212	0.61	2.9E-01	AI769472.1	EST_HUMAN	W14d10.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402803 3' similar to WP:C34F6.7 CE15376;
4183	17333	30325	0.61	2.9E-01	AB016428.1	NT	Cavia porcellus mRNA for glutathione S-transferase, complete cds
4195	17345		0.79	2.9E-01	AW002902.1	EST_HUMAN	wr02f10.x1 NCL_CGAP_GCB8 Homo sapiens cDNA clone IMAGE:2480385 3'
4808	17745	30724	0.88	2.9E-01	AA284468.1	EST_HUMAN	z857d12.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;
4805	17940		0.73	2.9E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4957	18087	31083	0.59	2.9E-01	AB019029.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5222	18344		0.89	2.9E-01	AI670899.1	EST_HUMAN	w80603.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2287309 3' similar to contains L1.L2.L1 repetitive element;
5320	18087	31063	0.65	2.9E-01	AB019029.1	NT	Mus musculus gene, complete cds, similar to EXLM1
5372	18576		1.59	2.9E-01	R37485.1	EST_HUMAN	y177e12.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28281 3'
5511	20137	33555	0.88	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
5884	18073	32381	5.27	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5884	18073	32382	5.27	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16,18,28,30 and levanase
5897	19085	32397	5.53	2.9E-01	6879662	NT	Mus musculus Eph receptor A8 (Epha8), mRNA
6181	18357	32705	1.55	2.9E-01	AA418145.1	EST_HUMAN	z197b12.r1 Soares NIHMPUL ST Homo sapiens cDNA clone IMAGE:78771 5'
6411	19580	32941	1.07	2.9E-01	AI797128.1	EST_HUMAN	w827c05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.L1.L1 repetitive element;
6456	19622	32986	2.22	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
7001	20137	33555	0.71	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
7126	18552	31468	1.4	2.9E-01	AF142329.1	NT	Mus musculus Filin protein (Filin) gene, complete cds; and Ligh protein (Ligh) gene, partial cds
7245	20328	33773	3.11	2.9E-01	Q04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR506C
7310	20362	33852	1.54	2.9E-01	AF100958.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bng1 (BING1), tapasin (tapasin), Rel3D5-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3- galactosyl transferase (beta1,3-galactosyl tr>
8104	21168	34705	1.61	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8104	21166	34706	1.61	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'



Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8343	21424	34949	0.84	2.9E-01	AJ237637.1	NT	Bos taurus partial stat5A gene, exons 5-19
8343	21424	34950	0.64	2.9E-01	AJ237637.1	NT	Bos taurus partial stat5A gene, exons 5-19
8356	21437		0.75	2.8E-01	BF217743.1	EST_HUMAN	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085113 5'
							Buchnera aphidicola plasmid pLyu Isolate M1 2-Isopropylmalate synthase (IeuA) gene, partial cds; 3-Isopropylmalate dehydrogenase (IeuB) gene, complete cds; and Isopropylmalate dehydratase subunit (IeuC) gene, partial cds
8534	21615		0.53	2.9E-01	AF197456.1	NT	AL150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
8784	21873	35412	0.82	2.9E-01	AU160810.1	EST_HUMAN	Arabidopsis thaliana sulfonyleurea receptor-like protein mRNA, complete cds
9125	22204	35747	1.09	2.8E-01	AF225908.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9233	22311	35853	0.81	2.9E-01	M22452.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9447	22563	36125	0.98	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9447	22563	36126	0.98	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
10405	23440	37047	0.46	2.9E-01	AW294100.1	EST_HUMAN	UI-H-BJ2-shg-b-02-0-UI.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2723714 3'
10405	23440	37048	0.46	2.9E-01	AW294100.1	EST_HUMAN	UI-H-BJ2-shg-b-02-0-UI.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2723714 3'
11133	24205	37830	1.94	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11433	24494	38159	1.79	2.9E-01	V01394.1	NT	Tarpedo californica mRNA encoding acetylcholine receptor gamma subunit
11433	24494	38160	1.79	2.9E-01	V01394.1	NT	Tarpedo californica mRNA encoding acetylcholine receptor gamma subunit
11881	24869	38568	2.71	2.9E-01	AA095373.1	EST_HUMAN	my35102.s1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8 repetitive element;
11888	24874	38571	3.12	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
11900	24888	38587	2.09	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
11900	24888	38588	2.09	2.9E-01	U35025.1	NT	Rattus norvegicus activin receptor-like kinase 7 (ALK7) mRNA, complete cds
							w288105.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element MER28 repetitive element;
12677	25452	32017	1.85	2.9E-01	AW005671.1	EST_HUMAN	D. melanogaster: part of the 44D cuticle gene cluster encoding cuticle gene 1
12774	25516		1.89	2.9E-01	V00202.1	NT	Homo sapiens TNF- $\alpha$ -inducible RNA binding protein (TIRP) gene, complete cds
12777	25519	32001	2.23	2.9E-01	AF082453.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
13126	25734	31944	1.24	2.9E-01	V08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
13126	25734	31945	1.24	2.9E-01	V08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
13204	25785	31819	1.4	2.9E-01	AF200418.1	NT	Callinectes sapidus cadmium-inducible metallothionein CdMT-1 mRNA, complete cds
862	13774		2.04	2.9E-01	U67138.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
567	13778		1.86	2.8E-01	L28145.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1107	14272	27331	3.34	2.8E-01	AF168080.1	NT	Guinea guinea oocyte maturation factor Moe (c-moe) gene, partial cds
1306	14462	27528	2.19	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 6'
1306	14462	27530	2.19	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1319	14475	27541	1.2	2.8E-01	D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1766	14915	28011	1.87	2.8E-01	AW860020.1	EST_HUMAN	QV1-CT0384-12020-065-505 CT0384 Homo sapiens cDNA
2069	15210	28326	1.49	2.8E-01	AL047620.1	EST_HUMAN	DKFZp586i2321_r1 386 (synonym: huter1) Homo sapiens cDNA clone DKFZp586i2321
2200	15335	28462	1.51	2.8E-01	AW611195.1	EST_HUMAN	hd44b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2542	15567	28781	2.98	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2542	15567	28792	2.98	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2812	15736		2.95	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2730	15948	28988	1.16	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
3035	16211		1.37	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
3036	16212	29234	2.52	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3036	16212	29235	2.52	2.8E-01	Z14037.1	NT	B. taurus microsatellite (ETH121)
3468	16633	29652	1.05	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt, position (4/7)
4103	17257	30257	1.67	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 68 of 70) of the complete genome
4240	17389		0.6	2.8E-01	AE004430.1	NT	Pseudomonas aeruginosa PA01, section 11 of 629 of the complete genome
4315	17458		2.17	2.8E-01	AI090868.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640228 3' similar to contains Alu repetitive element; contains element MER22, repetitive element;
4582	17719	30702	2	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4944	18074	31049	0.92	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4950	18080	31056	4.95	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4984	18113	31080	1.52	2.8E-01	BF528188.1	EST_HUMAN	802042601F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4160129 5'
5008	18135	31108	3.66	2.8E-01	AI272680.1	EST_HUMAN	q159c11.x1 Soares_NhlHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element;
5318	18473	31404	0.61	2.8E-01	X60787.1	NT	Mouse Kv3.3 gene for potassium channel protein, exon 2
5426	18604	31602	23.81	2.8E-01	AA349897.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA, 5' end
5723	18916	32211	2.57	2.8E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
5938	19124		0.93	2.8E-01	AW992583.1	EST_HUMAN	GM1-BN0024-150200-118-912 BN0024 Homo sapiens cDNA
6042	19225	32548	0.66	2.8E-01	AA765296.1	EST_HUMAN	oa01d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to qb:M34639 FK608-BINDING PROTEIN (HUMAN);
6059	19241		0.64	2.8E-01	AA404676.1	EST_HUMAN	z141f01.11 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724921 5' similar to contains Alu repetitive element;
6305	19212		0.67	2.8E-01	M36868.1	NT	Bovine 680 bp repeated unit of 1,723 satellite DNA
6347	19517	32874	1.85	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6347	19517	32875	1.65	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6870	20022	33432	7.84	2.8E-01	BF611216.1	EST_HUMAN	UI-H-B14-adi-F-04-0-U1.st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3086182 3'

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7145	20280	33721	0.64	2.8E-01	U65300.1	NT	Orthomyx heterodius cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
7599	20669		1.14	2.8E-01	U05633.1	NT	Mareilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, chloroplast gene encoding chloroplast protein, partial cds
8284	21366	34884	1.31	2.8E-01	AJ348126.1	EST_HUMAN	qp48h01.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1928289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8284	21366	34885	1.31	2.8E-01	AJ348126.1	EST_HUMAN	qp48h01.x1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1928289 3' similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8404	21485	35014	2.31	2.8E-01	U51688.1	NT	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
8712	21792	35328	0.6	2.8E-01	AA911929.1	EST_HUMAN	af02h05.s1 NCL_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1418983 3' similar to gb:M87789 IG GAMMA-1 CHAIN C REGION (HUMAN);
8780	21868		7.72	2.8E-01	BF347847.1	EST_HUMAN	602022687F1 NCL_CGAP_Bir67 Homo sapiens cDNA clone IMAGE:4158523 5'
8668	22628	36100	1.14	2.8E-01	U17251.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scn-2) gene, complete cds
8912	22952		1.16	2.8E-01	L13654.1	NT	Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
10092	23130	36733	0.88	2.8E-01	AF132728.1	NT	Escherichia coli translocated htrA receptor Tir (tir) gene, complete cds
10092	23130	36734	0.88	2.8E-01	AF132728.1	NT	Escherichia coli translocated htrA receptor Tir (tir) gene, complete cds
10152	23189	36766	0.46	2.8E-01	AE001310.1	NT	Chlamydia trachomatis section 37 of 87 of the complete genome
10156	23193	36789	0.7	2.8E-01	AF294393.1	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
10285	23300	36888	3.8	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319), mRNA
10319	23594		1.1	2.8E-01	8626184	NT	Fujinami sarcoma virus, complete genome
10361	23596	37202	0.5	2.8E-01	BE969727.2	EST_HUMAN	601654822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3639705 3'
10882	24061	37605	1.88	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
10882	24061	37686	1.88	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
11011	24080	37727	3.01	2.8E-01	BF695970.1	EST_HUMAN	601852148F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4076026 5'
11119	24191	37823	1.53	2.8E-01	AF051662.1	NT	Drosophila heteronema fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11556	24811		3.58	2.8E-01	BF674023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
11851	24840	38533	1.55	2.8E-01	AJ248285.1	NT	Pyrococcus abyssi complete genome; segment 3/6
11851	24840	38534	1.55	2.8E-01	AJ248285.1	NT	Pyrococcus abyssi complete genome; segment 3/6
12715	25475		12.79	2.8E-01	D88329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12846	25552	31987	7.61	2.8E-01	BE178699.1	EST_HUMAN	PM4-HT0606-030400-001-a07 HT0606 Homo sapiens cDNA
12876	25682	31996	1.29	2.8E-01	BE800116.1	EST_HUMAN	601673020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955996 5'
13052	26069		1.59	2.8E-01	11433628	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
489	13693	26717	4.34	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
628	13613	26835	13.84	2.7E-01	AA450061.1	EST_HUMAN	zxc3b710 at Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element;
1280	14448	27512	2.04	2.7E-01	AB004906.1	NT	[pomoea purpurea transposable element Tip100 gene for transposase, complete cds
1650	14803		1.63	2.7E-01	X79815.1	NT	Giantbilia SR2 gene
1788	14917	28012	3.16	2.7E-01	W58067.1	EST_HUMAN	zd22h10.1f Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1817	14866	28059	1.46	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2204	15057		3.1	2.7E-01	AF047676.1	NT	Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1
2250	15383	28510	0.94	2.7E-01	A1372772.1	EST_HUMAN	EST175679 Infant brain, Bento Soares Homo sapiens cDNA clone UH1B01R 5' end
2250	15383	28511	0.94	2.7E-01	A1372772.1	EST_HUMAN	EST175679 Infant brain, Bento Soares Homo sapiens cDNA clone UH1B01R 5' end
2440	15568	28695	7.07	2.7E-01	Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITTO088PIU (M88), partial
2526	16651	28775	4.36	2.7E-01	A1310858.1	EST_HUMAN	le43o1.1.x2 NCL CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element;
3049	16225		0.98	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
3361	16533	29547	0.66	2.7E-01	8393820	NT	Rattus norvegicus Insulin receptor (Insr), mRNA
4118	17272	30271	1.94	2.7E-01	A1928015.1	EST_HUMAN	wc92e11.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4133	17286	30281	0.68	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4133	17286	30282	0.68	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4140	17292	30286	2.39	2.7E-01	L77669.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
5153	18275		4.46	2.7E-01	AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 GT0286 Homo sapiens cDNA
5391	18583	31452	1.98	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (CHOX-1/4)
5607	18802		1.31	2.7E-01	AB033171.1	NT	Asiaporea mytilophthalma mitochondrial cytb gene for cytochrome b, partial cds
6472	19539	32898	0.86	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6472	19539	32899	0.86	2.7E-01	Q00918	SWISSPROT	LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1-BP-1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT)
6745	19801	33293	1.05	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6745	19801	33294	1.05	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6918	20233	33667	1.74	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
7197	20062		0.77	2.7E-01	A1540070.1	EST_HUMAN	id08h08.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2075103 3'
7611	20565	34058	0.92	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X

Table 4  
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7734	20785	34283	0.87	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7734	20785	34284	0.87	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7885	20919	34425	2.1	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cde
7885	20919	34426	2.1	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7917	20958	34474	0.72	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to similar to myosin-binding protein H
7917	20958	34475	0.72	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to similar to myosin-binding protein H
7978	21026	34540	0.68	2.7E-01	L01081.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
8048	21131	34651	0.68	2.7E-01	AA013147.1	EST_HUMAN	zsa3b11. s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360857 3' similar to contains Alu repetitive element;
8330	21412	34938	0.56	2.7E-01	AW66803.1	EST_HUMAN	MR1-SN0062-100500-002-d09 SN0062 Homo sapiens cDNA
8380	21461	34984	0.60	2.7E-01	R39257.1	EST_HUMAN	yeg1h06. s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:23511 3'
8486	21567	35104	0.83	2.7E-01	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8959	22038	35580	1.4	2.7E-01	Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MV2) (LUNG RESISTANCE-RELATED PROTEIN)
9534	22599	36171	10.56	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9534	22599	36172	10.56	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9537	22602		2.68	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
10005	23043	36636	0.8	2.7E-01	D88660.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
10286	23321	36923	0.9	2.7E-01	AF091948.1	NT	Oryctolagus cuniculus calgranulin C mRNA; partial cds
10323	23358	36968	2.06	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-A1c isoform a (NF-A1c) mRNA, complete cds
10455	23490	37099	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10456	23490	37100	1.06	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 8
10749	23782		0.51	2.7E-01	AB011678.1	NT	Rattus norvegicus mRNA for class I beta-tubulin, complete cds
10765	23798	37418	0.58	2.7E-01	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
10765	23798	37419	0.58	2.7E-01	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
11050	24127	37761	1.99	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11050	24127	37762	1.99	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
11081	24137	37772	2.58	2.7E-01	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12816	25942		1.49	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
13034	25681		2.75	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
482	18013	28710	2.8	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
493	13688		1.94	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1424	14578	27651	1.77	2.6E-01	BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1468	14622	27705	1.09	2.6E-01	AB013280.1	NT	Glycine max pseudogene for Bd 30K
1845	15088	28188	7.69	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1846	15088	28189	7.69	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2858451 3' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2159	15295		10.39	2.6E-01	AW733152.1	EST_HUMAN	Human prealbumin gene, complete cds
2220	15354	28485	1.13	2.6E-01	M11844.1	NT	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2950043 5'
2811	16735		11.66	2.6E-01	BE272440.1	EST_HUMAN	EST3386835 IMAGE resequences, MAGM Homo sapiens cDNA
3161	18336		1.11	2.6E-01	AW974531.1	EST_HUMAN	Bacteriophage T2 DNA-(adenine-N8)methyltransferase (dam) gene, complete cds
3871	18834	29845	0.84	2.6E-01	M22342.1	NT	
3733	18894	29899	1.67	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
4215	17384	30352	0.79	2.6E-01	AW959510.1	EST_HUMAN	EST371580 IMAGE resequences, MAGF Homo sapiens cDNA
4270	17415	30404	16.93	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
							Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4478	17619	30597	1.71	2.6E-01	AF175283.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4817	17754	30735	0.69	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4617	17754	30736	0.69	2.6E-01	AB021180.1	NT	
4870	17805	30794	1.14	2.6E-01	AA457817.1	EST_HUMAN	ae89d07.r1 Strabagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:839477 5'
4770	17905	30887	2.25	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
4837	17970	30958	1.15	2.6E-01	AF142703.1	NT	Ophrestia radiosa maturase-like protein (mtkK) gene, complete cds; chloroplast gene for chloroplast product id16a03.x1 NC1 CGAP_C018 Homo sapiens cDNA clone IMAGE:152288 5'
5086	18214	31187	3.63	2.6E-01	H04858.1	EST_HUMAN	yf51e05.r1 Soares placenta Nb2-HP Homo sapiens cDNA clone IMAGE:152288 5'
6165	18277		0.81	2.6E-01	AA884625.1	EST_HUMAN	am33b11.e1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1468605 3'
5457	18657		1.28	2.6E-01	AB035972.1	NT	Paramecium caudatum gene for PAP, complete cds
5565	18702	31802	0.97	2.6E-01	M96060.1	NT	Acetabacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CcpAx genes, complete cds id16a03.x1 NC1 CGAP_C018 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element;
5689	18883		0.84	2.6E-01	AI862398.1	EST_HUMAN	Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, plin-2 protooncogene homolog pim-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor IGHM enhancer 3 genes, partial cds; and unknown g?
5895	19083	32394	0.64	2.6E-01	AF207560.1	NT	

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6186	26211		2.57	2.6E-01	AE001811.1	NT	Thermoboga maritima section 123 of 138 of the complete genome
6330	19501	32859	1.96	2.6E-01	AI582557.1	EST_HUMAN	Is02512.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q04289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element;
6330	19501	32860	1.98	2.6E-01	AI582557.1	EST_HUMAN	Is02512.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q04289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element;
8552	19714	33080	0.98	2.6E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 617
8807	19961	33384	0.74	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936158 5'
8807	19961	33366	0.74	2.6E-01	BE792052.1	EST_HUMAN	601581754F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936158 5'
7183	20315	33758	1.04	2.6E-01	AI914380.1	EST_HUMAN	w448c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331368 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPH-A-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7549	20621	34098	0.7	2.6E-01	BE148991.1	EST_HUMAN	CMD-HT0246-031189-086-04 HT0245 Homo sapiens cDNA
7587	20648		0.98	2.6E-01	AL139077.2	NT	Campylobacter jejuni NGT/C11168 complete genome; segment 418
7826	20695		0.78	2.6E-01	AA186149.1	EST_HUMAN	z992e01.r1 Stragene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:128004 3' similar to y37a03.s1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:124212 5'
7918	20969	34476	1.73	2.6E-01	R10365.1	EST_HUMAN	gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
8033	21116	34634	1.18	2.6E-01	R02411.1	EST_HUMAN	y82a07.r1 Soares fetal liver spleen 1N1FLS Homo sapiens cDNA clone IMAGE:124212 5'
8088	21170	34685	1.3	2.6E-01	BE144331.1	EST_HUMAN	MRO-HT0168-181199-003-012 HT0168 Homo sapiens cDNA
8528	21610	35148	2.97	2.6E-01	BF343868.1	EST_HUMAN	602014422F1 NCL_CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4150398 5'
8605	21686	36223	1.74	2.6E-01	Q10199	SWISSPROT	HYPOTHETICAL 76.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
8892	21971	35506	4.06	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8892	21971	35507	4.06	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9687	22629	36200	0.92	2.6E-01	X17604.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.26)
9940	22979		0.5	2.6E-01	AF057121.1	NT	Lentia canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10072	23110	36713	1.13	2.6E-01	P87368	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G)
10072	23110	36714	1.13	2.6E-01	P87368	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G)
10393	23428		0.83	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10777	23760		1.09	2.6E-01	Y10186.1	NT	Homo sapiens PHEX gene
10840	23873		0.48	2.6E-01	Y15874.2	NT	Danio rerio mRNA for RP-TP-alpha protein
11816	24804		31.14	2.6E-01	X51765.1	NT	Human lambda-immunoglobulin constant region complex (germline)
12468	26070		4.14	2.6E-01	BE838491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12635	25365	32069	3.88	2.6E-01	AF16896.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXYD2) gene, complete cds, alternatively spliced

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12922	25607		2.04	2.0E-01	D88425.1	NT	Cavia cubana mRNA for serine/threonine kinase, complete cds
13007	25603		1.78	2.0E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
13057	25692		2.36	2.0E-01	AF141325.2	NT	Homo sapiens insulin polyphosphatase 1-phosphatase (INPP1) gene, complete cds
13098	15735		1.43	2.0E-01	BE272440.1	EST_HUMAN	601126076F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990043 5'
13107	25722		2.04	2.0E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
13150	25748		2.4	2.0E-01	U30729.1	NT	Arabidopsis thaliana floral homeotic (AP3) gene, promoter region and partial cds
251	13472	28503	1.87	2.5E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA
252	13472	28503	1.7	2.5E-01	4502298	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA
265	13484		2.51	2.0E-01	M29501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
855	14032	27093	1.23	2.5E-01	U09984.1	NT	Mus musculus ICR/Swiss glycerol dehydrogenase (Gpd-S) gene, complete cds
1085	14251		1.75	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1145	14310	27367	5.45	2.5E-01	T89837.1	EST_HUMAN	ye11607.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:117468 5'
1767	14916		4.63	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
2479	15608		11.21	2.5E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2563	15698	28814	1.22	2.5E-01	6679216	NT	Mus musculus protein-L-isopentate (D-aspartate) O-methyltransferase 1 (Pcm1), mRNA
2585	15699		1.02	2.5E-01	AA251987.1	EST_HUMAN	zai11a12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
2702	15820	28936	1	2.5E-01	X95310.1	NT	B. taurus mRNA for D-aspartate oxidase
3489	16656		3.34	2.5E-01	AW973471.1	EST_HUMAN	EST385464 IMAGE ressequences, MAGM Homo sapiens cDNA
3639	16803	28816	7.18	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3950	17108	30106	1.25	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
3950	17108	30106	1.25	2.5E-01	A1741483.1	EST_HUMAN	wg11c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780 3'
4438	17678		0.88	2.5E-01	Q03314	SWISSPROT	RHIB PROTEIN
4737	17872	30855	0.7	2.5E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Nai6) gene, complete cds; and Nai6 gene, exons 2-9 and 11-16
4871	18004		1.13	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4878	18009	30993	3.99	2.5E-01	AF007768.1	NT	Charisbonera tumefera diapause associated protein 2 (DAP2) mRNA, complete cds
4904	18034	31023	2.3	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4926	18056		3.54	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4954	18084	31080	0.8	2.5E-01	BE986785.1	EST_HUMAN	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5'



Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4994	18123	31101	0.61	2.5E-01	U83656.1	NT	Rattus norvegicus NF-KB gene, promoter region
5212	18333	31303	0.82	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5212	18333	31304	0.82	2.5E-01	P27023	SWISSPROT	MAJOR SURFACE GLYCOPROTEIN G (ATTACHMENT GLYCOPROTEIN G)
5337	18450		1.08	2.5E-01	AA419208.1	EST_HUMAN	zc35a05.r1 Scores ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:755900 5' similar to gb:M88279
5441	18641	31620	12.21	2.5E-01	S83390.1	NT	P99 PROTEIN (HUMAN);
6080	19282	32691	0.6	2.5E-01	AJ006345.1	NT	T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]
6081	19283		0.81	2.5E-01	AL163207.2	NT	Homo sapiens KVLQ11 gene
6762	19918	33313	0.82	2.5E-01	AJ251973.1	NT	Homo sapiens chromosome 21 segment HS21C007
7180	20055	33485	0.64	2.5E-01	8394138	NT	Homo sapiens partial steerin-1 gene
7507	20581	34084	0.71	2.5E-01	U13902.1	NT	Rattus norvegicus steerin-1 gene
7536	20609		1.13	2.5E-01	AF134119.1	NT	Feline calicivirus CF/68 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polypeptide precursor and capsid protein precursor, genes, complete cds; and unknown gene
7770	20828	34319	0.82	2.5E-01	AL161508.2	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7814	20869	34365	4.23	2.5E-01	AL163282.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
8028	21111	34630	2.22	2.5E-01	BF108040.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
8039	21122	34642	0.61	2.5E-01	BE060712.1	EST_HUMAN	757a03.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
8421	21602	35034	1.9	2.5E-01	BF038595.1	EST_HUMAN	601653391R2 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3826188 3'
8591	21672	35210	0.8	2.5E-01	P04492	SWISSPROT	601459238F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3662809 5'
8837	21976	35494	4.07	2.5E-01	H53236.1	EST_HUMAN	ETB PROTEIN, SMALL T-ANTIGEN (E1B 18K)
9076	22155	35689	1.05	2.5E-01	M8828.1	NT	yc8407.r1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:202501 5'
9716	22781	36351	16.85	2.5E-01	U89651.2	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9716	22781	36352	16.85	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP-1 Rasi-1 gene, promoter region
9772	22769	36339	2.44	2.5E-01	AF085164.1	NT	Homo sapiens matrix metalloproteinase MMP-1 Rasi-1 gene, promoter region
9772	22769	36340	2.44	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10303	23338	36943	1.31	2.5E-01	AW581997.1	EST_HUMAN	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10560	23585	37193	0.51	2.5E-01	11465652	NT	RC3-ST0186-130100-015-a07 ST0186 Homo sapiens cDNA
10763	23788	37416	1.4	2.5E-01	AW152246.1	EST_HUMAN	Porphyra purpurea chloroplast, complete genome
10767	23800	37422	1.61	2.5E-01	X58491.1	NT	xg40c10.x1 NC1_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
11332	24395	38043	2.86	2.5E-01	D50914.1	NT	Mouse L1Md LINE DNA
12204	25158	39834	6.16	2.5E-01	AF200528.1	NT	Human mRNA for KIAA0124 gene, partial cds
12233	26167		6.12	2.5E-01	AL161641.2	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13024	25674		1.22	2.6E-01	AF326363.1	NT	Della brassica cytochrome oxidase subunit II (COII) gene, partial cds; mitochondrial gene for mitochondrial product
567	13759	26783	1.41	2.4E-01	AA936316.1	EST_HUMAN	on70d04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
871	14047	27113	4.4	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1332	14489	27657	16.83	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1332	14489	27558	16.83	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
1415	14669	27642	0.97	2.4E-01	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1898	15041		29.78	2.4E-01	AF207753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1949	15092	28183	1.43	2.4E-01	AF251708.1	NT	Zaocys dhumnades fructose-1,6-bisphosphatase mRNA, complete cds
2091	15231	28353	1.64	2.4E-01	AJ742958.1	EST_HUMAN	wg76d05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371017 3' similar to TR:O80287 O80287 KIAA0512 PROTEIN
2206	15340	28467	1.17	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, submit 11 gene, complete cds; and unknown genes
2237	15370		1.25	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2338	15467	28602	2.29	2.4E-01	AE000680.1	NT	Aquifex acidicus section 12 of 109 of the complete genome
2602	15726	28845	3.13	2.4E-01	Z36534.1	NT	D. discoideum (AX3-K) ponA gene
2820	15934	29046	2.22	2.4E-01	X71783.1	NT	S. pombe swif gene
2846	15960	29069	6.27	2.4E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
3202	16377		3.03	2.4E-01	U72726.1	NT	Ornithine longistaminata receptor Kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3217	16391	29402	1.51	2.4E-01	X74209.1	NT	H. sapiens AGT gene, Peti fragment of intron 4
3655	17018	30018	0.97	2.4E-01	AE000312.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
4141	17263		0.65	2.4E-01	D29360.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
5181	18303	31268	0.55	2.4E-01	AW076596.1	EST_HUMAN	xb18a02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
5181	18303	31267	0.65	2.4E-01	AW076596.1	EST_HUMAN	xb18a02.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:2576618 3'
							Bacillus firmus hypothetical 34.0 kDa protein, hypothetical 8.9 kDa protein, hypothetical 10.1 kDa protein, hypothetical 21.0 kDa protein, putative thiosulfate sulfotransferase, hypothetical 18.1 kDa transcriptional regulator and hypothetical 18.2 kDa>
5334	18447	31415	1.89	2.4E-01	U88914.1	NT	Homo sapiens gene for TU12B1-TY, exon 13
5336	18448	31416	1.46	2.4E-01	AB032786.1	NT	Homo sapiens gene for TU12B1-TY, exon 13
5335	18448	31417	1.48	2.4E-01	AB032785.1	NT	Homo sapiens gene for TU12B1-TY, exon 13
5578	18773	31818	0.9	2.4E-01	A1925707.1	EST_HUMAN	wc33405.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5578	18773	31819	0.9	2.4E-01	A1925707.1	EST_HUMAN	wc33405.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5602	18797	31847	0.59	2.4E-01	D5087.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5772	18964	32268	12.85	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5772	18964	32267	12.86	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5800	18950		0.7	2.4E-01	M83377.1	NT	Gallus gallus brain-derived neurotrophic factor (BDNF) gene, 5' end
6010	26815		0.87	2.4E-01	A1133836.2	NT	Branchiostoma floridae mRNA for calmodulin 2 (cam2 gene)
6016	19200	32517	2.54	2.4E-01	BF592338.1	EST_HUMAN	715404.x1 NCL_CGAP_Br10 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW-SFR4_HUMAN Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4; contains element TAR1 TAR1 repetitive element
6106	19286	32520	2.47	2.4E-01	AF035546.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
6215	19390	32738	2.48	2.4E-01	7661801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6289	19443	32792	0.94	2.4E-01	AV733787.1	EST_HUMAN	AV733787 cda Homo sapiens cDNA clone cdaADE11 5'
6516	19881	33051	0.87	2.4E-01	AA339872.1	EST_HUMAN	z77002.s1 Soares_besla_NHT Homo sapiens cDNA clone IMAGE:727683 3'
6665	19824	33212	1.59	2.4E-01	AI698989.1	EST_HUMAN	w622c11.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb.J03464 PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7498	20573	34046	7.79	2.4E-01	L43001.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
7802	20554	34461	0.68	2.4E-01	AF229844.1	NT	Mus musculus DX1mx48e protein (DX1mx48e) mRNA, complete cds
8271	21353	34868	0.5	2.4E-01	X97252.1	NT	M.musculus pah gene and promoter
8271	21353	34869	0.5	2.4E-01	X97252.1	NT	M.musculus pah gene and promoter
8392	21473	34899	1.48	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae r08 and h08 genes; two component system 08
8392	21473	35000	1.48	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae r08 and h08 genes; two component system 08
8544	21825	35162	1.29	2.4E-01	AJ012585.1	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
8798	21877	35416	1.18	2.4E-01	BF242794.1	EST_HUMAN	60187678F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106298 5'
9332	22408	35961	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9332	22408	35962	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9763	22701	36267	8.39	2.4E-01	AI693515.1	EST_HUMAN	wd43602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330908 3' similar to contains MER22.b1 TAR1 repetitive element;
9905	22945	36530	0.68	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
9905	22945	36531	0.68	2.4E-01	AF220067.1	NT	Drosophila melanogaster SKPB gene, complete cds
10654	23688	37287	1.8	2.4E-01	Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11006	24085	37722	2.15	2.4E-01	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig.fragment No. 6
11074	24149	37788	1.96	2.4E-01	AF030199.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11447	24608	38174	1.8	2.4E-01	BE206917.1	EST_HUMAN	601176415F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531843 5'
11447	24508	38175	1.8	2.4E-01	BE206917.1	EST_HUMAN	601176415F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531843 5'
11478	24537		8.04	2.4E-01	Z21847.1	NT	P.asiatica mosaic virus genomic RNA
12159	25127	38827	1.75	2.4E-01	AF217491.1	NT	Homo sapiens fragile 16D oddo reductase (FOR) gene, exon 6
12999	25632		1.35	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive1-like1 (EIL1) mRNA, complete cds
12360	25256		1.62	2.4E-01	AJ278191.1	NT	Mus musculus mRNA for putative me7 protein (me7 gene)

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12588	25914		1.95	2.4E-01	V01507.1	NT	Gallus gallus gene coding for a-actin
12839	28161		1.37	2.4E-01	BF228975.1	EST_HUMAN	RC3-CT0413-100800-023-b08 CT0413 Homo sapiens cDNA
13072	28701		1.4	2.4E-01	AJ238044.1	NT	Homo sapiens mRNA for bradykinin B1 receptor (B1BKR gene)
13102	28718		4.16	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
400	13597	28633	1.39	2.3E-01	S76698.1	NT	aromatase [Poephilia guttata=zebra finches, ovary, mRNA, 3188 nt]
654	13840		5.53	2.3E-01	U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
684	13859	26900	29.31	2.3E-01	U67598.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
857	14130	27188	3.57	2.3E-01	BE311893.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1634	14786	27872	1.11	2.3E-01	AJ246480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
1881	14813	27898	1.72	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
2103	16242		1.78	2.3E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene
2317	15943	28764	1.85	2.3E-01	BE287718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2717	15935	28945	0.88	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2885	14573	27646	1.5	2.3E-01	AB015033.1	NT	Methicillin agarosecens gyrB gene for DNA gyrase subunit B, partial cds, strain:FO 14967
3028	18204	28227	1.08	2.3E-01	AA601379.1	EST_HUMAN	no16d06.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element THR repetitive element;
3153	16328		7.06	2.3E-01	R21732.1	EST_HUMAN	yh21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3498	18623	28844	1.32	2.3E-01	H69836.1	EST_HUMAN	yh7h10.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:213283 5'
3944	17103	30100	0.88	2.3E-01	S82821.1	NT	GSTA5-glutathione S-transferase Yc2 subunit [5' region, intron 1] [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
4046	17202		5.15	2.3E-01	7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4470	17610	30588	0.88	2.3E-01	R82252.1	EST_HUMAN	yh7f01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4520	17659		1.81	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4573	17710	30693	1.12	2.3E-01	D90899.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4811	17748	30728	2.76	2.3E-01	AF082535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKMT3) mRNA, complete cds
4878	17811	30800	5.65	2.3E-01	5031884	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5159	18281	31248	0.87	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5223	18345		1.03	2.3E-01	M18964.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
5260	18379	31345	0.63	2.3E-01	BF574804.1	EST_HUMAN	602132210F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271547 5'
5419	18620	31598	2.47	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5545	18742	31776	2.03	2.3E-01	BF058381.1	EST_HUMAN	7k3b068.x1 NCI_CGAP_OY18 Homo sapiens cDNA clone IMAGE:3478699 3' similar to SW:GAG_SMSAV P0330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10];

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6647	18841	32122	5.26	2.3E-01	X8587.1	NT	C.familiaris rom1 gene
6768	18858		0.98	2.3E-01	L39112.1	NT	Vitiforma corneum small subunit ribosomal RNA gene
5870	19060	32367	1.32	2.3E-01	S60371.1	NT	23S rRNA [Leuconostoc carnosum, Genotype, 2868 nt]
6062	19244	32569	1.98	2.3E-01	AJ708840.1	EST_HUMAN	ss27e12.x1 Barslead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
6062	19244	32570	1.98	2.3E-01	AJ708840.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6794	19949	33348	0.68	2.3E-01	AF188089.1	NT	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7017	20153	33573	4.63	2.3E-01	AJ718148.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7260	20343	33786	0.88	2.3E-01	8923323	NT	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7440	20517	33989	0.76	2.3E-01	AF000227.1	NT	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7573	20645	34123	2.84	2.3E-01	AF175389.1	NT	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7576	20648	34125	5.37	2.3E-01	AV719681.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7576	20648	34126	5.37	2.3E-01	AV719681.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7784	20840		4.28	2.3E-01	8754719	NT	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7789	20845	34338	1.56	2.3E-01	BE888071.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7831	20981		2.8	2.3E-01	N80983.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7968	21018	34530	0.71	2.3E-01	11418821	NT	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
7968	21018	34531	0.71	2.3E-01	11418821	NT	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
8035	21118	34637	0.52	2.3E-01	AL161558.2	NT	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
8183	21265	34788	1.73	2.3E-01	M68931.1	NT	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
8690	21770	35300	0.52	2.3E-01	U57999.1	NT	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
8972	22051	35594	0.58	2.3E-01	AW090541.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
9089	22168	35715	0.52	2.3E-01	AW094460.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
9341	22417	35970	0.64	2.3E-01	AA372164.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
9341	22417	35971	0.64	2.3E-01	AA372164.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
9780	22820	36388	0.5	2.3E-01	6879318	NT	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
9830	22970	36559	0.53	2.3E-01	BE277860.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
9885	23024	36616	0.81	2.3E-01	AW084460.1	EST_HUMAN	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
10037	23075	36875	1.57	2.3E-01	X52124.1	NT	CYTCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10071	23109	36712	0.63	2.3E-01	AW364633.1	EST_HUMAN	PM2-DT0036-281299-001-004 DT0036 Homo sapiens cDNA
10138	23176	36773	2.62	2.3E-01	BE173060.1	EST_HUMAN	MRO-HT0559-240400-014-g11 HT0559 Homo sapiens cDNA
10197	23234	36823	2.48	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10658	23692	37302	0.94	2.3E-01	AF201929.1	NT	Murine hepatitis virus strain 2, complete genome
10871	23705		5.89	2.3E-01	BF133577.1	EST_HUMAN	601646165R2 NIH_MGC 59 Homo sapiens cDNA clone IMAGE:4102092 3'
11465	24524	38195	2.24	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11465	24524	38196	2.24	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11633	24713	38404	2.43	2.3E-01	AE002167.2	NT	Chlamydomonas reinhardtii AR39, section 4 of 84 of the complete genome
12099	25078		1.38	2.3E-01	AV709736.1	EST_HUMAN	AV709736 ADG Homo sapiens cDNA clone ADCAGH01 5'
12281	25210		3.07	2.3E-01	U45428.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
12370	25264		48.78	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT20M8 Homo sapiens cDNA clone HCOE44 5'
12395	25873		1.23	2.3E-01	AA093819.1	EST_HUMAN	clnt1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
12464	26086	31657	4.08	2.3E-01	AW303623.1	EST_HUMAN	xv21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175
12500	26143	31552	7.05	2.3E-01	BE882494.1	EST_HUMAN	Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTR5.b2 TAR1 repetitive element;
12553	26376		1.77	2.3E-01	BF663319.1	EST_HUMAN	601507202F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3908689 5'
12612	25411		2.74	2.3E-01	AJ006519.1	NT	602144459F1 NIH_MGC 48 Homo sapiens cDNA clone IMAGE:4297719 5'
12708	25470		1.22	2.3E-01	U49645.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12712	25411		1.84	2.3E-01	AJ006519.1	NT	Plautodeles walli distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
13009	25685		2.36	2.3E-01	BF475611.1	EST_HUMAN	Rattus norvegicus mRNA for acid gated ion channel
92	13327	26355	1.13	2.2E-01	A052190.1	EST_HUMAN	nec39h12.x1 Lupski_octalio_nerve Homo sapiens cDNA clone IMAGE:3395850 3' similar to contains element
1596	14749	27833	2.74	2.2E-01	AF187850.1	EST_HUMAN	MER39 repetitive element;
2155	15281	28418	2.19	2.2E-01	M34640.1	NT	ozt4810.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1675280 3' similar to
2476	15603	28728	7.16	2.2E-01	BF677638.1	EST_HUMAN	TR-Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN;
2654	15777	28890	1.63	2.2E-01	BE618258.1	EST_HUMAN	Homo sapiens PPAR delta gene, promoter region
2654	15777	28891	1.63	2.2E-01	BE618258.1	EST_HUMAN	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2846	16123	29136	4.94	2.2E-01	BE156625.1	EST_HUMAN	60208608F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4249969 5'
2946	16123	29137	4.94	2.2E-01	BE156625.1	EST_HUMAN	601482629F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3886190 5'
2987	16163		2.07	2.2E-01	AF020503.1	NT	601482629F1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3886190 5'
3479	16846		2.35	2.2E-01	AL161562.2	NT	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
							PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
							Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62

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Table 4

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3848	17008	30009	0.62	2.2E-01	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4211	17360	30349	0.69	2.2E-01	AF213391.1	NT	Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds
4242	17388		0.8	2.2E-01	U68174.1	NT	Mus musculus breast/ovarian cancer susceptibility protein (BRCA1) mRNA, complete cds
4328	17471		1.07	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4335	17478	30460	0.62	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4378	17522	30502	2.74	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4379	17622	30603	2.74	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4475	17615	30595	1.07	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4475	17615	30596	1.07	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4947	18077		1.08	2.2E-01	D50804.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4952	18082	31058	2.2	2.2E-01	AA212116.1	EST_HUMAN	z887c05.1 Stratagene hNT neuron (#837233) Homo sapiens cDNA IMAGE:648968 5'
5156	18278		1.57	2.2E-01	L13299.1	NT	Mus musculus vinculin gene, exon 3
5226	18348	31319	1.34	2.2E-01	BE141035.1	EST_HUMAN	MRO-HT0067-201 099-002-c10 HT0067 Homo sapiens cDNA
5863	19053	32360	1.89	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog 2 (DIAPH2), transcript variant 156, mRNA
5874	19064		3.75	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
6122	19301	32640	0.78	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds
6122	19301	32641	0.78	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-TbxT) mRNA, complete cds
6845	19998	33405	0.77	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
7166	20299	33742	10.63	2.2E-01	AV756238.1	EST_HUMAN	AY756238 BM Homo sapiens cDNA clone BMFAHC06 5'
7278	20362	33815	1.61	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds, and unknown genes
7278	20362	33816	1.61	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds, and unknown genes
7442	20519	33991	2.36	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7442	20519	33992	2.36	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7655	20723	34198	0.62	2.2E-01	AE000035.2	NT	Human glycophorin B gene, exon 4
7878	20930	34436	0.88	2.2E-01	AF287987.1	NT	Mycoplasma pneumoniae M129 section 45 of 63 of the complete genome
7905	20957	34463	0.71	2.2E-01	AB024553.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
8210	21292		2.45	2.2E-01	AF155143.1	NT	Bacillus halodurens DNA, complete and partial cds, strain C-125
8280	21362	34881	2.68	2.2E-01	Z48933.1	NT	Mus musculus nm23-M1 gene, promoter region
8748	21827	35363	0.61	2.2E-01	AJ132918.1	NT	E. coli sepA and sepB genes
9083	22162	35705	0.52	2.2E-01	L23312.1	NT	Pan troglodytes MeCP2 gene 3'UTR
							Mouse HD protein mRNA, complete cds

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8083	22162	35706	0.52	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
8097	22176	35720	4.58	2.2E-01	AE001713.1	NT	Thermobia maritima section 25 of 136 of the complete genome
9117	22166	35740	0.48	2.2E-01	U09364.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Capd-S) gene, complete cds
9224	22302		2.88	2.2E-01	AW855036.1	EST_HUMAN	PM3-CT0263-241269-009-507 CT0263 Homo sapiens cDNA
9319	22391	35942	1.98	2.2E-01	8983247	EST_HUMAN	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
9369	22473	36039	1.13	2.2E-01	BF376354.1	EST_HUMAN	MRI-TN0045-110900-008-c02 TN0045 Homo sapiens cDNA
9489	22646	36109	1.42	2.2E-01	W02988.1	EST_HUMAN	zfp408.l1 Scarsa melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:291591 5'
9507	22773	36345	15.08	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
8552	22617	36187	0.76	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xklp3)
8563	22705	36271	1.05	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
8578	22718	36286	4.29	2.2E-01	M89843.1	NT	Brachydanio rerio apendymin beta and gamma chains (Epd) gene, complete cds
8820	22860	36441	0.65	2.2E-01	Q80980	SWISSPROT	CYCLOC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)
10020	23058	36654	3.84	2.2E-01	AF197841.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CP-sHSP21) mRNA, complete cds;
10159	23198	36792	1.53	2.2E-01	BF206507.1	EST_HUMAN	nuclear gene for chloroplast product
10380	23415	37024	1.11	2.2E-01	9826671	NT	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10540	23575	37182	0.65	2.2E-01	T59472.1	EST_HUMAN	Human herpesvirus 5, complete genome
10560	23575	37183	0.65	2.2E-01	T59472.1	EST_HUMAN	y683d08.r1 Stragene ovary (y6837217) Homo sapiens cDNA clone IMAGE:75855 5'
10580	23615	37220	0.6	2.2E-01	AF068264.1	NT	Pseudomonas aeruginosa quinoprotein ethanol dehydrogenase (exaA) gene, partial cds; cytochrome c550 precursor (exaB), NAD+ dependent acetaldehyde dehydrogenase (exaC), and pyrroloquinone synthase A (pqdA) genes, complete cds; and pyrroloquin>
10659	23693		0.79	2.2E-01	AF071001.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds
10707	23740	37344	0.57	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10707	23740	37345	0.67	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
10853	23888	37605	0.48	2.2E-01	AF049720.1	NT	Homo sapiens neuronal nitric oxide synthase (NOS1) gene, alternative exon 11 and AS
11389	24460	38111	1.65	2.2E-01	AF25772.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11707	24704	38396	5.09	2.2E-01	X01918.1	NT	Drosophila 68C glue gene cluster
11748	23834	37560	3.7	2.2E-01	7708215	NT	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
12207	25161		1.33	2.2E-01	BE870859.1	EST_HUMAN	601448957F1 NIH_MGC_05 Homo sapiens cDNA clone IMAGE:3850670 5'
12319	26156		1.96	2.2E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>



Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12407	25286		3.24	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12518	18492	31531	1.86	2.2E-01	AW361098.1	EST_HUMAN	RC1-CT0249-141189-021-g04 CT0249 Homo sapiens cDNA
12519	25353		1.47	2.2E-01	AW661822.1	EST_HUMAN	h17602.x1 NCJ_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972523 3'
13116	26148		3.08	2.2E-01	AV684801.1	EST_HUMAN	AV684801 GK6 Homo sapiens cDNA clone GKCAHB02 5'
893	14165	27228	1.88	2.1E-01	AA569289.1	EST_HUMAN	nm316t1.st NCJ_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1081804
998	14167	27228	0.72	2.1E-01	AL181604.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1148	14312		2.43	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1225	14385	27448	1.46	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1226	14385	27447	1.45	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1640	14692	27771	4.29	2.1E-01	AJ240895.1	NT	Mus musculus mas proto-oncogene and lgt2 gene for insulin-like growth factor type 2 and L41po and Au76 pseudogenes
1983	15106	28206	2.15	2.1E-01	AA906824.1	EST_HUMAN	d73a02.e1 NCJ_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519810 3' similar to gb:K02785
2224	15358	28488	3.55	2.1E-01	BF695073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2891	16167	29183	2.52	2.1E-01	6912445	NT	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
3533	16998	29709	6.1	2.1E-01	AA639482.1	EST_HUMAN	Homo sapiens potassium voltage-gated channel, subfamily H (KCNH4), mRNA
3908	17067		6.61	2.1E-01	9838361	NT	nc90b10.s1 NCJ_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1195579 3'
4125	17279		0.67	2.1E-01	AE001793.1	NT	Beta vulgaris mitochondrion, complete genome
4165	17315	30310	1.57	2.1E-01	PI11675	SWISSPROT	Thermoboga maritima section 105 of 138 of the complete genome
4165	17315	30311	1.57	2.1E-01	PI1675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4495	17635		1.63	2.1E-01	AB033041.1	NT	IMMEDIATE-EARLY PROTEIN IE180
4699	17834	30819	1.82	2.1E-01	AB010273.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4767	17892	30871	0.93	2.1E-01	X63161.1	NT	Homo sapiens pshep47 gene, complete cds
5138	18261	31228	0.7	2.1E-01	D13567.1	NT	P.falciparum mRNA for small GTPase rab11
5416	18818	31692	6.31	2.1E-01	BF672695.1	EST_HUMAN	Homo sapiens mRNA for alpha-2-macroglobulin, complete cds
7027	20163	33565	1.06	2.1E-01	AJ223392.1	NT	Lampetra japonica mRNA for alpha-2-macroglobulin, complete cds
7038	20091	33508	1.8	2.1E-01	U04642.1	NT	60215201F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283001 5'
7564	20636	34111	0.77	2.1E-01	Q01956	SWISSPROT	Drosophila melanogaster 16S rRNA gene, partial
7584	20636	34112	0.77	2.1E-01	Q01956	SWISSPROT	Human olfactory receptor (OR17-2) gene, partial cds
7576	20647		1.88	2.1E-01	AE000972.1	NT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7863	20935	34441	1.54	2.1E-01	AF000849.1	NT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7930	20980	34488	1.38	2.1E-01	AF068887.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
							Canis familiaris keratin (KRT9) gene, complete cds
							Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7630	20980	34489	1.38	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8263	21345		1.21	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1b), mRNA
8700	21780	36313	4.78	2.1E-01	U68399.1	NT	
8897	22076	35615	0.91	2.1E-01	AL040537.1	EST_HUMAN	DKFZp334H0814.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp334H0814.5
8997	22076	35616	0.91	2.1E-01	AL040537.1	EST_HUMAN	DKFZp334H0814.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp334H0814.5
9169	22237		0.5	2.1E-01	AB022524.1	NT	Homo sapiens APCOL gene, exon 9
9237	22314	35656	6.7	2.1E-01	235786.1	NT	S. cerevisiae chromosome II reading frame ORF YBL025w
9704	22763	36323	0.66	2.1E-01	N42336.1	EST_HUMAN	Y711e10.1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270954.5
9704	22763	36324	0.66	2.1E-01	N42336.1	EST_HUMAN	Y711e10.1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:270954.5
9713	22778	36348	2.72	2.1E-01	X97378.1	NT	Althallapa mRNA for AURanBP-1b protein
9817	22857	36437	1.02	2.1E-01	AB036529.1	NT	Homo sapiens p3R2 gene for ribonucleotide reductase, exon 6
10535	23570	37178	1.31	2.1E-01	297067.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10569	23604	37209	1.97	2.1E-01	PE2824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10576	23611	37216	0.72	2.1E-01	BF574254.1	EST_HUMAN	(60 KD DIACYLGLYCEROL KINASE)
11778	24768		1.34	2.1E-01	AI141875.1	EST_HUMAN	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831.5
11882	24850		1.68	2.1E-01	11036847	NT	qag6008.x1 Soares_fetal_heart_NbHH19W, Homo sapiens cDNA clone IMAGE:1691751.3
11879	24867	38565	2.6	2.1E-01	BE180422.1	EST_HUMAN	Homo sapiens pancreatic polypeptide 2 (PpY2), mRNA
12888	25459		1.82	2.1E-01	AF217490.1	NT	RC3-HT0622-040500-013-b11 H T0622 Homo sapiens cDNA
12994	25646		1.39	2.1E-01	BE622149.1	EST_HUMAN	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
13158	25753	31928	1.19	2.1E-01	AJ276505.1	NT	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915675.6
205	13428	28460	1.92	2.0E-01	AB017437.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
547	13740		1.97	2.0E-01	7705801	NT	Gallus gallus mRNA for avena, complete cds
717	13869	26937	1.37	2.0E-01	IM77088.1	NT	Homo sapiens C3I-18 protein (LOC51008), mRNA
833	14011	27067	2.09	2.0E-01	AF027865.1	NT	O. cuniculus germline IgH heavy chain V-H pseudogene, allotype VHa2
1036	14204	27261	1.83	2.0E-01	D90905.1	NT	Mus musculus Major Histocompatibility Locus class II region
1149	14313	27369	2.81	2.0E-01	AL163213.2	NT	Synechocystis sp. PCC6803 complete genome, 7/27, 761440-620815
1283	14439	27508	1.19	2.0E-01	AJ192695.6	NT	Homo sapiens chromosome 21 segment HS21C013
1336	14493	27563	1.99	2.0E-01	AW384937.1	EST_HUMAN	Homo sapiens rec1 gene
1516	14658	27752	22.4	2.0E-01	4503408	NT	PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA
1582	14734	27816	2.68	2.0E-01	AB007974.1	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
						NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1588	14740	27821	3.48	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1732	14892	27873	0.98	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1755	14904		2.58	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds, and unknown gene
1786	14945		3.87	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1941	15084	28185	1.46	2.0E-01	8922238	NT	Homo sapiens hypothetical protein FLJ10120 (FLJ10120), mRNA
2423	15552		1.9	2.0E-01	X82877.1	NT	H. sapiens Na+-D-glucose cotransport regulator gene
2955	16132		0.79	2.0E-01	AF074690.1	NT	Homo sapiens full length insert cDNA YH85A11
3576	16741	28758	0.72	2.0E-01	P48607	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3658	16821		0.91	2.0E-01	AY238005.1	EST_HUMAN	xp15b02.x1 NCL_CGAP_HIN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element
3708	16959	29063	0.86	2.0E-01	P34641	SWISSPROT	MER21 repetitive element:
3802	16963		0.8	2.0E-01	8880787	NT	CED-11 PROTEIN
4888	17823		8.71	2.0E-01	BE826165.1	EST_HUMAN	Mus musculus bone morphogenetic protein 8 (Bmp8), mRNA
5152	18274	31243	8.41	2.0E-01	8822080	NT	QV4-EN0032-180500-223-ed3 EN0032 Homo sapiens cDNA
5243	18959	26963	0.6	2.0E-01	P34641	SWISSPROT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5561	18758	31787	2.55	2.0E-01	X66600.1	NT	CED-11 PROTEIN
5559	18049	32355	2.08	2.0E-01	11432540	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5963	19149	32464	0.82	2.0E-01	X91856.1	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
6185	19361	32703	5.89	2.0E-01	U16300.1	NT	F. rubripes DNA encoding for vally-IRNA synthetase
6303	19476		0.74	2.0E-01	M75967.1	NT	Secchiaromyces cerevisiae Hal3p (HAL5) mRNA, complete cds
6569	19721	33098	47.65	2.0E-01	X61033.1	NT	Human hepatocyte growth factor gene, exon 1
8659	18818	33206	3.74	2.0E-01	AW360865.1	EST_HUMAN	M. laureatus mu class glutathione transferase gene
7445	20522	33995	1.41	2.0E-01	AF250371.1	NT	PM1-CT0247-141099-001-g06 CT0247 Homo sapiens cDNA
7603	20673	34147	0.83	2.0E-01	P64422	SWISSPROT	Mus musculus phosphofructokinase-1 C isozyme (P-1ko) gene, exons 3 through 7
8139	21221		6.16	2.0E-01	AF028026.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE PRECURSOR
8395	21478	35003	3.12	2.0E-01	X91151.1	NT	Andes virus strain O123133 glycoprotein G1 and G2 precursor, gene, partial cds
8921	22000		0.48	2.0E-01	BE592247.1	EST_HUMAN	M. musculus ec2 gene exon 14
9551	22818	36188	1.17	2.0E-01	U82511.1	NT	601344648F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677784 5'
9590	22845	36215	0.82	2.0E-01	U71122.1	NT	Dicystotellum discoidium random alg cDNA19 protein (sc19) mRNA, partial cds
9756	22854		5.42	2.0E-01	AE001278.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9947	22988	36579	0.52	2.0E-01	P11420	SWISSPROT	Chlamydia trachomatis section 5 of 87 of the complete genome
9947	22988	36580	0.52	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
10095	23133		2.24	2.0E-01	AF146992.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds

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Table 4

Single Exon Probes Expressed in Placenta

Probe Seq ID NO:	Exon Seq ID NO:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10247	23282	36878	1.89	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10247	23282	36879	1.89	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10371	23406	37016	0.67	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10371	23406	37017	0.67	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10419	23464		0.8	2.0E-01	X78388.1	NT	D.melanogaster DNA mobile element (hoppe)
10616	23650	37259	0.88	2.0E-01	X97121.1	NT	R.norvegicus mRNA for NTR2 receptor
11079	24154	37791	2.12	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11079	24154	37792	2.12	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
11908	24895	36597	1.33	2.0E-01		7524759 NT	Chlorella vulgaris chloroplast, complete genome
11908	24895	36598	1.33	2.0E-01		7524759 NT	Chlorella vulgaris chloroplast, complete genome
12666	25443		1.24	2.0E-01	AF206637.2	NT	Pimphales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12666	25443		1.64	2.0E-01	AF302773.2	NT	Homo sapiens ninein-Lm isoform (ninein) mRNA, complete cds
12912	25876	31851	1.63	2.0E-01	AW975287.1	EST_HUMAN	EST3707405 MAGe resequences, MAGN Homo sapiens cDNA
12952	25862	31956	1.63	2.0E-01	A023592.1	EST_HUMAN	ov80410.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
12977	25636		17.48	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
113	13344		4.89	1.9E-01		7548743 NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Arl1), mRNA
362	13573	26604	5.58	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
673	13859	26889	1.54	1.9E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
673	13859	26890	1.54	1.9E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
680	13866	26897	8.31	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-281189-011-d01 BT0502 Homo sapiens cDNA
681	13866	26897	8.7	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
1010	14181		1.72	1.9E-01		7305180 NT	Mus musculus Interleukin 2 receptor, gamma chain (il2rg), mRNA
1128	14293	27349	5.63	1.9E-01	AA358813.1	EST_HUMAN	EST07784 Fetal lung II Homo sapiens cDNA 5' end
1401	14555	27629	2.42	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kaffir cluster
1456	14620		4.34	1.9E-01	AF184823.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2456	15584	28711	3.66	1.9E-01	U66068.1	NT	Homo sapiens hypothetical protein FLJ10531 (FLJ10581), mRNA
2899	16165	28181	3.81	1.9E-01	U66068.1	NT	Stomoxys hispidus p53 gene, partial cds
3004	16179		7.53	1.9E-01	U60922.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3482	16650	28666	4.07	1.9E-01	D13197.1	NT	Mouse gene for immunoglobulin diversity region D1
3559	16734	29760	4.94	1.9E-01	R16467.1	EST_HUMAN	Y42F10.1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:128547 5'
3907	17066	30066	1.08	1.9E-01	AF284017.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
4100	17253	30256	3.68	1.9E-01	AB008784.1	NT	Schistosoma haematobium DNA for cytoplasmic dynein heavy chain, complete cds
4183	17343	30336	1.51	1.9E-01	AW754106.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4261	17397		1.31	1.9E-01	AE001812.1	NT	Deinoceratops radiodurans R1 section 49 of 229 of the complete chromosome 1

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4346	17489	30471	0.89	1.8E-01	BE834943.1	EST_HUMAN	MRI-FN0010-280700-007-404 FN0010 Homo sapiens cDNA
4592	17728	30711	0.8	1.8E-01	AL161463.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
5124	18260		1.08	1.8E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5721	18914		5.19	1.8E-01	AW130149.1	EST_HUMAN	AF28407.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
5761	18953	32256	8.03	1.8E-01	AF127937.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
5862	19148	32463	1.08	1.8E-01	AF091218.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
6006	19181		2.45	1.8E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6457	19624	32987	1.03	1.8E-01	AI762391.1	EST_HUMAN	wf4h02.x1 NCL_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2394099 3'
6518	19683	33054	1.1	1.8E-01	AW148452.1	EST_HUMAN	AF14608.x1 NCL_CGAP_K108 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7112	18538	31495	1.54	1.8E-01	R43212.1	EST_HUMAN	Y839a12.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element;
7138	20273	33712	0.74	1.8E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 8-11
7138	20273	33713	0.74	1.8E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7408	20487	33957	0.92	1.8E-01	U73946.1	NT	Drosophila melanogaster testis-specific RNA-binding protein (bruno) mRNA, complete cds
7638	20707	34186	0.78	1.8E-01	U93988.1	NT	Staphylococcus aureus toxic shock syndrome toxin-1 (tsst), enterotoxin (ent), and integrase (int) genes, complete cds
7661	20728	34204	1.38	1.8E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
7708	20773	34258	2.64	1.8E-01	AF072724.1	NT	Zea mays starch branching enzyme 1 (sber1) gene, complete cds
8174	21256	34778	1.83	1.8E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8885	21864	35500	13.56	1.8E-01	AB03024.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
9146	22225	35768	1.5	1.8E-01	MT4968.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
9146	22225	35769	1.5	1.8E-01	MT4568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
10079	23117	36719	0.77	1.8E-01	AA912488.1	EST_HUMAN	089g10.e1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1637506 3' similar to contains Alu repetitive element;
10447	23482	37090	0.81	1.8E-01	BE830353.1	EST_HUMAN	RC5-E70082-060700-022-A02 E70082 Homo sapiens cDNA
10447	23482	37091	0.81	1.8E-01	BE830353.1	EST_HUMAN	RC5-E70082-060700-022-A02 E70082 Homo sapiens cDNA
10880	23665	37594	1.38	1.8E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10880	23665	37594	1.38	1.8E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10892	24071	37704	2.18	1.8E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12025	25008	38711	2.21	1.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12047	25028	38735	1.48	1.8E-01	LO7344.1	NT	Influenza A/Guangdong/243/72 nucleoprotein (seg 5) gene, 5' end

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
32	13270	28274	1.85	1.8E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
270	18009	28519	1.47	1.8E-01	AB022090.1	NT	Mus musculus Ccig gene for chaperonin containing TCP-1 gamma subunit, partial cds
381	13589	28625	1.9	1.8E-01	4502532	NT	Homo sapiens calicium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
765	13046	28693	0.78	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
1009	14178	27235	1.8	1.8E-01	AB12212.1	EST_HUMAN	wf7102.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1115	14278	27335	2.14	1.8E-01	AF000580.1	NT	Dicotyledon discoidium plasmid Ddp5, complete genome
1317	14473	27640	6.87	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
1533	14686	27765	1.49	1.8E-01	8753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1633	14688	27769	1.49	1.8E-01	8753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1915	15059		1.91	1.8E-01	AF733708.1	EST_HUMAN	gq22d10 x5 NCL CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:075936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE ;
1965	15108	28208	2.28	1.8E-01	AB051897.1	NT	Mus musculus Scya8, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A8 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2756	16973		3.34	1.8E-01	AW635726.1	EST_HUMAN	QV3-DT0018-081289-038-g04 DT0018 Homo sapiens cDNA
2903	16140		2.3	1.8E-01	AF184589.1	NT	Ionopsidium acetule LEAFY protein (LEAFY2) gene, partial cds
2968	16144	29163	1.16	1.8E-01	AW182300.1	EST_HUMAN	X41a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3194	16389	29375	1.61	1.8E-01	AW995179.1	EST_HUMAN	QV6-BN0041-070300-147-e04 BN0041 Homo sapiens cDNA
3452	16619	29638	0.77	1.8E-01	BF183582.1	EST_HUMAN	601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040821 3'
3712	16673	29877	0.87	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3712	16673	29878	0.87	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4453	17683		0.92	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (Bcl-A-DQB), complete cds
4678	17813	30801	5.61	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
4895	18025	31011	2.68	1.8E-01	AB051897.1	NT	Mus musculus Scya8, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A8 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5128	18254	31219	0.65	1.8E-01	X79784.1	NT	N. tabacum mRNA pNLA-36
5158	18280	31245	1.79	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151289-112-g08 ST0203 Homo sapiens cDNA
5206	18327	31297	2.55	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5218	18340	31313	0.89	1.8E-01	AF439881.1	EST_HUMAN	u67e04.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134580 3'
5291	18409	31376	1.2	1.8E-01	Y08310.1	NT	M.barkeri mlaC and mlaB genes

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Table 4

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5413	18616	31589	0.61	1.8E-01	BE082628.1	EST_HUMAN	RC8-BT0841-300300-011-H03 BT0841 Homo sapiens cDNA
5929	19115	32428	1.19	1.8E-01	AL161694.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6047	18230	32554	0.95	1.8E-01	N28629.1	EST_HUMAN	Y38H08.r1 Soares melanocyte 2NBM Homo sapiens cDNA clone IMAGE:284063 5'
6256	19430	32776	0.89	1.8E-01	6078428	NT	Mus musculus Trif receptor-associated factor 8 (Tra8), mRNA
6256	19430	32777	0.89	1.8E-01	6078428	NT	Mus musculus Trif receptor-associated factor 8 (Tra8), mRNA
6841	19800	33189	1.18	1.8E-01	Q9QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
6598	19846		2.12	1.8E-01	N94853.1	EST_HUMAN	Y62H02.r1 Soares, multiple sclerosis_2NblMSP Homo sapiens cDNA clone IMAGE:278163 6'
7148	20281	33722	1.11	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wus, complete cds
7148	20281	33723	1.11	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wus, complete cds
7202	20671	33477	0.67	1.8E-01	BE981353.1	EST_HUMAN	601848361R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3932247 3'
7604	20674	34148	0.81	1.8E-01	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
8810	21989	35431	0.58	1.8E-01	AW968118.1	EST_HUMAN	EST1378191 MAGE rescue sequences, MAG1 Homo sapiens cDNA
9543	22608	36176	1.58	1.8E-01	M73268.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9374	22716	36284	1.52	1.8E-01	9826232	NT	Bacteriophage Ika, complete genome
9892	22741		0.6	1.8E-01	AA483761.1	EST_HUMAN	nt02a05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:843088 similar to contains L1:13 L1
9774	22814	36392	0.95	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9774	22814	36393	0.95	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9814	22854	36432	1.02	1.8E-01	M26019.1	NT	S. commune orotidine-5-phosphate decarboxylase (URA1) gene, complete cds
9814	22854	36433	1.02	1.8E-01	M26019.1	NT	S. commune orotidine-5-phosphate decarboxylase (URA1) gene, complete cds
9881	23020	36613	0.81	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9886	23026	36617	0.71	1.8E-01	U67548.1	NT	Methanococcus jannaschii section 90 of 150 of the complete genome
10337	23372		0.67	1.8E-01	AF200252.1	NT	Aquarius amplius cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10578	23613	37218	1.48	1.8E-01	X63440.1	NT	M. musculus mRNA for P19-protein tyrosine phosphatase
10785	23818	37441	1.21	1.8E-01	AB011171.1	NT	Homo sapiens mRNA for KIAA0599 protein, partial cds
10873	23938	37588	2.02	1.8E-01	X77336.1	NT	A. thaliana mRNA for ribonucleotide reductase R2
10917	24000	37693	5	1.8E-01	U38906.1	NT	Bacteriophage r1 integrase, repressor protein (iro), dUTPase, hsdR and lysin genes, complete cds
10974	20281	33722	3.05	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wus, complete cds
10974	20281	33723	3.05	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wus, complete cds
10975	24054	37688	4.41	1.8E-01	AF019107.1	NT	Dictyostelium discoideum unknown (DGI041) gene, complete cds
11270	24338	37976	2.08	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11551	24608	38284	1.41	1.8E-01	AW275728.1	EST_HUMAN	xp40n10.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2742883 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11750	23936	37663	8.94	1.8E-01	X57033.1	NT	B.taurus mRNA for potassium channel
12061	25042	38751	3.48	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx27), mRNA
12124	25104	38808	1.77	1.8E-01	AA095094.1	EST_HUMAN	cp2788 seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
12289	25183		1.79	1.8E-01	10086561	NT	Bovine ephemeral fever virus, complete genome
12306	25224	32103	1.26	1.8E-01	BF348623.1	EST_HUMAN	602018928F1 NCI_CGAP_Bm07 Homo sapiens cDNA clone IMAGE:4156318 5'
12719	14473	27540	1.18	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
12811	25541		3.28	1.8E-01	Q96682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12842	25620		20.8	1.8E-01	R24494.1	EST_HUMAN	YH48H10.1 Soares placenta Nb2-IP Homo sapiens cDNA clone IMAGE:133027 5'
12988	25843		4.88	1.8E-01	Y11114.1	NT	E.coli pspA mRNA for hexokinase (hpk1)
13036	26134	31548	1.7	1.8E-01	9506952	NT	Rattus norvegicus procollagen C-proteinase enhancer protein (Pcdee), mRNA
591	13762	26801	8.4	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3815768 5'
828	14006	27063	3.16	1.7E-01	X63330.1	NT	P.dumetilli histone gene cluster for core histones H2A, H2B, H3 and H4
983	14158		1.79	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
1083	14249	27305	0.89	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolyhedrovirus, complete genome
1083	14249	27308	0.89	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolyhedrovirus, complete genome
1880	15006	28113	2.44	1.7E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
2038	16178		3.23	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2922	16100	29112	2.13	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2922	16100	29113					Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2993	16169	29166	2.13	1.7E-01	AF000716.1	NT	regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
3061	16237	29257	1.47	1.7E-01	AA336909.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
3061	16237	29257	1.09	1.7E-01	AJ238738.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3081	16237	29258	1.09	1.7E-01	AJ238738.1	NT	Naja naja atra cdx-1 gene, exons 1-3
3174	16349	29356	1.65	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3451	16618	29637	0.81	1.7E-01	N56763.1	EST_HUMAN	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3534	16699	29710	1.52	1.7E-01	AJ269505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
4049	17205	30215	8.08	1.7E-01	AJ236377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4581	17816		2.48	1.7E-01	X52936.1	NT	Schistosoma gregaria alpha repetitive DNA
4884	18014	30898	0.59	1.7E-01	AF217480.1	NT	Homo sapiens fragile 18D oxidoreductase (FOR) gene, exons 8, 9, and partial cds



Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4981	18090	31068	1.31	1.7E-01	A1247635.1	EST_HUMAN	q57a09.x1 Soares_fetal_liver_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains OFR.b1 OFR repetitive element;
5231	18353		1.07	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 1b (ae) gene, complete cds
5272	18391	31359	0.72	1.7E-01	BF030010.1	EST_HUMAN	601597250F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827187 5'
5312	18429	31399	0.61	1.7E-01	D37951.1	NT	Rattus norvegicus mRNA for MIBP1 (C-myc intron binding protein 1), complete cds
5524	18721	31737	1.88	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17888 60S
5524	18721	31738	1.88	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17888 60S
5710	18803	32198	0.82	1.7E-01	U43599.1	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
6469	18828	32888	12.64	1.7E-01	H72118.1	EST_HUMAN	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6517	18882	33052	0.72	1.7E-01	A1370978.1	EST_HUMAN	y502a06.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:213858 3'
6517	18882	33053	0.72	1.7E-01	A1370978.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W_Homo sapiens cDNA clone IMAGE:2045492 3'
6992	18511	31503	0.75	1.7E-01	BE300286.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NbHL19W_Homo sapiens cDNA clone IMAGE:2046782 3'
7010	20155		1.84	1.7E-01	AF026562.3	NT	00094408771 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2560248 3'
7140	20276		0.69	1.7E-01	ZB2910.1	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
7369	20448	33911	1.38	1.7E-01	AF000422.1	NT	Homo sapiens HFE gene
7448	20525	33998	8.91	1.7E-01	BE734178.1	EST_HUMAN	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7849	20718	34185	1.21	1.7E-01	P18724	SWISSPROT	601589022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843864 5'
7666	25850	34208	0.64	1.7E-01	Q01855	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HFLF0 PROTEIN)
8045	21128	34648	1.28	1.7E-01	AF000573.1	NT	COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR
8150	21232	34752	0.75	1.7E-01	AF160669.1	NT	Homo sapiens homogenisate 1,2-dioxigenase gene, complete cds
8472	21953	35083	7.35	1.7E-01	7708426	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadL) gene, complete cds
8472	21953	35084	7.35	1.7E-01	7708426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8895	21874	35511	0.5	1.7E-01	AW892873.1	EST_HUMAN	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8925	22004	35543	1.83	1.7E-01	D00384.1	NT	RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
8945	22124	35668	0.94	1.7E-01	AF217413.1	NT	Rat (SHR strain) SXL gene
9045	22124	35667	0.94	1.7E-01	AF217413.1	NT	Homo sapiens neuriligin 3 isoform gene, complete cds, alternatively spliced
9198	22276	35814	0.91	1.7E-01	R77002.1	EST_HUMAN	Homo sapiens neuriligin 3 isoform gene, complete cds, alternatively spliced
9369	22444	36005	0.53	1.7E-01	BE253142.1	EST_HUMAN	y68g02.r1 Soares_placenta_Nb2HP_Homo sapiens cDNA clone IMAGE:144242 5'
9369	22444	36006	0.53	1.7E-01	BE253142.1	EST_HUMAN	601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9789	22829	36407	9.03	1.7E-01	AP001508.1	NT	601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9899	22939	36524	0.54	1.7E-01	AW877455.1	EST_HUMAN	Bacillus halodurans genomic DNA, section 2/14
9899	22939	36526	0.54	1.7E-01	AW877455.1	EST_HUMAN	EST389564 IMAGE resequences, MAGO Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8916	22858	36543	2.08	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
8982	23031	36621	0.47	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
9992	23031	36622	0.47	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
10013	23051	36645	0.93	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10438	23473		2.77	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10605	23639	37247	1.58	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y <sup>+</sup> system), member 2 (SLC7A2), mRNA
10607	23641	37249	1.66	1.7E-01	AA627972.1	EST_HUMAN	nc60a07.s1 NCL CGAP_C08 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:U25081 TRANSFORMING PROTEIN RHOC (HUMAN);
10918	24002	37638	9.54	1.7E-01	BE380835.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
11045	24122	37766	2.12	1.7E-01	AA814817.1	EST_HUMAN	d43a03.s1 NCL CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1428924 3'
11373	24434	38090	6.81	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11373	24434	38091	6.81	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11657	24736	38427	1.71	1.7E-01	AA883375.1	EST_HUMAN	d4509.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460297 3'
12011	24908		1.5	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
12042	25023	38727	1.87	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FORN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12042	25023	38728	1.87	1.7E-01	P55899	SWISSPROT	IGG RECEPTOR FORN LARGE SUBUNIT P51 PRECURSOR (FCRN) (NEONATAL FC RECEPTOR) (IGG FC FRAGMENT RECEPTOR TRANSPORTER, ALPHA CHAIN)
12142	25117	38825	2	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
12275	26087		1.45	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12567	25920		1.18	1.7E-01	A1824404.1	EST_HUMAN	b68g05.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHA-1 (HUMAN);
12907	25900	31972	7.24	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
128	13356	26388	1.7	1.6E-01	AF217532.1	NT	Homo sapiens myeloblast kinase gene, exon 6 and 7
687	15985	26913	1.16	1.6E-01	R31497.1	EST_HUMAN	yA7512.T Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:135599 5'
1651	14703	27783	4.25	1.6E-01	AF298117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1810	15053		1.27	1.6E-01	AJ235272.1	NT	Rickettsia prowazekii strain Madrid E. complete genome; segment 3/4
1877	15120	28221	2.14	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2041	15182		1.43	1.6E-01	U10334.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2457	16063	28712	1.09	1.6E-01	X64232.1	NT	H. sapiens mRNA for novel T-cell activation protein
2562	16887	28813	2.73	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2957	16134	29149	14.1	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2957	16134	29150	14.1	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3723	16884	28889	1.23	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3723	16884	28890	1.23	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3872	17031	30030	0.82	1.6E-01	AE000862.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4107	17261		2.8	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4144	17236	30288	1.21	1.6E-01	AF084456.1	NT	Citridia fasciculata trypanothione 1 (bnt1) gene, complete cds
4448	17588	30569	10.91	1.6E-01	AF179880.1	NT	Homo sapiens apelin gene, complete cds
4578	17715		2.49	1.6E-01	AW968601.1	EST_HUMAN	EST380877 IMAGE resequences, MAGU Homo sapiens cDNA
4586	17723		4.39	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Ccp3), mRNA
5060	18188	31182	1.39	1.6E-01	AA088343.1	EST_HUMAN	E224109 at Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221956
5083	18211	31183	1.8	1.6E-01	AJ006359.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV.;
5083	18211	31184	1.8	1.6E-01	AJ006356.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region
5345	18458		0.93	1.6E-01	AF045283.1	NT	Lycopodium obscurum RsaI fragment 2, satellite region
5503	18702	31719	0.81	1.6E-01	L46508.1	NT	Gallus gallus smooth muscle/non-muscle myosin light chain kinase gene, exon 28
5539	18833	31909	2.9	1.6E-01	AW197496.1	EST_HUMAN	Plesmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5639	18833	31910	2.9	1.6E-01	AW197496.1	EST_HUMAN	Xm43101.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2686869 3' similar to TR:O75984 O75984
5651	18845	32126	1.99	1.6E-01	AF034716.1	NT	HYPOTHETICAL 127.6 KD PROTEIN ;
6152	18928	32674	0.73	1.6E-01	BE925803.1	EST_HUMAN	Xm43101.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2686869 3' similar to TR:O75984 O75984
6358	19720	33096	2.06	1.6E-01	AL161588.2	NT	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
6358	19720	33097	2.06	1.6E-01	AL161588.2	NT	RC3-BN0034-310800-113-101 BN0034 Homo sapiens cDNA
6359	20252	33688	0.70	1.6E-01	AB046786.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. B4
6985	20213		0.68	1.6E-01	BF683630.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. B4
7103	18530	31485	4.15	1.6E-01	AW291215.1	EST_HUMAN	Homo sapiens mRNA for KIAA1556 protein, partial cds
7451	20528	34001	0.71	1.6E-01	Z49632.1	NT	602139855F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301004 5'
7565	21005	34518	1.63	1.6E-01	AW246359.1	EST_HUMAN	U1-H-BI2-agt-b-08-0-U1.s1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7982	21031	34544	0.84	1.6E-01	6753237	NT	S.cerevisiae chromosome X reading frame ORF YJR132w
7986	21035		1.03	1.6E-01	AU136525.1	EST_HUMAN	2822248.6prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
8053	21136	34657	1.62	1.6E-01	L46349.1	NT	Mus musculus Ca-2+ dependent activator protein for secretion (Cadps), mRNA
8215	21297		0.53	1.6E-01	BE244087.1	EST_HUMAN	AU136525 PLAGE1 Homo sapiens cDNA clone PLAGE1004466 5'
8310	21392	34816	0.77	1.6E-01	U39243.1	NT	Gorilla gorilla androgen receptor gene, partial exon
							TCBAP1E0607 Pediatric pro-B cell acute lymphoblastic leukemia Baydar-HQSC project=TCBA Homo sapiens cDNA clone TCBAP0607
							Bacteroides vulgatus beta-lactamase (ctxA) gene, complete cds and mobilization protein (mobA) gene, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8833	21912	35450	1.08	1.6E-01	ZB9119.1	NT	Bacillus subtilis complete genome (section 16 of 21): from 2897771 to 3213410
8028	22105	35648	0.77	1.6E-01	R13873.1	EST_HUMAN	y6c0408.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:26873 5'
9133	22122		0.74	1.6E-01	L38681.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
9171	22249	35702	1.85	1.6E-01	Z49501.1	NT	S. cerevisiae chromosome X reading frame ORF YJR001w
9311	22387		0.76	1.6E-01	AF11167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9851	22891		1.77	1.6E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041189-011-H01 ST0200 Homo sapiens cDNA
9854	22894	36475	1.98	1.6E-01	Z48501.1	NT	S. cerevisiae chromosome X reading frame ORF YJR001w
9891	22931		1.18	1.6E-01	BE165664.1	EST_HUMAN	PM2-HT0353-270100-004411 HT0353 Homo sapiens cDNA
10828	23859	37482	0.5	1.6E-01	11128018	NT	Homo sapiens nuclear autoantigen (GS2NA), mRNA
10893	23977	37609	2.34	1.6E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
11244	24313	37951	1.34	1.6E-01	O14847	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11244	24313	37952	1.34	1.6E-01	O14947	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
11249	24318	37958	1.62	1.6E-01	BE259849.1	EST_HUMAN	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
11377	24438		3.8	1.6E-01	AF106064.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11697	24894	38388	7.53	1.6E-01	6871552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Ap1b1), mRNA
12277	25207	38363	3.89	1.6E-01	AV719585.1	EST_HUMAN	Mus musculus GLC Homo sapiens cDNA clone GLCEMF07 5'
12597	26402	32043	2	1.6E-01	L14933.1	NT	Rat convertase PC5 mRNA, 5' end
12830	25423		1.38	1.6E-01	AW639711.1	EST_HUMAN	RC1-LT0074-120200-014-H01_1 LT0074 Homo sapiens cDNA
12733	25893		11.84	1.6E-01	AB045310.1	NT	Cucumis sativus KS mRNA for ent-kaurene synthase, complete cds
12933	25816		2.71	1.6E-01	AK024498.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
13028	25878		5.04	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 9428 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
13054	25850	31984	1.69	1.6E-01	9506922	NT	Rattus norvegicus chondroin sulfate proteoglycan 5 (neuroglycan C) (Cepg5), mRNA
13080	25894		1.4	1.6E-01	BE267894.1	EST_HUMAN	601125459F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345038 5'
13159	25782		1.29	1.6E-01	BF672698.1	EST_HUMAN	602152004F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283145 5'
258	13477	26508	1.7	1.6E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
268	13477	26508	1.7	1.6E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
600	15984		2.8	1.5E-01	AV711698.1	EST_HUMAN	AV711698 DCA Homo sapiens cDNA clone DCAADH06 5'
805	13985	27037	1.38	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS210084
1116	14281	27337	1.44	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGG322 myosin heavy chain, 3'UTR
1121	14286	27941	2.7	1.5E-01	AJ251885.1	NT	Homo sapiens partial SL C22A2 gene for organic cation transporter (OCT2), exon 1
1137	14302		1.85	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1243	14402	27463	2.37	1.5E-01	AW195518.1	EST_HUMAN	xs98411.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2688085 3'

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1304	14480	27526	3.22	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1304	14480	27527	3.22	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1511	14864	27749	1.38	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
1857	15100	28200	0.98	1.5E-01	AW444451.1	EST_HUMAN	UI-H-B13-ekb-b-09-0-0-J1.s1 NCL CGAP_Sulp5 Homo sapiens cDNA clone IMAGE:2733941 3'
2980	16166		0.9	1.5E-01	AW572516.1	EST_HUMAN	xx56a02.2 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:X65072_ma1
3100	16276	29290	0.81	1.5E-01	M81441.1	NT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN);
3118	16294	29308	0.62	1.5E-01	O78697	SWISSPROT	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3433	16601	29820	6.78	1.5E-01	AA685049.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
3434	16621	29841	0.73	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN);
3454	16621	29842	0.73	1.5E-01	Z23104.1	NT	L. stagnalis mRNA for G protein-coupled receptor
3851	17011	30011	2.35	1.5E-01	U09984.1	NT	L. stagnalis mRNA for G protein-coupled receptor
3897	17026	30025	0.83	1.5E-01	7108358	NT	Mus musculus CR/Swiss glyceraledehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3881	17040	30037	0.77	1.5E-01	M97882.1	NT	Homo sapiens pyruvate dehydrogenase kinase, isoform 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3970	17128	30131	2.45	1.5E-01	AW665983.1	EST_HUMAN	XYN1A; Thermotoga bacterium; xynA; 4182 base-pairs
3987	17144	30149	0.68	1.5E-01	AJ003165.1	NT	h10106.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
3987	17144	30160	0.68	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
4181	17312	30308	1.16	1.5E-01	AW368659.1	EST_HUMAN	Populus trichocarpa cv. Trichobel ABI3 gene
4210	17359	30348	0.67	1.5E-01	Z12928.1	NT	RC2.HT0149-101059-012-c09 H10149 Homo sapiens cDNA
4299	17442	30428	9.85	1.5E-01	AL163284.2	NT	B. napus mitochondrion DNA for ORF158
4847	17680	30669	1.64	1.5E-01	BF687665.1	EST_HUMAN	Homo sapiens chromosome 21 segment H321C084
4874	15891	29002	2.33	1.5E-01	BF695381.1	EST_HUMAN	602067192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086223 5'
5114	18242	31207	1.5	1.5E-01	AL161560.2	NT	602083289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
5370	18573	31441	1.91	1.5E-01	P07998	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5399	18601	31571	1.33	1.5E-01	AF256352.1	NT	THROMBOSPONDIN 1 PRECURSOR
5443	18843		5.95	1.5E-01	P15196	SWISSPROT	Calman crocodilus MHC class II beta chain (hclibeta) gene, complete cds
5655	18949	32131	4.8	1.5E-01	AW850754.1	EST_HUMAN	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5697	18881	32182	6.68	1.5E-01	U65016.1	NT	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
5697	18881	32183	6.68	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
6029	19212	32532	0.82	1.5E-01	4506810	NT	Mus musculus transforming growth factor alpha (TGFA) mRNA, complete cds
							Homo sapiens sodium channel, voltage-gated, type VI, alpha polypeptide (SCN6A) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6128	19307	32947	1.71	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnm12), mRNA
6128	19307	32948	1.71	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnm12), mRNA
6188	19344	32680	2.19	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6324	19496	32862	3.49	1.5E-01	BE727658.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3933981 5'
6376	19545		1.68	1.6E-01	4608398	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6474	19641	33002	1.74	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/490/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6831	25828	33179	3.58	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6861	18820	33207	4.73	1.5E-01	11417238	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
6872	18831	33220	1.51	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6719	19876	33267	2.35	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6823	19876	33383	0.86	1.5E-01	AAT14760.1	EST_HUMAN	nv30d10.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241871 3'
6852	20006	33414	2.24	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7118	18544	31500	6	1.5E-01	AW070295.1	EST_HUMAN	EST382376 IMAGE resequences, MAGK Homo sapiens cDNA
7158	25840		0.8	1.5E-01	A4811545.1	EST_HUMAN	cb7302.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337019 3' similar to contains element LTR2 repetitive element.
7395	20444		4.73	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7550	20822	34099	1.63	1.5E-01	A1873157.1	EST_HUMAN	wf62a08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
7764	20823	34314	0.88	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7764	20823	34315	0.88	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7775	20832	34322	1.68	1.5E-01	AW500811.1	EST_HUMAN	U1HF-BN0-akk-d-05-Q-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7775	20832	34323	1.68	1.5E-01	AW500811.1	EST_HUMAN	U1HF-BN0-akk-d-05-Q-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7919	20970	34477	0.79	1.5E-01	U46590.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of bsl-1 (SOL3) gene, complete cds
8248	21330	34846	0.99	1.5E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK68 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)
8414	21495	35026	1.1	1.5E-01	A4970317.1	EST_HUMAN	cc85g12.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26082
8507	21588		1.06	1.5E-01	BE884799.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN)
8594	21675		14.14	1.5E-01	C16800.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8628	21708	35245	1.87	1.5E-01	L27835.1	NT	C16800 Clontech human aorta polyA+ mRNA (#8572) Homo sapiens cDNA clone GEN-529H09 5'
8763	21872	35411	2.17	1.5E-01	D84478.1	NT	P angelomonon gligas growth hormone (GH) mRNA, complete cds
8814	21893		0.76	1.5E-01	P43446	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
9038	22117	35860	3.12	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
							Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8305	22381	35932	2.58	1.5E-01	N74226.1	EST_HUMAN	z559e08.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:298866 3' similar to PIR:S44443 S44443 RAD23 protein homolog2 - human ;
8394	22469	36033	1.34	1.5E-01	BF595465.1	EST_HUMAN	GVO00404 Human Poriolosis Differential Display Homo sapiens cDNA
9401	22475		2.52	1.5E-01	AV754819.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAB12 5'
8605	22660		0.64	1.6E-01	AU190007.1	EST_HUMAN	AU190007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5'
9652	21055	34609	6.7	1.5E-01	U00455.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
10022	23060	36656	0.71	1.5E-01	M77144.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
10125	23163	36761	7.82	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10126	23163	36762	7.82	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10407	23442	37049	2.59	1.5E-01	X98852.1	NT	P. lentusculi mRNA for integrin beta subunit
10498	23630		0.51	1.5E-01	AB027759.1	NT	Mesocricetus auratus mRNA for collagen type XVII, complete cds
10516	23551	37161	2.36	1.5E-01	A1814048.1	EST_HUMAN	wk53h12.x1 NCL CGAP_P122 Homo sapiens cDNA clone IMAGE:2419176 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10516	23551	37162	2.36	1.5E-01	A1814048.1	EST_HUMAN	wk53h12.x1 NCL CGAP_P122 Homo sapiens cDNA clone IMAGE:2419176 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10588	23633	37242	1.22	1.6E-01	U40382.1	NT	Danio rerio transcription factor Pax8b (Pax8) mRNA, complete cds.
10761	23784	37413	1.69	1.6E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
10761	23784	37414	1.69	1.6E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
10935	24017	37649	1.67	1.6E-01	BE088492.1	EST_HUMAN	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
10935	24017	37650	1.67	1.6E-01	BE088492.1	EST_HUMAN	CM2-BT0688-210300-122-f11 BT0688 Homo sapiens cDNA
11063	24139	37773	4.46	1.6E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11063	24139	37774	4.46	1.6E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
11331	24394	38042	1.38	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
11925	24911		1.34	1.5E-01	AU193704.1	EST_HUMAN	qe72e01.x1 Soares fetal_lung_NbhL19W Homo sapiens cDNA clone IMAGE:1744538 3' similar to gb:U17887 80S ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);
12332	25963		38.98	1.5E-01	BF700582.1	EST_HUMAN	602123753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
12628	25422		1.64	1.6E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12633	25428		1.23	1.5E-01	AJ238332.1	NT	Mus musculus mRNA for death inducer-obiterator-1 (Dio-1)
12696	25976		6.64	1.5E-01	R63077.1	EST_HUMAN	yp87e04.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:194430 5'
12749	25468		1.52	1.5E-01	AP001514.1	NT	Bacillus halodurans genomic DNA, section 8/14
12778	25520	32002	1.41	1.5E-01	9695413	NT	Lymphocystis disease virus 1, complete genome
12807	26000		2.59	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDA004 5'
12932	25898	31857	7.68	1.5E-01	AL139074.2	NT	Campylobacter jejuni NC:TC11168 complete genome, segment 1/8

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13183	25769	31932	6.61	1.6E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
13227	26138		2.26	1.6E-01	8631294	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
310	13526		1.23	1.4E-01	AF008863.1	NT	Homo sapiens T cell receptor beta locus, TCRBV8S6P to TCRBV21S2A2 region
933	14108		3.24	1.4E-01	U78838.1	NT	Xenopus laevis mRNA for DNA (cytosine-5)-methyltransferase, complete cds
1288	14444		2.89	1.4E-01	T01864.1	EST_HUMAN	Y05401.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'
1787	14936		1.48	1.4E-01	6676960	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1790	14939	28032	1.84	1.4E-01	AE001710.1	NT	Thermoboga maritima section 22 of 136 of the complete genome
1954	15097		1.27	1.4E-01	AW13741.1	EST_HUMAN	U1-H-B1-act-a-09-0-U1.s1 NCL CGAP_Sub33 Homo sapiens cDNA clone IMAGE:2714009 3'
2042	15183		14.84	1.4E-01	AA720815.1	EST_HUMAN	U72407.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283921 3'
2544	16669	28783	1.02	1.4E-01	P30708	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2853	16987	28077	3.34	1.4E-01	A1933498.1	EST_HUMAN	wm74d01.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2441865 3'
4289	17434	30421	9.45	1.4E-01	A1695084.1	EST_HUMAN	b66602.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4289	17434	30422	9.45	1.4E-01	A1695084.1	EST_HUMAN	b66602.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4362	17495	30475	4.28	1.4E-01	AE001710.1	NT	Thermoboga maritima section 22 of 136 of the complete genome
4531	17669		0.7	1.4E-01	AA776287.1	EST_HUMAN	z60601.s1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:453673 3' similar to gb:X01057_mai INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element;
4788	17933	30920	0.79	1.4E-01	5453861	NT	Homo sapiens phosphodiesterase 4A, cAMP-specific (durae) (Drosophila)-homolog phosphodiesterase E2) (PDE4A), mRNA
5322	18436	31406	0.62	1.4E-01	AJ005180.1	NT	Lycopodium esculentum genomic RAPD band 26
5421	18622	31698	5.21	1.4E-01	T90677.1	EST_HUMAN	y615c11.s1 Stralagene lung (R337210) Homo sapiens cDNA clone IMAGE:117812 3'
5444	18644	31621	4.33	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5444	18644	31622	4.33	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
8427	18595	32861	3.17	1.4E-01	BE326891.1	EST_HUMAN	hr87c02.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
8611	19771	33161	4.45	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone IMAGE:1000769 5'
8611	19771	33162	4.45	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone IMAGE:1000769 5'
8701	19859	33249	3.7	1.4E-01	AW082766.1	EST_HUMAN	x671d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
8715	19873		1.51	1.4E-01	BE26536.1	EST_HUMAN	QV1-UM0036-080300-103-d03 UM0036 Homo sapiens cDNA
8739	19895	33286	2.48	1.4E-01	BF378533.1	EST_HUMAN	DKFZb761A0810.r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZb761A0910 5'
7276	20359		0.71	1.4E-01	AL118568.1	EST_HUMAN	U1-H-B10-act-c-09-0-U1.s1 NCL CGAP_Sub31 Homo sapiens cDNA clone IMAGE:2710289 3'
7645	20617		1.78	1.4E-01	AW016373.1	EST_HUMAN	w04f12.x1 NCL CGAP_C11 Homo sapiens cDNA clone IMAGE:2389295 3' similar to SW:ICE4_HUMAN
7818	20888		0.73	1.4E-01	AI762827.1	EST_HUMAN	P48662 CASPASE-4 PRECURSOR;



Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7621	20861	34167	0.83	1.4E-01	T53770.1	EST_HUMAN	y80H11.r2 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:68973 5' similar to contains
7769	20855	34345	0.95	1.4E-01	U85645.1	NT	Alu repetitive element
7832	20982	34490	1.02	1.4E-01	A130512.1	EST_HUMAN	Oryctolagus cuniculus fructose 1,6, biphosphate aldolase (AldB) gene, complete cde
8162	21244		0.54	1.4E-01	BF310258.1	EST_HUMAN	q180b12.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:187893 3'
8870	21750		1.32	1.4E-01	AV659047.1	EST_HUMAN	601894760.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124199 5'
8984	22063		0.6	1.4E-01	A1436093.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCFSH08 3'
9114	22183	35738	4.94	1.4E-01	AA307073.1	EST_HUMAN	th92b12.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2128111 3' similar to
9194	22272	36810	0.76	1.4E-01	AW023638.1	EST_HUMAN	TR:O02710 O02710 GAG POLYPROTEIN. ;
9322	22398	35951	1.07	1.4E-01	R62746.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9322	22398	35952	1.07	1.4E-01	R62746.1	EST_HUMAN	d158b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9388	22463	36027	8.62	1.4E-01	BF310959.1	EST_HUMAN	y10c05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9475	22532	36098	1.72	1.4E-01	W63411.1	EST_HUMAN	y10c05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9547	22612	36180	0.54	1.4E-01	X73293.1	NT	60189465.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9558	22623	36194	1.65	1.4E-01	Y10196.1	NT	z69404.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains
9558	22623	36195	1.65	1.4E-01	Y10196.1	NT	element KER repetitive element ;
9849	21092	34607	1.81	1.4E-01	AF121381.1	NT	M.vannelli genes rpoH, rpoB and rpoA
10009	23047	36641	0.54	1.4E-01	X66092.1	NT	M.vannelli genes rpoH, rpoB and rpoA
10192	23229	36821	0.89	1.4E-01	AF023813.1	NT	Homo sapiens PHEX gene
10293	23328	36931	0.81	1.4E-01	AW021908.1	EST_HUMAN	Homo sapiens PHEX gene
10293	23328	36932	0.81	1.4E-01	AW021908.1	EST_HUMAN	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase lal (IAL), and
10463	23498	37109	0.76	1.4E-01	BF376285.1	EST_HUMAN	zinc finger protein (DNZ1) genes, complete cds
10463	23498	37110	0.76	1.4E-01	BF376285.1	EST_HUMAN	C.porfingens ORF for putative membrane transport protein
10690	23714		0.51	1.4E-01	T84293.1	EST_HUMAN	Macromitrium levatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein,
10825	23858	37481	0.7	1.4E-01	Z69117.1	NT	partial cds
10948	24030		1.32	1.4E-01	AA811480.1	EST_HUMAN	d128h03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
11081	24156	37783	2.57	1.4E-01	R63400.1	EST_HUMAN	d128h03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
11282	24348	37985	1.69	1.4E-01	AW104982.1	EST_HUMAN	MF3-S10218-211299-013-a08 S10218 Homo sapiens cDNA
11354	24416	38071	1.88	1.4E-01	T66102.1	EST_HUMAN	MF3-S10218-211299-013-a08 S10218 Homo sapiens cDNA
							MF3-S10218-211299-013-a08 S10218 Homo sapiens cDNA
							y47403.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:111365 5'
							Bacillus subtilis complete genome (section 14 of 21): from 2699461 to 2812870
							ca89a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3'
							y17c05.r1 Soares breast 2NbHb1 Homo sapiens cDNA clone IMAGE:154088 5'
							x373e10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603274 3'
							y47g10.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:120930 5'

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11354	24416	38072	1.53	1.4E-01	T88102.1	EST_HUMAN	ye47g10.17 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:120530 5'
11356	24418	38075	2.38	1.4E-01	P08848	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-F) (VLA-5) (CD49E)
11572	24627	38306	1.85	1.4E-01	X68092.1	NT	C.parietogens ORF for putative membrane transport protein
11613	20617		1.57	1.4E-01	AW015373.1	EST_HUMAN	UHP10-act-c-09-01.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11757	23943	37570	2.07	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
11816	24808		1.51	1.4E-01	X52102.1	NT	M.musculus p16K gene for 16 kDa protein
12038	25020	38724	10.18	1.4E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; iPhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and HSAR (Hsar) gene, complete cds
12560	25382	32038	4.68	1.4E-01	X74773.1	NT	P.salina plastid gene secY
12574	25360		3.28	1.4E-01	11968117	NT	Rattus norvegicus desmin (Dco), mRNA
12605	25405		1.71	1.4E-01	BE984835.2	EST_HUMAN	601659490R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3885671 3'
12827	26178		2.83	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
12724	25482		7.52	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycylamide ribonucleotide transferase (GART) genes, complete cds
12742	25493		4.02	1.4E-01	D64004.1	NT	Synchoocytis ep. PC6803 complete genome, 23/27, 2888767-3002965
12834	26193		3.2	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12928	25812		1.45	1.4E-01	X69192.1	NT	V.plantifolia mRNA for methyltransferase
13084	25977		3.38	1.4E-01	D82883.1	NT	Mus musculus mRNA for prolidase, complete cds
13178	25765		1.68	1.4E-01	AW377898.1	EST_HUMAN	MR0-HT0208-221299-204-608 HT0208 Homo sapiens cDNA
332	13546	26578	2.27	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
332	13546	26577	2.27	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
542	13735	26769	1.88	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
653	13838	26868	2.43	1.3E-01	AJ277606.1	NT	Human calicivirus HUJNLV/Girlington/93/UJK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/93/UJK
653	13839	26867	2.43	1.3E-01	AJ277606.1	NT	Human calicivirus HUJNLV/Girlington/93/UJK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/93/UJK
867	14043	27108	1.55	1.3E-01	X53330.1	NT	P.dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
917	14092	27167	1.28	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1092	14218	27274	2.14	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1151	14315		2.04	1.3E-01	AL115265.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1242	14401	27482	1.87	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAFF05 5'

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Table 4

## Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1475	14628		0.97	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein QMS mRNA, complete cds
1905	15048	28159	1.02	1.3E-01	6680957	NT	Mus musculus procollagen, type XI, alpha 1 (Col11a1), mRNA
2014	15154	28259	2.73	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2239	15372		1.08	1.3E-01	AJ243578.1	NT	Rhodospirillum rubrum acidophila pucB5, pucA5, pucB6, pucA7, pucB8, pucA8 and pucC genes and ORF151
2364	15485		1.38	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191069-032-412 ST0173 Homo sapiens cDNA
2455	15583		3.31	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2653	15776	28889	2.78	1.3E-01	M85918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3440	16608	29628	1.21	1.3E-01	AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 8, and synepthophysin genes, complete cds; and L-type calcium channel 3p
3539	16704	29715	1.11	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3816	16976	29979	0.85	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3816	16978	29980	0.85	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3822	16982	29985	1.55	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrolipoyl dehydrogenase 4 [AKR1C4], exon 2
3905	17064	30063	0.88	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
4098	17251		1.08	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4162	13639	26866	0.88	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington93/UK
4162	13639	26867	0.88	1.3E-01	AJ277608.1	NT	Human calicivirus HUNLV/Girlington93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington93/UK
4257	17402		0.82	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4274	17419		3.74	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081209-036-403 DT0018 Homo sapiens cDNA
4281	17426	30415	1.82	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4302	17446	30431	21.62	1.3E-01	AW273741.1	EST_HUMAN	xx2310.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4434	17574		1.19	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4601	17738	30717	0.61	1.3E-01	M21672.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4656	17792	30776	2.64	1.3E-01	BE272339.1	EST_HUMAN	601126088F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:2890063 5'
4748	17883	30869	0.73	1.3E-01	BF078854.1	EST_HUMAN	602164308F1 NIH_MGC 39 Homo sapiens cDNA clone IMAGE:4265544 5'
5314	18431	31401	0.78	1.3E-01	AF000005.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 994901-1168000 nt. position (577)
5440	18840	31619	1.01	1.3E-01	AW466888.1	EST_HUMAN	he07006.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1
5478	18677	31690	1.83	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM0093-100400-189-a06 UM0093 Homo sapiens cDNA
5618	18812		0.92	1.3E-01	AF107703.1	NT	Emeticella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5702	18885		0.87	1.3E-01	AF056880.1	NT	Hepatitis C virus 68 Cl-10 genome polyprotein gene, partial cds
5842	19032	32338	0.72	1.3E-01	BF210920.1	EST_HUMAN	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6107	19287	32621	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4177233 5'
6107	19287	32622	0.58	1.3E-01	BF527281.1	EST_HUMAN	602039337F2 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4177233 5'
6612	19772	33163	18.92	1.3E-01	AB031328.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6698	18856	33246	2.26	1.3E-01	X88891.1	NT	C.jacchus intron 4 of visual pigment gene (red allele)
6927	20242		0.74	1.3E-01	W26367.1	EST_HUMAN	2873 Human retina cDNA randomly primed/sublibrary Homo sapiens cDNA
6974	20202	33628	0.7	1.3E-01	BE782928.1	EST_HUMAN	601465957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3889079 5'
6974	20202	33629	0.7	1.3E-01	BE782928.1	EST_HUMAN	601465957F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3889079 5'
7155	20289		0.74	1.3E-01	BF629560.1	EST_HUMAN	602044345F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4181868 5'
7412	20490		1.97	1.3E-01	H48664.1	EST_HUMAN	y33602.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207076 5'
8146	21228		0.79	1.3E-01	BE272330.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2990063 5'
8160	21242	34762	1.68	1.3E-01	11423284	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
8192	21274	34787	1.32	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
8469	21550	35080	0.66	1.3E-01	11421556	NT	Homo sapiens TED protein (TED), mRNA
8540	21621		4.24	1.3E-01	Z74102.1	NT	S. cerevisiae chromosome IV reading frame ORF YDLO54c
8580	21661		4.86	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8725	21805	35342	1.26	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'
9149	22227	35770	0.57	1.3E-01	R11172.1	EST_HUMAN	y339g11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129284 5' similar to
9149	22227	35771	0.57	1.3E-01	R11172.1	EST_HUMAN	SP:RL2B RAT P29316 90S RIBOSOMAL PROTEIN ;
9420	22484	36060	0.69	1.3E-01	11068003	NT	SP:RL2B RAT P29316 90S RIBOSOMAL PROTEIN ;
9420	22484	36061	0.69	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9872	22634	36204	4.19	1.3E-01	AF023128.1	NT	Plutella xylostella granulovirus, complete genome
9873	23012		0.73	1.3E-01	N86948.1	EST_HUMAN	Oryzopsis cuniculatus H+K+ATPase alpha 2c subunit mRNA, complete cds
10267	23262		1.07	1.3E-01	8393940	NT	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL
10335	23370	36980	0.95	1.3E-01	AW851599.1	EST_HUMAN	RECEPTOR ASSOCIATED PROTEIN (BAP) 29
10603	25864	37244	1.08	1.3E-01	AL163246.2	NT	Rattus norvegicus peptidyl arginine deiminase, type IV (Pdi4), mRNA
10743	23778	37389	0.65	1.3E-01	AW121237.1	EST_HUMAN	MR2-CT0222-201099-001-e01 CT0222 Homo sapiens cDNA
10797	23830	37454	0.45	1.3E-01	AW247838.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
10866	23963		2.31	1.3E-01	BF330989.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
11455	24515		1.34	1.3E-01	BF092708.1	EST_HUMAN	2820637.3p1fme NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820637 3'

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11529	24585		3.2	1.3E-01	6571745	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
11616	24667	38354	2.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11616	24667	38355	2.42	1.3E-01	BF677328.1	EST_HUMAN	602087045F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251346 5'
11895	24883	38581	7.06	1.3E-01	BE279449.1	EST_HUMAN	601198052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
12000	24885		1.41	1.3E-01	AF012836.1	NT	Thermococcus litoralis trehalose/maltose transporter operon including trehalose/maltose binding protein (malE) and inner membrane proteins MalF (malF) and MalG (malG) genes, complete cds
12023	25007	39708	1.72	1.3E-01	BE618364.1	EST_HUMAN	601473989F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876208 5'
12052	25033	38739	1.52	1.3E-01	BF683555.1	EST_HUMAN	602139760F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300883 5'
12399	25279	32080	2.13	1.3E-01	BE618346.1	EST_HUMAN	601482741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'
12543	25368		6.39	1.3E-01	AJ242780.1	NT	Gallus gallus syo1 gene for lymphocytin, exons 1-3
12984	25627		1.31	1.3E-01	AB028829.1	NT	Ephydra fluviatilis mRNA for sALK-B, complete cds
12995	25647		1.87	1.3E-01	AW001114.1	EST_HUMAN	wu24409.x1 Scores_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:O80287 O80287 KIAA0639 PROTEIN, ;
394	13631	25688	13.87	1.2E-01	AK21744.1	EST_HUMAN	t339002.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2096539 3' similar to gb:U05760_rna1 ANNEXIN V (HUMAN);
437	13237		1.42	1.2E-01	U66912.1	NT	Dictyostellium discoideum ORF DG1016 gene, partial cds
561	13753		3.82	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CQ-45 mRNA, partial cds
1408	14662	27638	2.32	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1408	14662	27637	2.32	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1414	14568		3.35	1.2E-01	AV735249.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdaAJB11 5'
1419	14572		0.94	1.2E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome, segment 4/5
1536	14689		0.94	1.2E-01	AA897474.1	EST_HUMAN	al48609.s1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1480584 3' similar to TR:Q16671 Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR, ;
1660	14812	27897	1.1	1.2E-01	Q14834	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1682	14834	27819	2.88	1.2E-01	AI285402.1	EST_HUMAN	q38909.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1980563 3'
1808	14857		25.75	1.2E-01	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
1970	15113		1.66	1.2E-01	AW448368.1	EST_HUMAN	U1H-BI3-adv-e-10-0-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2253	15386	28514	1.68	1.2E-01	BF248490.1	EST_HUMAN	601821667F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2450	15378		0.99	1.2E-01	Z21403.1	EST_HUMAN	HSAAABE2T TEST1, Human adult Testis tissue Homo sapiens cDNA
2636	15779	28693	1.84	1.2E-01	AW695566.1	EST_HUMAN	QV3-BN0040-129-f10 BN0046 Homo sapiens cDNA
2805	16083	28088	1.18	1.2E-01	U18018.1	NT	Human ETA enhancer binding protein (ETA-F) mRNA, partial cds
2867	16143	28162	1.9	1.2E-01	A1720470.1	EST_HUMAN	aa80c09.x1 Barstead colon HPLB87 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05085 GOS RIBOSOMAL PROTEIN L30 (HUMAN);

Table 4

## Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3001	18177	29188	3.44	1.2E-01	M16364.1	NT	Human creatine kinase-B mRNA, complete cds
3068	16244	29265	0.91	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3302	18476	29488	2.52	1.2E-01	AW370668.1	EST_HUMAN	QV1-BT0259-281089-021-405 BT0259 Homo sapiens cDNA
3330	18503		0.74	1.2E-01	U67900.1	NT	Methanococcus jannaschii, section 142 of 180 of the complete genome
3588	18733		0.66	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3610	18774	29789	1.12	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3610	18774	29789	1.12	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3694	18733		1.22	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3865	17024		0.95	1.2E-01	BF128551.1	EST_HUMAN	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4083668 3'
4298	17441	30426	2.1	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MRT7)
4298	17441	30427	2.1	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MRT7)
4431	17571	30552	0.59	1.2E-01	M15861.1	NT	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
4942	18072		1.94	1.2E-01	X73416.1	NT	W. suavis mitochondria off1
5364	18557	31433	0.89	1.2E-01	AA744369.1	EST_HUMAN	ny63c04.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'
5415	18617	31591	0.93	1.2E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5425	18626	31601	2.5	1.2E-01	W33035.1	EST_HUMAN	zc08d02.r1 Soares_papillary_tumor_Nb1HPA Homo sapiens cDNA clone IMAGE:321689 5'
5484	18683	31700	1.65	1.2E-01	Z98268.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
5622	18916	31885	1.14	1.2E-01	Z48234.1	NT	M.domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6329	19500	32858	1.9	1.2E-01	BE820945.1	EST_HUMAN	60149381BF1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6377	19546	32903	0.81	1.2E-01	P10842	SWISSPROT	MATING-TYPE P-SPECIFIC POLYPEPTIDE P1
6428	19596	32862	2.28	1.2E-01	AW845275.1	EST_HUMAN	IL0-CT0031-221089-113-e04 CT0031 Homo sapiens cDNA
6493	19659	33022	1.52	1.2E-01	M26926.1	NT	Mouse galactosyltransferase mRNA, complete cds
6591	19723	33101	0.58	1.2E-01	AA747635.1	EST_HUMAN	rx85c01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1269024 3'
6785	19940	33338	1.18	1.2E-01	BF347985.1	EST_HUMAN	602023112F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158388 5'
7154	20288	33731	0.64	1.2E-01	H47799.1	EST_HUMAN	yp80f04.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:183759 5'
7164	20288	33732	0.64	1.2E-01	H47799.1	EST_HUMAN	yp80f04.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:183759 5'
7772	20829	34320	0.62	1.2E-01	AJ271741.1	NT	Homo sapiens partial ILF3 gene for Interleukin enhancer binding factor 3 (alternative transcripts dbp76, dbp76 gamma, dbp76 alpha and ILF3)
8076	21168		1.13	1.2E-01	BE007072.1	EST_HUMAN	PM3-BN0137-280300-002-409 BN0137 Homo sapiens cDNA
8149	21231	34751	2.45	1.2E-01	AI913753.1	EST_HUMAN	wc99g03.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN
8197	21278	34801	0.64	1.2E-01	Q02369	SWISSPROT	Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II
8604	21655	35119	0.66	1.2E-01	AI832881.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (Cl-B22)

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST-E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8590	21671		10.78	1.2E-01	AW083652.1	EST_HUMAN	xc49d07.x1 NCL_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
8611	21691		3.76	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8649	21729	36266	1.09	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8649	21729	35287	1.09	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8800	21879		1.02	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
8887	21868		1.44	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 103 of the complete genome
8920	21868		0.77	1.2E-01	X15191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
9771	22767	36338	1.3	1.2E-01	X77961.1	NT	S.cerevisiae HXT5 gene
10209	23245	36835	0.9	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone GUAKE08 5'
11125	24197		2.55	1.2E-01	D26184.1	NT	Yeast MPT5 gene for suppressor protein, complete cds
11320	24363		3.03	1.2E-01	BE662324.2	EST_HUMAN	Y6055578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
11414	24475		1.73	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11533	24589	38264	2.78	1.2E-01	AF160493.1	NT	Homo sapiens dynein intermediate chain DNA11 (DNA11) gene, exon 17
11593	24646	38329	1.72	1.2E-01	R40249.1	EST_HUMAN	Y80c02.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28880 3'
11798	24768		2.47	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
12161	25128		2.09	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCFIB12 3'
12522	25355		4.37	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
12614	26126	31544	2	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
12732	25488		1.65	1.2E-01	AF188932.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaxin gene, partial cds
12734	13763		18.32	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12863	25574		1.4	1.2E-01	X63091.1	NT	R.norvegicus NF68 gene for 68kDa neurofilament
12868	25629	31681	4.89	1.2E-01	A1299003.1	EST_HUMAN	qn20g05.x1 NCL_CGAP_Lus Homo sapiens cDNA clone IMAGE:1898840 3'
12892	25844		3.46	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12897	26050		6.44	1.2E-01	O80433	SWISSPROT	CYCLIN T
13031	25670	31060	1.47	1.2E-01	AE004426.1	NT	Vibrio cholerae chromosome II, section 86 of 63 of the complete chromosome
13221	25795		1.23	1.2E-01	AF090141.1	NT	Chryseobacterium meningosepticum GOB-1 carboxypeptidase gene, complete cds
578	13770	26792	1.56	1.1E-01	AJ581003.1	EST_HUMAN	hm08g11.s1 NCL_CGAP_Brn28 Homo sapiens cDNA clone IMAGE:2167983 3'
630	13815	26838	1.33	1.1E-01	AA569006.1	EST_HUMAN	nm08g11.s1 NCL_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1069620 3' similar to gb:X06985_rna1 HEME OXYGENASE 1 (HUMAN);

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1079	14245	27302	1.51	1.1E-01	BF697308.1	EST_HUMAN	602129847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1109	14274		1.85	1.1E-01	AL181560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1185	16031	27405	3.87	1.1E-01	AW972198.1	EST_HUMAN	EST384142 MAGE resequences, MAGL Homo sapiens cDNA
1278	14435	27505	1.88	1.1E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002865
1549	14701	27780	2.75	1.1E-01	AU140363.1	EST_HUMAN	AUT40363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2255	15368		1.73	1.1E-01	AJ008701.1	NT	Homo sapiens mRNA for putative serine/threonine protein kinase, partial
2368	15519		2.02	1.1E-01	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Pctra), mRNA
2603	16999		1.08	1.1E-01	6978578	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2633	15756		1.27	1.1E-01	AW821909.1	EST_HUMAN	RC0-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
2817	16095	29107	0.89	1.1E-01	S92418.1	NT	Interleukin-12 p35 subunit [mice, Genomic], 700 nt, segment 4 of 6]
3088	16274	29286	0.81	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
3422	16591		1.56	1.1E-01	6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Ca $\alpha$ 1g), mRNA
3508	16676	29885	2.09	1.1E-01	BE393186.1	EST_HUMAN	60130867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627066 5'
3540	16705	29718	1.47	1.1E-01	X62135.1	NT	C.reinhardtii nuclear gene on linkage group XIX
3580	16745	29763	0.71	1.1E-01	R96946.1	EST_HUMAN	yq62g08.s1 Soares fetal liver spleen 1NF1S3 Homo sapiens cDNA clone IMAGE:200414 3' similar to contains Alu repetitive element
3673	16836	29846	0.7	1.1E-01	Y07695.1	NT	A.immersus gene for transposase
3791	16952		0.96	1.1E-01	P97394	SWISSPROT	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
3800	16961	29865	1.28	1.1E-01	X52708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4226	17374	30359	1.2	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
4226	17374	30360	1.2	1.1E-01	AW819412.1	EST_HUMAN	MR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
4233	17380		0.83	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds;
4367	17510		11.45	1.1E-01	AF157086.1	NT	Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complex
4401	17544	30528	0.76	1.1E-01	AW802058.1	EST_HUMAN	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4782	17897	30877	0.92	1.1E-01	S44957.1	NT	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
4953	18083	31059	1.23	1.1E-01	Y07695.1	NT	Tape-1=integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
5134	17380		0.75	1.1E-01	AF030001.1	NT	A.immersus gene for transposase
5787	18978		2.59	1.1E-01	AA747216.1	EST_HUMAN	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complex
							nt76a03.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1288140 similar to contains Alu repetitive element; contains element MER35 repetitive element;



Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5857	18047	32353	1.32	1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5894	18082	32393	0.87	1.1E-01	AL110985.1	NT	Bdella ciherea strain T4 cDNA library under conditions of nitrogen deprivation
5927	19113	32425	0.95	1.1E-01	BF339518.1	EST_HUMAN	602039176F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:416818 5'
5927	19113	32426	0.96	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:416818 5'
5958	19144	32469	1.79	1.1E-01	X68851.1	NT	S. pombe est8 gene encoding protein kinase
5992	19177	32498	5.15	1.1E-01	M86533.1	NT	Providencia rettgeri penicillin G amidase gene
6150	18226	32671	1.68	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
6171	19347	32893	1.37	1.1E-01	BE769162.1	EST_HUMAN	PM3-FT0024-130600-004-f12 FT0024 Homo sapiens cDNA
6191	19367	32716	7.73	1.1E-01	AW653699.1	EST_HUMAN	RC3-CT0254-280989-011-a01 CT0254 Homo sapiens cDNA
6554	19716	33082	0.61	1.1E-01	AL183282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6562	19724	33102	1.52	1.1E-01	AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6602	19762	33150	0.84	1.1E-01	A1216307.1	EST_HUMAN	qg78408.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6742	19898	33289	3.68	1.1E-01	O69635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6843	19996		2.73	1.1E-01	AF032922.1	NT	Homo sapiens syntrophin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6884	20249	33684	2.74	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7193	20058	33468	0.74	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7193	20058	33469	0.74	1.1E-01	AE002155.1	NT	Ureaplasma urealyticum section 56 of 59 of the complete genome
7337	26217		1.01	1.1E-01	BF332798.1	EST_HUMAN	601816624F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050853 5'
7456	258-5	34007	0.98	1.1E-01	AF000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (87)
7706	20771	34255	7.51	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7706	20771	34268	7.51	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7833	20888	34391	2.16	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
7872	20928		0.64	1.1E-01	Z14098.1	NT	B. subtilis gene encoding hypothetical polyketide synthase
7873	20927	34433	3.08	1.1E-01	AA788784.1	EST_HUMAN	af31506.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone 1240403 3' similar to gb.J03483
8155	21237	34758	1.58	1.1E-01	U67492.1	NT	CHROMOGGRANIN A PRECURSOR (HUMAN);
8403	21484	35012	1.96	1.1E-01	AA493574.1	EST_HUMAN	Methanococcus jannaschii section 34 of 150 of the complete genome
8403	21484	35013	1.55	1.1E-01	AA493574.1	EST_HUMAN	rh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943382
8448	21530	35059	1.28	1.1E-01	X91233.1	NT	rh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943382
8489	21570		0.94	1.1E-01	AW81791E.1	EST_HUMAN	H. sapiens IL15 gene
8546	21627	35165	2.31	1.1E-01	AL134349.1	EST_HUMAN	PM1-ST0270-080200-001-f08 ST0270 Homo sapiens cDNA
8018	22097	35637	5.07	1.1E-01	U02482.1	NT	DKFZp547P194_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547P194 5'
							Pediococcus acidilactici H plasmid pSMB74 pediocin (pap) gene cluster papA, papB, papC and papD genes, complete cds

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9113	22192	35737	1.04	1.1E-01	AI807474.1	EST_HUMAN	wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element;
9210	22288	35830	0.5	1.1E-01	AF030081.1	NT	Homo sapiens C16orf3 large protein mRNA, complete cds
9243	22320	35863	2.25	1.1E-01	AA192153.1	EST_HUMAN	z983b12.f1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:827743 5'
9243	22320	35864	2.25	1.1E-01	AA192153.1	EST_HUMAN	z983b12.f1 Stralagene muscle 937209 Homo sapiens cDNA clone IMAGE:827743 5'
9338	22411	35884	0.71	1.1E-01	Y12127.1	NT	P.furiosus partial dph5 gene and atpF gene
9388	22441	36001	2.76	1.1E-01	T72875.1	EST_HUMAN	y419f03.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gdpM81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9392	22467		0.83	1.1E-01	BE893260.1	EST_HUMAN	601436972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
9622	22677		0.89	1.1E-01	BE142305.1	EST_HUMAN	GM3-H10142-271059-028-g11 HT0142 Homo sapiens cDNA
9698	22745		2.33	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
10114	23152		0.77	1.1E-01	AL161643.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10410	23445		1.23	1.1E-01	R60590.1	EST_HUMAN	y98a00.o1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:147064 3'
10544	23579	37188	1.29	1.1E-01	U03529.1	NT	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
10914	23987	37631	1.38	1.1E-01	AF245277.1	NT	Dicotyledon discoidium Khresin Unc104/JUF-1a homolog (Unc104) mRNA, complete cds
11044	16274	29288	1.78	1.1E-01	F03285.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
11182	24233		2.47	1.1E-01	AF169032.1	NT	Carassius auratus actin/beta A precursor mRNA, complete cds
11300	24368	38007	3.11	1.1E-01	R23708.1	EST_HUMAN	y356f12.f1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
11483	24542	38212	2.8	1.1E-01	Z11910.1	NT	Z.mobilis tat and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11483	24542	38213	2.6	1.1E-01	Z11910.1	NT	Z.mobilis tat and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11510	24568	38245	1.69	1.1E-01	BE602974.1	EST_HUMAN	601676924F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959668 5'
11588	24639	38318	3.21	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11971	24958		1.33	1.1E-01	AL161511.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
12378	25269		3.78	1.1E-01	BE787023.1	EST_HUMAN	RC2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA
12849	25910		3.18	1.1E-01	BE974556.1	EST_HUMAN	601680651R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'
13136	25738	31847	1.98	1.1E-01	BF239753.1	EST_HUMAN	601806350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1228	14388		1.61	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1301	14457	27523	2.18	1.0E-01	AI985499.1	EST_HUMAN	wc08d01.x1 NCI_CGAP_K111 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MER7.13
1423	14577	27650	2.3	1.0E-01	AL161504.2	NT	MER7 repetitive element;
2558	15883	28808	1.01	1.0E-01	AV451365.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3813	16973	29978	1.11	1.0E-01	BF239818.1	EST_HUMAN	U1-H-B13-alc-d-07-o-U1.s1 NCI_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2736420 3'
4064	17220	30228	2.6	1.0E-01	BF365703.1	EST_HUMAN	601806489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4627	17665	30651	1.44	1.0E-01	AE002265.2	NT	Chlamydia pneumoniae AR39, section 91 of 94 of the complete genome
4677	17812		0.78	1.0E-01	AI792349.1	EST_HUMAN	en32c04.y6 Geesler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4834	17967	30955	2.17	1.0E-01	U90450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (far) mRNA, complete cds
5039	18167	31143	2.17	1.0E-01	AW952344.1	EST_HUMAN	EST1364414 IMAGE resequences, MAGB Homo sapiens cDNA
5261	18390	31346	0.81	1.0E-01	BE389100.1	EST_HUMAN	601288959F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613552 5'
5436	18636		9.49	1.0E-01	W88490.1	EST_HUMAN	zh82h04.s1 Scores_fetal_liver_spleen_TNFS_S1 Homo sapiens cDNA clone IMAGE:418695 3'
5534	18731		0.87	1.0E-01	XG4015.1	NT	X campestris genes for sensor and regulator protein
6001	19188		1.08	1.0E-01	AK024472.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
6148	19325	32670	13.08	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6465	19632	32993	0.9	1.0E-01	AA481879.1	EST_HUMAN	241g10.s1 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:766258 3' similar to contains L1.13 L1 repetitive element
6479	19846	33008	0.72	1.0E-01	AA406039.1	EST_HUMAN	2467c12.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:743082 3'
7164	20297		1.87	1.0E-01	R23821.1	EST_HUMAN	yh34h06.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element
7814	20665		2.39	1.0E-01	Y12488.1	NT	M.musculus wtn gene
8118	21200	34721	0.69	1.0E-01	AA881091.1	EST_HUMAN	al32g01.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1407898 3' similar to gb.M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8141	21223	34741	2.17	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8141	21223	34742	2.17	1.0E-01	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8689	21769		0.96	1.0E-01	AW189797.1	EST_HUMAN	X09501.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb.X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.13 TAR1 repetitive element
9387	22482	36026	1.12	1.0E-01	AF102856.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synatron mRNA, complete cds
9695	22744	36314	0.87	1.0E-01	R44993.1	EST_HUMAN	y933h04.s1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:34549 3'
9707	22766		1.9	1.0E-01	M76729.1	NT	Human pro-alpha-1(V) collagen mRNA, complete cds
9750	22888		3.15	1.0E-01	AE001501.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
9764	22761	36331	0.95	1.0E-01	W01955.1	EST_HUMAN	zo66c10.s1 Scores_fetal_heart_NBH110W Homo sapiens cDNA clone IMAGE:327282 3'
10026	23094	36661	1.88	1.0E-01	BF240154.1	EST_HUMAN	601805681F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
10139	23177	36774	8.92	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10139	23177	36775	8.92	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10347	23382		1.06	1.0E-01	AW957425.1	EST_HUMAN	EST369615 IMAGE resequences, MAGB Homo sapiens cDNA
10351	23388	36956	0.62	1.0E-01	T51952.1	EST_HUMAN	y529a06.s1 Stragelene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element
10537	23572	37179	1.27	1.0E-01	BE782750.1	EST_HUMAN	601584504F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938098 5'
10894	23978		1.77	1.0E-01	AU159127.1	EST_HUMAN	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000695 3'

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11286	24352	37991	2.17	1.0E-01	BF242948.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11288	24352	37992	2.17	1.0E-01	BF242948.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11885	24884	38374	3.64	1.0E-01	BE780543.1	EST_HUMAN	601582588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938734 5'
11814	24803		1.75	1.0E-01	AP000400.1	NT	Escherichia coli O167:H7 genomic DNA, prophage (Sakai-VT1) inserted region, substrain:RIMD 0509952
12384	25833		1.73	1.0E-01	BE537719.1	EST_HUMAN	601085554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12609	25408		1.73	1.0E-01	7662165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12938	26119		3.11	1.0E-01	U52991.1	NT	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
12973	25833		1.8	1.0E-01	BE537719.1	EST_HUMAN	601085554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
13045	26085		25.82	1.0E-01	U68834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
13117	25728		6.58	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
13219	26106		1.45	1.0E-01	AE002138.1	NT	Ureaplasma urealyticum section 39 of 59 of the complete genome
2839	15953	28060	0.96	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pke-RII) mRNA, complete cds
2847	15861	28070	0.94	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2847	15861	28071	0.94	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
3340	16913	29528	1.31	9.9E-02	AF098810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
7110	18536	31492	8.86	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blasticidin S deaminase, complete cds
8099	21181	34899	0.69	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCL CGAP_OV23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element;
8099	21181	34700	0.69	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCL CGAP_OV23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element;
8457	22573	36139	1.36	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
12132	25112	38816	3.87	9.9E-02	D86980.1	NT	Human mRNA for KIAA0227 gene, partial cds
677	13769		2.18	9.9E-02	X56338.1	NT	O. sativa RAmY3C gene for alpha-amylase
3214	16388	29398	3.68	9.9E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4339	17492	30463	9.93	9.9E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4339	17492	30464	9.93	9.9E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7651	20719		0.98	9.9E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9454	22570		1.18	9.9E-02	M61943.1	NT	Human laminin B1 chain gene, exon 26
11747	23933	37559	1.73	9.9E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3884287 5'
12332	26240		1.29	9.9E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
1381	14536	27611	1.92	9.7E-02	AB006808.1	NT	Alce arborescens mRNA for NADP-malic enzyme, complete cds

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1617	14769		1.01	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2335	15468	28601	2.68	9.7E-02	BE188860.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA
4091	17248		4.05	9.7E-02	Q99795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5461	18661	31639	0.59	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5461	18661		0.59	9.7E-02	AF099189.1	NT	Caulobacter crescentus thymidylate kinase (tnk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
6138	19316	32657	1.39	9.7E-02	AW954476.1	EST_HUMAN	EST389548 MAGC resequences, MAGC Homo sapiens cDNA
7450	20527	34000	3.05	9.7E-02	Z69119.1	NT	Bacillus subtilis complete genome (section 16 of 21), from 2897771 to 3213410
8171	21253	34774	1.54	9.7E-02	N22768.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254786 3'
8171	21253	34775	1.54	9.7E-02	N22768.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
9050	22129	35673	1.49	9.7E-02	A1953984.1	EST_HUMAN	wx78508.x1 NCJ CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gbX52851_maf1
11472	24531		1.72	9.7E-02	U68337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN); Mus musculus ligalgin (Lgln) mRNA, partial cds
2073	15213	28330	1.33	9.6E-02	A1080721.1	EST_HUMAN	oz47d11.x1 Soares_NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
2073	15213	28331	1.33	9.6E-02	A1080721.1	EST_HUMAN	oz47d11.x1 Soares_NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4464	17604	30582	6.67	9.6E-02	Z32886.2	NT	Proteus mirabilis fibrinolytic operon, strain HI4320
5117	18244	31209	0.95	9.6E-02	AW966230.1	EST_HUMAN	EST378303 MAGC resequences, MAGC Homo sapiens cDNA
6231	19406		2.76	9.6E-02	BE910039.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
8017	21068		0.78	9.6E-02	6878763	NT	Mus musculus lymphocyte antigen 78 (Ly78), mRNA
8571	21652		0.65	9.6E-02	AU137084.1	EST_HUMAN	AU137084 PLACET Homo sapiens cDNA clone PLACE1005740 5'
9744	22808	36386	1.48	9.6E-02	AV687898.1	EST_HUMAN	AV687898 GKGO Homo sapiens cDNA clone GKCAAH02 5'
10076	23114		1.34	9.6E-02	BE694895.1	EST_HUMAN	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5'
10245	23280	36878	1.04	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10245	23280	36877	1.04	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10325	23360	36970	0.92	9.6E-02	BF677270.1	EST_HUMAN	602086769F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250969 5'
10354	23389	36998	1.56	9.6E-02	AB013595.1	NT	Anthrithum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10354	23389	36999	1.56	9.6E-02	AB013595.1	NT	Anthrithum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10465	23500	37113	3.43	9.6E-02	P08174	SWISSPROT	COMPLEMENT DECAT-ACCELERATING FACTOR PRECURSOR (CD56)
10881	24090	37694	6.27	9.6E-02	Z76702.1	NT	Myobacterium tuberculosis H37Rv complete genome, segment 102/162
12019	25003	38704	2.8	9.6E-02	AA82755.1	EST_HUMAN	zid1g01.s1 Soares_NHT Homo sapiens cDNA clone IMAGE:745392 3'
13015	25638		1.7	9.6E-02	H14598.1	EST_HUMAN	ym18h03.s1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:48653 3'

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13143	25743	31949	1.41	9.6E-02	AJ25624.1	NT	Gallus gallus ALPHA 10 nAChR gene for alpha 10 subunit of nicotinic acetylcholine receptor, exons 1-5
4217	17366	30355	2.16	9.5E-02	AW892395.1	EST_HUMAN	CM2-BN0023-050200-087-412 BN0023 Homo sapiens cDNA
5782	18974	32280	0.88	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7455	20532	34006	4.64	9.6E-02	AB003473.1	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
7741	20802	34282	7.77	9.5E-02	AL161538.2	NT	Arabidopsis thaliana DNA for phospholipase A2 inhibitor, complete cds
7876	18974	32280	0.81	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
8084	21146	34866	2.85	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8084	21146	34867	2.85	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10918	24001	37634	4.09	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10918	24001	37635	4.09	9.5E-02	BF035861.1	EST_HUMAN	601453842F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
12104	25084		1.82	9.5E-02	7657416	NT	Mus musculus odd Oz/ten-m homolog 3 (Drosophila) (Odz3), mRNA
13087	25715		2.81	9.5E-02	AF272732.1	NT	Arabidopsis thaliana putative transcription factor (MYB110) mRNA, complete cds
1880	15024	28130	3.95	9.4E-02	BF671063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281817 5'
3985	17142	30147	4.64	9.4E-02	Z33059.1	NT	M. capricolum DNA for CONTIG MCO73
6447	19814	32978	0.95	9.4E-02	AF097363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
7769	20827	34318	0.68	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and val genes, complete cds, and p135 gene, partial cds
8789	21878		2.5	9.4E-02	Z46883.1	NT	Acetobacter sp. cysD, cobQ, cobX, lyeS, rubA, rubB, estB, oxyR, ppk, migA, ORF2 and ORF3 genes
11174	20827	34318	1.9	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and val genes, complete cds, and p135 gene, partial cds
12214	26011		7.72	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
13198	25780	31938	4.84	9.4E-02	U27699.1	NT	Human pephBGT-1 beta-actin-GABA transporter mRNA, complete cds
3054	16230		2.37	9.3E-02	4808280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3094	16270		8.03	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3329	16902	28521	2.17	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4288	17413	30400	3.17	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4288	17413	30401	3.17	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4857	17890		1.82	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
5779	18971		0.67	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8442	21623	35052	0.56	9.3E-02	AW568007.1	EST_HUMAN	EST09 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
9324	22400		0.6	9.3E-02	AL113179.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
8911	22951	36537	2.3	9.3E-02	BE902681.2	EST_HUMAN	601656988F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'
10394	23428	37035	3.6	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10394	23428	37036	3.6	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10526	23561		3.98	9.3E-02	AW206117.1	EST_HUMAN	UI-H-B1-afx-h-05-Q-UI.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
12485	25533		2.08	9.3E-02	AJ249850.1	NT	Photobacterium damsela subsp. damsela partial gyrB gene for DNA gyrase B subunit
12905	25964		22.03	9.3E-02	AW468850.1	EST_HUMAN	hd28h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
13139	26010						Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), Rar3 (R3D-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
238	13460	26486	2.87	9.3E-02	AF100956.1	NT	Molluscum contagiosum virus subtype 1, complete genome
238	13460	26487	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
238	13460	26488	4.72	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2302	15434		3.08	9.2E-02	R54156.1	EST_HUMAN	y99807.r1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:41618 5'
3247	18421	26437	3.7	9.2E-02	Q28831	SWISSPROT	MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3378	18551	26564	1.01	9.2E-02	AA534354.1	EST_HUMAN	nt79d01.s1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:928136 3'
3676	16339		1.14	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptae), mRNA
4353	17486		1.05	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4425	17565		0.88	9.2E-02	BE299722.1	EST_HUMAN	600944365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980176 5'
4760	17685	30876	3.44	9.2E-02	X86402.1	NT	G. gallus Mia-CK gene
8188	21280	34802	1.82	9.2E-02	T49920.1	EST_HUMAN	y999c09.r1 Stratiagene placenta (#937225) Homo sapiens cDNA clone IMAGE:99808 5' similar to similar to gb:X66009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
8370	21451	34974	2.18	9.2E-02	X95250.1	NT	H. vulgare xylase isomerase gene
13120	28201		1.2	9.2E-02	11468872	NT	Podospora anserina mitochondrion, complete genome
438	13238	26237	2.23	9.1E-02	X77665.1	NT	O. cuniculus k12 keratin gene
3760	16921		0.97	9.1E-02	AW572569.1	EST_HUMAN	PM2-BT0349-161269-001-002 BT0349 Homo sapiens cDNA
4607	17744	30723	1.76	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5848	18038	32345	1.23	9.1E-02	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; aid CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7459	26218		0.61	9.1E-02	AF028308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and hypoxanthine gene families
7648	20818	34094	12.21	9.1E-02	AW160658.1	EST_HUMAN	ca74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781068 5'
7852	20907	34411	0.95	9.1E-02	AF000061.1	NT	Aeropyrum pernix genomic DNA, section 4/7
7887	20939	34445	1.02	9.1E-02	U39073.1	NT	Mus musculus thymopoietin zeta mRNA, complete cds
9124	22203	35746	0.96	9.1E-02	Y14379.1	NT	Homo sapiens gamma adducin gene, exon 9
10642	23678		1.46	9.1E-02	T02984.1	EST_HUMAN	FB19F10 Fetal brain, Stratiagene Homo sapiens cDNA clone FB19F10 3' end
10674	23708	37316	1.02	9.1E-02	S74059.1	NT	Tc916-Cyl actin [Tritpneustes gratilla-sea urchins, embryos, Genomic, 5275 nt]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10703	23736	37341	0.8	9.1E-02	Y11187.1	NT	A. thaliana RH1, TC1, G14587-5, G14587-3, and PRL1 genes
11441	24502	38170	2.13	9.1E-02	AF037625.1	NT	Rana catesbeiana dihydropyridine receptor, mRNA, complete cds
12151	25121		7.04	9.1E-02	8833404	NT	Bacteriophage Mu, complete genome
12393	28124		1.42	9.1E-02	AA178901.1	EST_HUMAN	223812.61 Stratiagene muscle 937209 Homo sapiens cDNA clone IMAGE:611763 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;
12473	26326		1.32	9.1E-02	AF052895.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
12956	23654		13.49	9.1E-02	AJ291350.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
13230	25789		1.27	9.1E-02	AF226988.1	NT	Bombay motif fibron heavy chain Fib-H (fib-H) gene, complete cds
763	13944	26990	5.89	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1694	14816	27699	7.33	9.0E-02	BE220482.1	EST_HUMAN	h39g10.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176842 3' similar to contains Alu repetitive element
2454	15562	28710	1.18	9.0E-02	AW801384.1	EST_HUMAN	IL5-UM0067-240300-050-008 UM0067 Homo sapiens cDNA
2864	15978	29088	4.99	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2864	15978	29088	4.99	9.0E-02	AF138522.1	NT	HIV-1 p8c095-08 from USA envelope glycoprotein (env) gene, partial cds
3417	18586	29003	1.11	9.0E-02	AF279135.1	NT	Dichyestellum discoidaleum spore coat structural protein SP65 (colE) gene, complete cds
4414	17555	30541	0.6	9.0E-02	S88757.1	NT	Corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4414	17555	30542	0.6	9.0E-02	S88757.1	NT	Corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4790	17925	30913	2.03	9.0E-02	X85740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
6118	19298	32834	7.2	9.0E-02	W56037.1	EST_HUMAN	za68a12.11 Soares_fetal_lung_NbHL19W/Homo sapiens cDNA clone IMAGE:297694 5' similar to PIR:S52171 S62171 small G protein - human ;
6880	20012		0.63	9.0E-02	BF082651.1	EST_HUMAN	7H63403.x1 NCL CGAP_Col16 Homo sapiens cDNA clone IMAGE:3320645 3' similar to contains Alu repetitive element
12819	25546		1.82	9.0E-02	AF022236.1	NT	Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscS (escS), EscT (escT), EscU (escU), CasD (casD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
1469	14623	27708	1.25	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1469	14623	27707	1.25	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2460	15587	28714	1.64	8.9E-02	BE153572.1	EST_HUMAN	PMO-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA
4316	17459		1.69	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranFla2 protein (AtranFla2) gene, partial cds
5972	19158	32474	2.7	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alo-f-08-0-JLs1 NCL CGAP_Sub55 Homo sapiens cDNA clone IMAGE:3068294 3'
5972	19158	32476	2.7	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alo-f-08-0-JLs1 NCL CGAP_Sub55 Homo sapiens cDNA clone IMAGE:3068294 3'
5987	19172	32494	3.34	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7343	20423	33886	1.6	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN (INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHENYL-TETRAHYDROFOLATE CYCLOHYDROLASE]
7731	20783		1.77	8.9E-02	Z78021.1	NT	H sapiens flow-sorted chromosome 6 HindIII fragment, SC9pA20f8
8240	21322	34839	1.19	8.9E-02	P29475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8323	21405	34932	0.76	8.9E-02	BF701665.1	EST_HUMAN	60212911F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8323	21405	34933	0.76	8.9E-02	BF701665.1	EST_HUMAN	60212911F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8797	21876	36416	6.85	8.9E-02	AA305319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
							qu55c05.x1 NCI CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1988680 3' similar to contains MER10.b1
9819	22659	36439	0.84	8.9E-02	AL285627.1	EST_HUMAN	MER10 repetitive element;
9819	22659	36440	0.84	8.9E-02	AL285627.1	EST_HUMAN	qu55c05.x1 NCI CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1988680 3' similar to contains MER10.b1
9934	22973	36565	0.63	8.9E-02	AA339366.1	EST_HUMAN	MER10 repetitive element;
12213	25862		1.8	8.9E-02	P19524	SWISSPROT	EST44454 Fetal brain I Homo sapiens cDNA 5' end
12386	25262		3.82	8.9E-02	BF696918.1	EST_HUMAN	MYOSIN-2 ISOFORM
12537	25368		2.76	8.9E-02	6680220	NT	602128682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
12584	25393		2	8.9E-02	U28895.1	NT	Mus musculus hippocampus abundant gene transcript 1 (Hiat1), mRNA
12827	26199		1.16	8.9E-02	U40493.1	NT	Human 4-hydroxyphenylpyruvate-dioxygenase gene, complete cds
12880	26133		1.54	8.9E-02	AE001514.1	NT	Ceratitis capitata mariner transposon transposase gene, complete cds
1404	14558	27832	0.96	8.9E-02	Q27474	SWISSPROT	Helicobacter pylori, strain J99 section 76 of 132 of the complete genome
4012	17169	30177	1.07	8.9E-02	AA299126.1	EST_HUMAN	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
							EST11695 Uleus Homo sapiens cDNA 5' end
							TRANSCRIPTION INITIATION FACTOR TFIID 135 KDa SUBUNIT (TAFII135) (TAFII130)
4145	17297		5.23	8.9E-02	O00288	SWISSPROT	(TAFII130)
4418	17559		0.75	8.9E-02	4580423	NT	Homo sapiens paired box gene 6 (antridia, keratitis) (PAX6), isoform b, mRNA
7716	20780		0.71	8.9E-02	D17520.1	NT	Sheep mRNA for arylalkylase, complete cds
9188	22256	35807	2.07	8.9E-02	AA151872.1	EST_HUMAN	z899a05.s1 Striatogene colon (#937204) Homo sapiens cDNA clone IMAGE:568288 3'
11380	24441	38099	2.79	8.9E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:335648 5'
11380	24441	38100	2.79	8.9E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:335648 5'
11541	24597	38273	6.26	8.9E-02	AL040126.1	EST_HUMAN	DKFZp434D1313_r1 434 (synonym: hlec3) Homo sapiens cDNA clone DKFZp434D1313 5'
12443	25314	32090	1.19	8.9E-02	Z71561.1	NT	S. cerevisiae chromosome XIV, reading frame ORF YNL285w
9785	18946	29853	4.17	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3785	16946	29854	4.17	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds, and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4829	17682	30050	1.4	8.7E-02	AF178638.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5211	18332		1.07	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189408 (section 101 of 148) of the complete genome
5429	18629	31603	5.49	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5429	18629	31608	5.49	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6884	20212	33642	0.63	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6884	20212	33643	0.63	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7188	20053	33463	0.67	8.7E-02	AF281342.1	NT	Oncorhynchus mykiss TAT-binding protein, 1 mRNA, partial cds
8046	21128		0.56	8.7E-02	AA284532.1	EST_HUMAN	z20c03.c1 Soares ovary tumor NthOT Homo sapiens cDNA clone IMAGE:713692 3'
8713	21783	35329	0.66	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
8713	21783	35330	0.66	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
10951	24033		2.01	8.7E-02	U04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
11591	24944		1.48	8.7E-02	AJ007763.1	NT	Glucorobacter oxydans RNA-1a and RNA-1a genes
12431	25306		2.2	8.7E-02	X17118.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12848	25432		2.85	8.7E-02	9878057	NT	Mus musculus nidogen 2 (Nid2), mRNA
13033	25680		2.05	8.7E-02	X65292.1	NT	G. gallus mRNA for vigilin
1281	14437	27508	7.73	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 22
2317	15449	28581	2.2	8.6E-02	BE408687.1	EST_HUMAN	601304016F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3638943 5'
3257	16431	29448	2.35	8.6E-02	U05468.1	NT	Trichomonas vaginalis beta-tubulin (btubt) gene, complete cds
3734	16895		3.69	8.6E-02	AF163382.1	NT	Dicystostellum discoidaleum adenyl cyclase (acrA) gene, complete cds
3880	17039		0.8	8.6E-02	U29187.1	NT	Mus musculus long incubation prion protein (Prnp) and prion-like protein (Prnd) genes, complete cds
4609	17746	30725	0.66	8.6E-02	U88178.1	NT	Oryctolagus cuniculus galectin-3 gene, untranslated exon and 5' flanking region
5330	18443		1.02	8.6E-02	AB011163.1	NT	Homo sapiens mRNA for KIAA0391 protein, partial cds
6219	18984	32743	4.74	8.6E-02	Y10826.1	NT	Homo sapiens LCN1b gene
6504	19870	33035	1.29	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6504	19870	33036	1.29	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7753	20814	34306	0.89	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
8115	21197	34718	1.09	8.6E-02	5730068	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8115	21197	34717	1.09	8.6E-02	5730068	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8261	21343	34860	0.58	8.6E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8324	21408		0.76	8.6E-02	U60188.1	NT	Dicystostellum discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds
9938	22677	36568	1.24	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
9975	23014		1.4	8.6E-02	AW682153.1	EST_HUMAN	H20c08.x1 NCI_CGAP_GUT Homo sapiens cDNA clone IMAGE:2872846 3'
10398	23391	37001	1.07	8.6E-02	AF028504.1	NT	Rattus norvegicus SPA-1 like protein p1284 mRNA, complete cds
11188	24257	37892	1.82	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11188	24257	37893	1.82	8.6E-02	AF208551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11627	24583	38259	3.02	8.6E-02	BF305806.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11627	24683	38260	3.02	8.6E-02	BF305806.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11724	23910	37534	7.67	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
11876	24983	38559	2.29	8.6E-02	AF283680.1	NT	Bacillus stearothermophilus Bsr71 methylase (Flm) and Bsr71 restriction endonuclease (FIR) genes, complete cds
2470	15597	28722	2.58	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5292	18410		0.68	8.5E-02	N76915.1	EST_HUMAN	yv48h08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245823 5'
5768	18978	32283	0.73	8.5E-02	AA985491.1	EST_HUMAN	cc83507.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1692917 3' similar to gbK01144 HLA
5826	18018		1.99	8.5E-02	P08089	SWISSPROT	CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN PRECURSOR (HUMAN);
6135	19314	32853	6.61	8.5E-02	AF233885.1	NT	M PROTEIN; SEROTYPE 6 PRECURSOR
8805	21884	35424	1.68	8.6E-02	6754779	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
10041	23079	36880	3.27	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10041	23079	36881	3.27	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10572	23607	37212	0.64	8.5E-02	X78731.1	NT	V.ammodytes gene for ammodytoxin C
10702	23735	37340	0.82	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11424	24485		8.03	8.5E-02	AF165510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11446	24507	38173	3.82	8.5E-02	AB001592.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12873	25886		2.76	8.9E-02	AJ005888.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor
13070	25700		2.44	8.5E-02	AA382894.1	EST_HUMAN	EST72736 Ovary II Homo sapiens cDNA 5' end
2732	16070	28961	4.05	8.4E-02	W69330.1	EST_HUMAN	z444e1.1.1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5'
5427	18827	31003	9.84	8.4E-02	BE267163.1	EST_HUMAN	601190436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
6828	18981	33388	1.40	8.4E-02	AK024456.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
8218	21300	34821	6.95	8.4E-02	BE095074.1	EST_HUMAN	GM3-BT0790-260400-162-d05 BT0790 Homo sapiens cDNA
8043	22122	35864	1.16	8.4E-02	AF218890.1	NT	Homo sapiens atracitin precursor (ATRN) gene, exon 2

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10571	23008	37211	1.84	8.4E-02	AI735184.1	EST_HUMAN	as88g10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
10831	23635		0.48	8.4E-02	AV730882.1	EST_HUMAN	O88312 GOB-4.;
12351	25264	32114	1.87	8.4E-02	R79408.1	EST_HUMAN	AV730882 HTF Homo sapiens cDNA clone HTFBMG04 5'
3682	16845	29553	7.77	8.3E-02	P7534	SWISSPROT	y63h12.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
3709	16870	29873	0.75	8.3E-02	AI439787.1	EST_HUMAN	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3709	16870	29874	0.75	8.3E-02	AI439787.1	EST_HUMAN	th82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
4417	17558		0.68	8.3E-02	M54884.1	NT	th82g08.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6389	19558	32917	0.74	8.3E-02	AI942338.1	EST_HUMAN	C.hummi A2b region open reading frame, complete cds
6496	19662	33025	2.87	8.3E-02	AF032683.1	NT	w079f11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
8169	21251	34771	3.08	8.3E-02	AF195787.1	NT	Homo sapiens protocadherin 43 gene, exon 1
8202	21284		1.06	8.3E-02	AA865285.1	EST_HUMAN	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dp2) mRNA, complete cds
8495	21576		1.31	8.3E-02	AA887873.1	EST_HUMAN	cg88g08.e1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.11 L1 L1
9738	22803	36377	1.09	8.3E-02	AW565303.1	EST_HUMAN	repetitive element
9751	22889		2.02	8.3E-02	AL151695.2	NT	cg81f10.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1582779 3'
10549	23884		0.72	8.3E-02	AF020409.1	NT	la03h10.x1 Human Pancreatic Islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA
12448	26128		1.81	8.3E-02	BE859458.1	EST_HUMAN	SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE.;
1410	14564		9.13	8.2E-02	Y08170.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 81
1525	14878	27759	2.03	8.2E-02	AF167077.2	NT	Dicotyledon discoidium Doca (dca) mRNA, complete cds
3141	16317		1.97	8.2E-02	AL163206.2	NT	G01644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928983 5'
3804	17063		1.35	8.2E-02	AL161498.2	NT	Gallus gallus mRNA for for OBCAM protein gamma isoform
4114	17268	30268	0.99	8.2E-02	AL163206.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
4369	17542	30523	6.58	8.2E-02	P48960	SWISSPROT	Homo sapiens chromosome 21 segment HS21C006
4399	17542	30524	6.58	8.2E-02	P48960	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
5182	18314	31282	3.43	8.2E-02	U76009.1	NT	Homo sapiens chromosome 21 segment HS21C006
5450	18650	31628	1.46	8.2E-02	BE897030.1	EST_HUMAN	LEUCOCYTE ANTIGEN CD97 PRECURSOR
7165	20298	33741	3.16	8.2E-02	AF309555.1	NT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
7910	20962		0.58	8.2E-02	AF743341.1	EST_HUMAN	LEUCOCYTE ANTIGEN CD97 PRECURSOR
8905	21984		0.59	8.2E-02	U28397.1	NT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
8971	22050	35593	3.24	8.2E-02	AW875128.1	EST_HUMAN	Mus musculus zinc transporter (ZnT-3) gene, complete cds
9789	22839	36416	4.88	8.2E-02	X04197.1	NT	G01439676F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'

Table 4

### Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9965	23004	38599	2.27	8.2E-02	BE254318.1	EST_HUMAN	601113055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355598 5'
12454	25318	32094	3.98	8.2E-02	AE002248.2	NT	Chlamydomonas reinhardtii AR38, section 73 of 94 of the complete genome
12686	25458	32021	1.43	8.2E-02	AW862195.1	EST_HUMAN	QV4-CT0361-021299-049-b01 CT0361 Homo sapiens cDNA
12909	25876		2.58	8.2E-02	AF276388.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 6 through 28, and complete cds, alternatively spliced
1524	14677	27758	0.96	8.1E-02	AB017138.1	NT	Pseudomonas putida malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdcH, mdcL and mdcM genes), complete cds
5873	18063	32371	1.03	8.1E-02	AE004008.1	NT	Xyella fastidiosa, section 152 of 228 of the complete genome
6509	18874	33043	0.89	8.1E-02	T11532.1	EST_HUMAN	A1494F Heart Homo sapiens cDNA clone A1484
7347	20427		0.83	8.1E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
7766	20816		0.99	8.1E-02	AI692681.1	EST_HUMAN	wd8908.XT NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8535	21616	35151	0.96	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10090 (FLJ10090), mRNA
8535	21616	35162	0.56	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10090 (FLJ10090), mRNA
10119	23154		1.83	8.1E-02	AY05150.1	NT	Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds
10685	23719		0.7	8.1E-02	AW269778.1	EST_HUMAN	ux45b11.XT Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816081 3'
10858	23891	37511	0.47	8.1E-02	AW450487.1	EST_HUMAN	UIH-B13-ako-g-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735040 3'
10858	23891	37512	0.47	8.1E-02	AW450487.1	EST_HUMAN	UIH-B13-ako-g-01-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2735040 3'
11790	24780	39477	1.99	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
16003	26246		7.61	8.0E-02	AW054653.1	EST_HUMAN	EST1366723 MAGE resequences, MAGE Homo sapiens cDNA
959	14132	27191	0.65	8.0E-02	U60315.1	NT	Molluscan contagiosum virus subtype 1, complete genome
1733	16046	27874	11.83	8.0E-02	D28535.1	NT	Human gene for dihydrodipicolinate succinyltransferase, complete cds (exon 1-16)
1733	16046	27976	11.83	8.0E-02	D28535.1	NT	Human gene for dihydrodipicolinate succinyltransferase, complete cds (exon 1-15)
1952	15095	28198	4.4	8.0E-02	BE067219.1	EST_HUMAN	PM3-B10347-170200-001-508 BT0347 Homo sapiens cDNA
2447	15575	28704	0.93	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2287259
2447	15575	28705	0.93	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2287259
2541	15666		3.21	8.0E-02	BF249744.1	EST_HUMAN	801855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4078618 5'
2881	14280	27338	1.55	8.0E-02	M23449.1	NT	Dicystidium discoidium cyclo nucleotide phosphodiesterase gene, complete cds
2965	16141	29159	1.06	8.0E-02	AL445087.1	NT	Thermoplasma acidophilum complete genome, segment 516
3919	17076	30075	0.93	8.0E-02	AW966118.1	EST_HUMAN	EST1378181 MAGE resequences, MAGI Homo sapiens cDNA
4182	17332		0.74	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREB2) mRNA
4935	18065		6.87	8.0E-02	X72794.1	NT	M.musculus gene for gelatinase B
5038	18169	31142	0.82	8.0E-02	M28071.1	NT	Herpesvirus esaimiri transformational-associated protein (STP), and dihydrodipicolinate reductase (DHFR) gene.s
6042	40404	32513	3.59	8.0E-02	AF276548.1	NT	complete cds, and small nuclear RNAs (snRNAs)
6042	40404	32513	3.59	8.0E-02	AF276548.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7330	19196	32513	1.61	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8319	21401	34928	2.41	8.0E-02	AL114993.1	NT	Edwards chereia strain T4 cDNA library under conditions of nitrogen deprivation
8589	22044	38213	1.38	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
8589	22844	38214	1.38	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10361	23366		0.49	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
11032	24111	37747	2.64	8.0E-02	AF217798.1	NT	Homo sapiens SCG10 like-protein, Helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
12127	25107	38811	1.69	8.0E-02	4507608	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 9 (TNFSF9) mRNA
12486	25337	32081	3.54	8.0E-02	AJ005376.1	NT	Drosophila oreana hunchback region
13134	17332		1.85	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2243	15376	28504	3.37	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859510 5'
3043	16219	29240	12.83	7.9E-02	AI582020.1	EST_HUMAN	ar8c08x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z26876
3953	17111	30110	4.47	7.9E-02	6681044	NT	60S RIBOSOMAL PROTEIN L38 (HUMAN);
3953	17111	30111	4.47	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
4932	18062		1.16	7.9E-02	AB008019.1	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
6836	19889		1.14	7.9E-02	BF368016.1	EST_HUMAN	Arabidopsis thaliana RXW24L mRNA, partial cds
8221	21303	34824	3.1	7.9E-02	U27832.1	NT	RC3-GN0042-310800-024-d11 GN0042 Homo sapiens cDNA
10234	23269	36859	5.6	7.9E-02	AI091644.1	EST_HUMAN	Saccharomyces cerevisiae suppressor of YIF2 Smt4p (SMT4) gene, complete cds
10234	23269	36860	5.6	7.9E-02	AI091644.1	EST_HUMAN	ou63003.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP.C37A2.2
13008	25864		1.27	7.9E-02	AI761639.1	EST_HUMAN	CE08611;
1237	14396	27457	1.49	7.8E-02	AI793276.1	EST_HUMAN	ou63005.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP.C37A2.2
1237	14396	27458	1.49	7.8E-02	AI793276.1	EST_HUMAN	CE08611;
4916	18045	31035	0.6	7.8E-02	BE830331.1	EST_HUMAN	wg68h01.x1 Scores_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370097 3'
5198	17003		2.97	7.8E-02	BE250048.1	EST_HUMAN	cc59d02.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570487 5' similar to contains L1.13 L1
7223	20037	33504	1.1	7.8E-02	U82695.2	NT	repetitive element;
							cc59d02.y5 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570487 5' similar to contains L1.13 L1
							repetitive element;
							PM3-FN0058-140700-005-f09 FN0058 Homo sapiens cDNA
							600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859893 5'
							Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7223	20087	33505	1.1	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8985	22064	33604	0.93	7.8E-02	BE897847.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
9081	22160	35702	0.59	7.8E-02	X78344.1	NT	S. cerevisiae CAT8 gene
9253	22330	35877	0.8	7.8E-02	AF23437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9253	22330	35878	0.8	7.8E-02	AF23437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9461	22703	36269	0.9	7.8E-02	AA489364.1	EST_HUMAN	nc88b08.r1 NCLCGAP_P1 Homo sapiens cDNA clone IMAGE:771731
10008	23044	36637	0.58	7.8E-02	Z89124.1	NT	Bacillus subtilis complete genome (section 21 of 21); from 3999281 to 4214814
10901	23985	37618	2.19	7.8E-02	U32823.1	NT	Human Interleukin-11 receptor alpha chain gene, complete cds
12910	25602	31873	1.36	7.8E-02	U72847.1	NT	Homo sapiens envoplakin (EVPK) gene, exons 15 through 18
1431	18038	27659	1.22	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3677	16840		2.01	7.7E-02	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
8093	21175	34890	5.38	7.7E-02	AA402949.1	EST_HUMAN	TR-G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN. ;
10040	23078	36679	4.88	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
10336	23371	36981	0.84	7.7E-02	AI318662.1	EST_HUMAN	ta80b08.x1 NCLCGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26878 60S
10336	23371	36982	0.84	7.7E-02	AI318662.1	EST_HUMAN	RIBOSOMAL PROTEIN L38 (HUMAN);
11262	24331	37972	3.98	7.7E-02	11422757	NT	ta80b08.x1 NCLCGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26878 60S
3474	16841	29660	3.1	7.6E-02	BE514432.1	EST_HUMAN	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
3494	16851	29673	0.98	7.6E-02	AA286447.1	EST_HUMAN	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3649	18812	29625	0.96	7.6E-02	AJ400877.1	NT	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
6222	18397	32748	0.69	7.6E-02	A081275.1	EST_HUMAN	Homo sapiens ASCL3 gene, C11orf14 gene, C11orf15 gene, C11orf17 gene
6486	18853	33015	1.14	7.6E-02	BE378328.1	EST_HUMAN	en26g02.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'
9570	22712	36280	1.11	7.6E-02	AJ131016.1	NT	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
10101	23139		0.99	7.6E-02	AL195078.2	NT	Homo sapiens SCL gene locus
10424	23459	37064	0.5	7.6E-02	BE708002.1	EST_HUMAN	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
10557	23592		1.04	7.6E-02	BE959638.2	EST_HUMAN	RC1-HT0645-020800-017-d06 HT0545 Homo sapiens cDNA
10815	23848	37489	0.97	7.6E-02	X92658.1	NT	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
							L.esculentum mRNA for triose phosphatase translocator

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10816	23848	37470	0.97	7.6E-02	X92858.1	NT	L. esculentum mRNA for triose phosphate translocator
11974	24959	38581	1.93	7.6E-02	AW896845.1	EST_HUMAN	QV3-BN0046-150400-151-e04 BN0046 Homo sapiens cDNA
807	13987	27039	1.66	7.5E-02	5902093	NT	Homo sapiens solute carrier family 9 (neurotransmitter transporter, glycine), member 9 (SLC9A9), mRNA
807	13987	27040	1.66	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC9A9), mRNA
1971	15114	28214	0.89	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment H521C078
4630	17766	30748	0.74	7.5E-02	AB015961.1	NT	Homo sapiens IL-18 gene for Interleukin-18, intron 1 and exon 2
5974	19169	32477	1.45	7.5E-02	AB48714.1	EST_HUMAN	wq24h09.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472257 3'
8533	21614	35150	1.28	7.6E-02	AB64387.1	EST_HUMAN	w52b02.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gbM14328 ALPHA ENOLASE (HUMAN);
8705	21785	35318	1.36	7.5E-02	AU116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5'
10238	23273		0.49	7.5E-02	BF221730.1	EST_HUMAN	7c61c05.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element
10711	23744	37550	0.73	7.5E-02	BF220609.1	EST_HUMAN	MER27 repetitive element;
10816	23849	37471	0.82	7.5E-02	X78460.1	NT	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
400	13884	26718	1.41	7.4E-02	AW838547.1	EST_HUMAN	C.fiml DSM 20113 16S rDNA
1489	14642		1.21	7.4E-02	AF030027.1	NT	RC5-LT0054-260100-011-H09 LT0054 Homo sapiens cDNA
2848	15771		0.96	7.4E-02	6755069	NT	Equine herpesvirus 4 strain NS80587, complete genome
3683	16846	29854	1.21	7.4E-02	AB07885.1	EST_HUMAN	Mus musculus paired-like homeodomain transcription factor 1 (Pib1), mRNA
4826	17959	30846	1.19	7.4E-02	L78810.1	NT	wf49h01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4914	18044	31034	2.65	7.4E-02		NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
5036	18184	31159	4.42	7.4E-02		NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
6824	19784		1.69	7.4E-02	R17477.1	EST_HUMAN	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrlp), mRNA
6717	19875	33268	0.68	7.4E-02	AF030422.1	NT	yg14g06.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
7636	20705	34184	0.64	7.4E-02	AA605132.1	EST_HUMAN	Electrophorus electricus acetylcholinesterase catalytic subunit precursor gene, complete cds
8035	21167	34683	1.11	7.4E-02	BE880112.1	EST_HUMAN	no71d02.e1 NCL CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112269 3'
8659	21779	35312	1.26	7.4E-02	U56089.1	NT	601483368F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895284 5'
9367	22442	36002	1.08	7.4E-02	AW629605.1	EST_HUMAN	Human peridolic tryptophan protein 2 (PWPF2) gene, exons 15 to 21, and complete cds
9367	22442	36003	1.08	7.4E-02	AW629605.1	EST_HUMAN	hh87d11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2987881 5' similar to SW:SCA2_HUMAN
9639	21082	34593	0.58	7.4E-02	AB72839.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.1
9639	21082	34594	0.58	7.4E-02	AB72839.1	EST_HUMAN	hh87d11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2987881 5' similar to SW:SCA2_HUMAN
							O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.1
							hh87d11.y1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2987881 5' similar to SW:SCA2_HUMAN
							we74d02.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
							we74d02.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'



Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10018	23057	36653	1	7.4E-02	U62293.1	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
10146	23184	36780	0.46	7.4E-02	BF512678.1	EST_HUMAN	U1H-BW1-emb-g-05-0-UJ.s1 NCL CGAP_Sub67 Homo sapiens cDNA clone IMAGE:3069888 3'
11266	24335	37875	1.46	7.4E-02	AA059167.1	EST_HUMAN	z64e01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381720 5'
							g011d07.s1 Barstead arista HPLRBS3 Homo sapiens cDNA clone IMAGE:1726285 3' similar to gb:M86492
11914	24601	38604	1.42	7.4E-02	AI125063.1	EST_HUMAN	GLIA MATURATION FACTOR BETA (HUMAN);
12409	25288		1.22	7.4E-02	11525893	NT	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12692	26101		3.74	7.4E-02	AW379431.1	EST_HUMAN	CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA
12870	25580	31895	2.61	7.4E-02	BF035099.1	EST_HUMAN	801453813F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857738 5'
12882	25595	31868	1.44	7.4E-02	AJ223459.2	NT	Aspergillus nidulans prnD, prnX, prnA genes
481	13676	26709	1.15	7.3E-02	BE064981.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889209 3'
481	13676	26709	1.15	7.3E-02	BE064981.2	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889209 3'
702	13685	26917	2.66	7.3E-02	AE001789.1	NT	Thermococcus maritima section 101 of 136 of the complete genome
1610	16040	27748	3.29	7.3E-02	AW900281.1	EST_HUMAN	CMO-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
1893	18050		15.79	7.3E-02	AL103302.2	NT	Homo sapiens chromosome 21 segment HS21C102
5112	18240		1.02	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
6582	19744	33126	1.46	7.3E-02	AA779977.1	EST_HUMAN	z24a02.s1 Soares_fetal_liver_spleen_1NF1S_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
7633	20702	34180	2.37	7.3E-02	P05143	SWISSPROT	gb:U02426 26S PROTEASE SUBUNIT 4 (HUMAN);
7633	20702	34181	2.37	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7981	21030		0.58	7.3E-02	BF316067.1	EST_HUMAN	601890047F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125515 5'
8361	21442		1.38	7.3E-02	7662107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
8596	21677	35214	0.5	7.3E-02	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
9411	22485		1.17	7.3E-02	AB011090.1	NT	Homo sapiens mRNA for KIAA0518 protein, partial cds
11492	19744	33126	1.78	7.3E-02	AA779977.1	EST_HUMAN	z24a02.s1 Soares_fetal_liver_spleen_1NF1S_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
							gb:U02426 26S PROTEASE SUBUNIT 4 (HUMAN);
122	13362	26382	0.5	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
122	13352	26383	0.5	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1505	14658	27739	2.6	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1505	14658	27740	2.6	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2814	15738		3.34	7.2E-02	U14794.1	NT	Human Immunodeficiency Virus type 1 isolate 28 reverse transcriptase (pol) gene, internal fragment, partial cds
3991	17148	30154	0.63	7.2E-02	AW298322.1	EST_HUMAN	U1H-BW0-ajl-a-05-0-UJ.s1 NCL CGAP_Sub66 Homo sapiens cDNA clone IMAGE:2732049 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4465	17605	30583	3.07	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
5402	18604	31576	2.73	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5403	18605	31577	8.76	7.2E-02	P11120	SWISSPROT	CALMODULIN
6244	19418		1.11	7.2E-02	BF217598.1	EST_HUMAN	601883305F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096224 5'
7318	20400	33863	1.32	7.2E-02	BF216086.1	EST_HUMAN	601883356F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7356	20416	33878	0.7	7.2E-02	AF221128.1	NT	Streptococcus pneumoniae putative response regulator (zmpR), putative histidine kinase (zmpS), and putative zinc metalloprotease (zmpB) genes, complete cds
7359	20438		1.53	7.2E-02	5834887	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8382	21463	34987	0.8	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8382	21463	34988	0.8	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8244	22341		0.57	7.2E-02	V17217.1	NT	Lactococcus lactis cspE gene
9775	22815		0.51	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9811	22851	36430	2.19	7.2E-02	AV712482.1	EST_HUMAN	AV712482 DCA Homo sapiens cDNA clone DCAAUG01 5'
9891	23000	36596	4.88	7.2E-02	L14581.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
10118	23166	36754	0.96	7.2E-02	BF125389.1	EST_HUMAN	601763623F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028438 5'
10206	23242	36833	2.34	7.2E-02	AW873187.1	EST_HUMAN	h024f11.x1 NCL CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340
10395	23430	37037	0.8	7.2E-02	AA768204.1	EST_HUMAN	ATYPICAL PKC SPECIFIC BINDING PROTEIN ; os62c07.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1316844 3'
10580	23595	37201	2.15	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10892	23725	37331	5.97	7.2E-02	BE565003.1	EST_HUMAN	601343926F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3685951 5'
10716	23749		3.47	7.2E-02	BE539214.1	EST_HUMAN	601085194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451659 5'
10837	23870	37492	0.55	7.2E-02	AA708897.1	EST_HUMAN	z28h05.s1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451641 3'
11153	24224	37853	4.14	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Miat1 (Miat1) gene, complete cds
12316	25230	32104	2.12	7.2E-02	AA773696.1	EST_HUMAN	af81a04.r1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
12350	25253		3.63	7.2E-02	AJ230786.1	EST_HUMAN	AJ230786 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PST3D5 3'
12411	25290		2.05	7.2E-02	AA584465.1	EST_HUMAN	nc05f08.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1099839 3'
12474	25327		4.23	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
12488	25937		7.37	7.2E-02	AW600962.1	EST_HUMAN	CM4-NN1008-200300-11b-c11 NN1009 Homo sapiens cDNA
13048	25887		1.63	7.2E-02	AA401779.1	EST_HUMAN	z57e12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728454 5'
1853	15088	28197	2.05	7.1E-02	L02280.1	NT	Human Immunodeficiency virus type 1 (Dp) proviral structural capsid protein (gag) gene, partial cds

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## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2368	15497	28623	8.8	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092881 5'
8091	21173	34687	1.08	7.1E-02	A1125264.1	EST_HUMAN	cd92a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3'
10888	23698	37521	0.53	7.1E-02	AL163246.2	NT	Homo sapiens chromosome 21 segment H321C049
12183	25150		6.46	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3091234 5'
541	13734	28758	1.4	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR
1528	14882		1.28	7.0E-02	X95877.1	NT	Martella Mibut-1 gene
1801	14960	28044	1.18	7.0E-02	AA056343.1	EST_HUMAN	z06f04.s1 Sitratogene codon (#637204) Homo sapiens cDNA clone IMAGE:509569 3'
3095	16271	29288	2.02	7.0E-02	AW138152.1	EST_HUMAN	UI-H-B11-acy-c-07-0-JL.s1 NCI_CGAP_Sub83 Homo sapiens cDNA clone IMAGE:2716020 3'
4004	17161	30167	0.65	7.0E-02	AA815438.1	EST_HUMAN	el65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376878 3' similar to gb:K03002 60S
4155	17307	30301	1.19	7.0E-02	BE070284.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4268	17403		1.14	7.0E-02	AW782962.1	EST_HUMAN	QV4-BT0407-280100-090-e10 BT0407 Homo sapiens cDNA
4330	17473	30468	1.19	7.0E-02	AF07821.1	NT	CMO-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA
5045	18173	31150	7.97	7.0E-02	BF381897.1	EST_HUMAN	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
5493	18692		0.82	7.0E-02	Y09143.2	NT	601816291F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4050071 5'
7560	20632	34107	0.9	7.0E-02	AV689285.1	EST_HUMAN	Lumbricus rubellus mRNA for cyclophilin B
7782	20838	34331	0.68	7.0E-02	Y19187.1	NT	AV689285 GKC Homo sapiens cDNA clone GKCCAE08 5'
9299	22375	35028	1.24	7.0E-02	Y19187.1	NT	Gallus gallus mRNA for partial ezrin, XL spliced variant (ecz gene)
9797	22837	38416	1.31	7.0E-02	K02901.1	NT	African swine fever virus, complete genome
10158	23195	36791	0.88	7.0E-02	U27266.1	NT	Rat Ig gamma epsilon H-chain gene C-region, 3' end
11654	24733	38424	2.6	7.0E-02	AAT24295.1	EST_HUMAN	Human myosin binding protein H (MyBP-H) gene, complete cds
13022	25973	31958	1.2	7.0E-02	11421638	NT	z06a05.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:L14837
527	13720	28744	7.08	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
527	13720	28745	7.08	6.9E-02	AL163210.2	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
1384	14318		1.56	6.9E-02	4507868	NT	Homo sapiens chromosome 21 segment HS21C010
3893	17052	30051	1.34	6.9E-02	Q06364	SWISSPROT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3893	17052	30052	1.34	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S2 (NUCLEAR ANTIGEN 21D7)
5302	18419	31389	4.11	6.9E-02	Z76163.1	NT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5316	18433	31403	0.83	6.9E-02	M34956.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA24F7
7793	20849		0.87	6.9E-02	AF04967.1	NT	M. hyarhinis 115 kDa protein (p115) gene, complete cds
8242	21324		1.14	6.9E-02	U12022.1	NT	Canine distemper virus strain A75/17, complete genome
8750	21829	35386	1.01	6.9E-02	BE567435.1	EST_HUMAN	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
							601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8760	21829	35987	1.01	6.9E-02	BE587435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8320	22398	35949	0.67	6.9E-02	U22887.1	NT	Barbado duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
11374	24435	38092	1.46	6.9E-02	381752.1	NT	DPH2L=candidate tumor suppressor gene (ovarian cancer critical region of deletion) [human, 9 week fetal and placental tissues, mRNA, 2233 nt]
11374	24435	38093	1.48	6.9E-02	S91752.1	NT	DPH2L=candidate tumor suppressor gene (ovarian cancer critical region of deletion) [human, 9 week fetal and placental tissues, mRNA, 2233 nt]
12348	25251		10.94	6.9E-02	X74315.1	NT	X.laevi XFD2 mRNA for fork head protein
12824	25357		1.58	6.9E-02	P44921	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOF6 HOMOLOG
12770	25513		3.37	6.9E-02	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1932	15076	28177	1.18	6.8E-02	AA496759.1	EST_HUMAN	es30102.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1932	15076	28178	1.18	6.8E-02	AA496759.1	EST_HUMAN	es30102.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1956	15099	28198	3.85	6.8E-02	AF156873.1	NT	MITOCHONDRIAL MATRIX PROTEIN P-1 PRECURSOR (HUMAN);
4676	17810		0.64	6.8E-02	BE141076.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSOR14) gene, complete cds
6768	19914		0.65	6.8E-02	P20792	SWISSPROT	CELL SURFACE RECEPTOR DAF-1 PRECURSOR
7040	20093		0.99	6.8E-02	BE061890.1	EST_HUMAN	RG1-BT0254-090300-017-d08 BT0254 Homo sapiens cDNA
7432	20509	33981	8.22	6.8E-02	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
7881	20915	34420	0.6	6.8E-02	AJ248287.1	NT	Dicotyledon discoidium myosin heavy chain kinase A (MHCK A) mRNA, complete cds
8483	21564	35099	6.03	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
8483	21564	35100	6.03	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
12141	28155		1.47	6.8E-02	T03214.1	EST_HUMAN	FB448 Fetal brain, Stragene Homo sapiens cDNA clone FB448 3' end similar to LINE-1
12276	25208		1.84	6.8E-02	AA758014.1	EST_HUMAN	ab0705.s1 Soares testis_NHT Homo sapiens cDNA clone 1320705 3'
12806	25599		1.34	6.8E-02	AW075839.1	EST_HUMAN	EST387848 IMAGE resequences, MAGN Homo sapiens cDNA
12972	26632		2.3	6.8E-02	9910885	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
13203	26091	31680	1.24	6.8E-02	6978885	NT	Rattus norvegicus Growth factor independent-1 (Gfi1), mRNA
1569	14711		2.71	6.7E-02	AF115938.1	NT	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds
1842	16095	28186	2.17	6.7E-02	AJ220285.1	EST_HUMAN	gq79e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone 1320705 3'
3811	16971	29973	4.48	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOXD-4 (HOXA-4)
4065	17221	30228	0.74	6.7E-02	U53783.1	NT	Cyprinus carpio Rap1b mRNA, complete cds
4065	17221	30230	0.74	6.7E-02	U53783.1	NT	Cyprinus carpio Rap1b mRNA, complete cds
7989	21019	34532	0.66	6.7E-02	W57759.1	EST_HUMAN	zid20g11.s1 Soares_fetal_heart_NbH191W Homo sapiens cDNA clone IMAGE:341252 3' similar to contains
8034	21117	34635	0.74	6.7E-02	X62895.1	NT	Alu repetitive element/contains element L1 repetitive element;
							H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8034	21117	34838	0.74	6.7E-02	X82685.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
8633	21713	35250	0.73	6.7E-02	AW082688.1	EST_HUMAN	x061c11.x1 Soares_NFL_T_C80C_S1 Homo sapiens cDNA clone IMAGE:2580788 3'
9800	22840	36417	0.59	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B1-act-g-01-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
9800	22840	36418	0.59	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B1-act-g-01-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
1379	14534	27608	0.98	6.6E-02	AI735509.1	EST_HUMAN	at12e09.x1 Barslead aorta HPLR88 Homo sapiens cDNA clone IMAGE:2384920 3' similar to
2262	16385	28513	3.73	6.6E-02	AJ289241.1	NT	SW:LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. ;
3552	18717	29731	12.38	6.6E-02	R64308.1	EST_HUMAN	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3567	18732	29748	3.11	6.6E-02	7108357	NT	y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3567	18732	29749	3.11	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4191	17341	30334	1.61	6.6E-02	AF260225.1	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
5093	18221	31181	12.07	6.6E-02	Q81703	SWISSPROT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5093	18221	31192	12.07	6.6E-02	Q81703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5130	18255	31220	0.64	6.6E-02	AA393244.1	EST_HUMAN	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5130	18255	31221	0.64	6.6E-02	AA393244.1	EST_HUMAN	NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6714	19872	33284	3.82	6.6E-02	X08411.1	NT	NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6749	19905	33288	0.62	6.6E-02	P25159	SWISSPROT	z174d07.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gbl.04270 TUMOR
6749	19905	33289	0.62	6.6E-02	P25159	SWISSPROT	NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6937	19905	33288	0.68	6.6E-02	P25159	SWISSPROT	NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6937	19905	33289	0.68	6.6E-02	P25159	SWISSPROT	NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
8133	21215	34736	1.51	6.6E-02	AF052572.1	NT	P. vulgaris mRNA for chalcone synthase
8669	21749	35287	0.77	6.6E-02	AF050555.1	NT	MATERNAL EFFECT PROTEIN STAUFEN
8979	22068		0.53	6.6E-02	Q60673	SWISSPROT	MATERNAL EFFECT PROTEIN STAUFEN
9121	22200	35741	1.28	6.6E-02	9629168	NT	MATERNAL EFFECT PROTEIN STAUFEN
9121	22200	35742	1.28	6.6E-02	9629168	NT	Homo sapiens chomokine receptor CXCR4 gene, promoter region and complete cds
10137	23194	36760	0.54	6.6E-02	A1458752.1	EST_HUMAN	Dicystellum discoideum darlin (darA) gene, complete cds
10292	23327	36630	1.5	6.6E-02	Y07848.1	NT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
10327	23362		0.65	6.6E-02	11430559	NT	Human respiratory syncytial virus, complete genome
10710	23743	37349	0.49	6.6E-02	BF694659.1	EST_HUMAN	Human respiratory syncytial virus, complete genome
11205	24274	37811	4.95	6.6E-02	BF374248.1	EST_HUMAN	Human respiratory syncytial virus, complete genome
12761	25506		4.64	6.6E-02	9937991	NT	Human respiratory syncytial virus, complete genome
13124	25793		1.28	6.6E-02	AF167430.1	NT	Homo sapiens EMS, gar22, rrp22 and bam22 genes
							Homo sapiens vinculin (VCL), mRNA
							602080808F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245336 5'
							MR1-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA
							Mus musculus DIPB gene (Dipb), mRNA
							Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
596	13785	28805	1.57	6.5E-02	BF027639.1	EST_HUMAN	601671046F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
1011	14183	27245	1.3	6.5E-02	7708088	NT	Homo sapiens E2F-like protein (LOC61270), mRNA
1422	14576	27649	3.38	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1773	14822	28018	2.04	6.5E-02	AE000764.1	NT	Aquifex aeolicus section 96 of 103 of the complete genome
6878	18870	32158	2.07	6.5E-02	AA443991.1	EST_HUMAN	z44h12.s1 Soares ovary tumor N6H0T Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038
6673	18832	33221	0.73	6.5E-02	BF685340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
7113	18539	31486	1.02	6.5E-02	U22881.1	NT	602118887F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4276029 5'
10147	23185	36781	0.57	6.5E-02	BE983200.2	EST_HUMAN	Azobacter vinelandii ATCC 5046 negative regulator NucB (mucB) gene, partial cds
10147	23185	36782	0.57	6.5E-02	BE983200.2	EST_HUMAN	601668817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10883	23171	37323	0.81	6.5E-02	BF106300.1	EST_HUMAN	601668817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865637 3'
10875	23960	37589	4.45	6.5E-02	AA195948.1	EST_HUMAN	60182351F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
12163	25129		3.78	6.5E-02	M21496.1	NT	z32g05.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12633	26363		3.87	6.5E-02	AF102993.1	NT	Rabbit microsomal epoxide hydrolase
589	13780	28789	1.49	6.4E-02	X94549.1	NT	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds
1770	14919	28013	0.99	6.4E-02	AE001777.1	NT	A. canerae precursor of peridinin-chlorophyll-protein (PCP) gene
1770	14919	28014	0.99	6.4E-02	AE001777.1	NT	Thermoboga maritima section 89 of 136 of the complete genome
							Thermoboga maritima section 89 of 136 of the complete genome
							q607b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR6.b3
5586	18763	31803	1.11	6.4E-02	A181958.1	EST_HUMAN	LTR8 repetitive element;
6239	19413	32761	2.64	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6239	19413	32762	2.64	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6332	18896	33069	1.23	6.4E-02	A1672896.1	EST_HUMAN	w673g12.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346780 3'
6957	20270	33708	4.11	6.4E-02	BE974448.1	EST_HUMAN	601880425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'
8631	21812		2.47	6.4E-02	6753323	NT	Mus musculus chaperonin subunit 6a (zebra) (Cct6a), mRNA
8865	21844	35478	4.17	6.4E-02	AA093305.1	EST_HUMAN	K1419.c6g.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9327	22403	35955	0.98	6.4E-02	AF150195.1	EST_HUMAN	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
9785	22828		0.61	6.4E-02	BE634083.1	EST_HUMAN	RC1-OT0083-150600-014-g06 OT0083 Homo sapiens cDNA
9918	22958	36545	1.87	6.4E-02	AB011128.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
10488	23503	37116	0.45	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10488	23503	37117	0.45	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
12008	24983	38597	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12008	24993	38698	1.86	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12427	28048		2.7	6.4E-02	AF107890.1	NT	Homo sapiens mitch 5B (MUC5B) gene, partial cds
12479	25331	32058	2.61	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1793	14942	28035	2.51	6.3E-02	AF109805.1	NT	Mus musculus major histocompatibility locus class III region Hsc70t gene, partial cds; smRNP, G7A, NG23, Muc5 homolog, CLCP, NG24, NG25, and NG28 genes, complete cds; and unknown genes
3892	18854		2.29	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6284	18438	32785	1.12	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4087498 5'
7391	20469		1.64	6.3E-02	X97869.1	NT	H. sapiens gene encoding La autoantigen
9491	22548	38111	0.99	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Dornin gene, exons 1-3
10218	23264	38843	3.52	6.3E-02	AB010182.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
10478	23513		1.31	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GKC Homo sapiens cDNA clone GKC4H1E01 5'
10954	18438	32785	2.36	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4087499 5'
2549	15874	28797	1.04	6.2E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
4395	17508	30489	4.22	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4458	17598		1.03	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Ne-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4705	17840		5.66	6.2E-02	Q82191	SWISSPROT	52 KD RO PROTEIN (SJOGEREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
6935	20250	33889	0.78	6.2E-02	D49530.1	NT	Spirulina platensis DNA for acetylase cyclase, complete cds.
7805	20861	34354	0.88	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8016	21087		0.58	6.2E-02	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
9148	28225		0.92	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9544	22609	36177	0.47	6.2E-02	AA778450.1	EST_HUMAN	af20a06.61 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
9681	22730	38300	1.19	6.2E-02	6877898	NT	Mus musculus stromal cell derived factor receptor 2 (Sdrf2), mRNA
11415	24476	38140	1.42	6.2E-02	AF217480.1	NT	Homo sapiens fragile 16D oddo reductase (FOR) gene, exons 8, 9, and partial cds
11629	24709	38401	1.54	6.2E-02	AJ242735.1	NT	Methanobrevibacter ruminantium (strain ATCC 35061) chymotrypsin (chyl) gene
12263	26191		3.63	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12817	26415		1.24	6.2E-02	BE793085.1	EST_HUMAN	601563773F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3887842 5'
12703	25487	32024	3.61	6.2E-02	BF112039.1	EST_HUMAN	737108.x1 Soares_NSF_F8_9w_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to
268	13485	26518	3.63	6.1E-02	D16471.1	NT	TR:Q9Y4S6 Q9Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1]:
4099	17294		2.86	6.1E-02	U73326.1	NT	Human mRNA, Xq terminal portion
							Arabidopsis thaliana K+ inward rectifying channel protein (AtKIC1) gene, complete cds

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Table 4  
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6240	19414		1.57	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8458	21539	35088	3.55	6.1E-02	X99268.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8861	21940	35474	0.6	6.1E-02	BE971853.1	EST_HUMAN	601651088R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934804 3'
8861	21940	35475	0.6	6.1E-02	BE971853.1	EST_HUMAN	601651088R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934804 3'
10967	24048	37681	3.9	6.1E-02	BE178543.1	EST_HUMAN	IL3-HT0618-110500-136-C08 HT0618 Homo sapiens cDNA
12134	25114	38818	1.68	6.1E-02	AB025333.1	NT	Eptatretus burgeri mRNA for RNA polymerase III largest subunit, partial cds
12218	26063		30.03	6.1E-02	X70669.1	NT	S. japonicum mRNA for serine-enzyme
12838	26957		1.58	6.1E-02	AI88661.1	EST_HUMAN	ts59f07 x1 NCL_CGAP_OV35 Homo sapiens cDNA clone IMAGE:2282901 3'
12983	25645		6.43	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment H3210007
1281	14447	27513	1.58	6.0E-02	AE001777.1	NT	Thermotoga maritima section 88 of 136 of the complete genome
2740	15857	28669	1.17	6.0E-02	AW56848.1	EST_HUMAN	EST380924 MAGE sequences, MAGJ Homo sapiens cDNA
2832	15946		1.43	6.0E-02	AB031289.1	NT	Mesocricetus corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
3002	13335	26382	1.53	6.0E-02	AA188730.1	EST_HUMAN	z978a04.r1 Stratagene HeLa cell s3 937215 Homo sapiens cDNA clone IMAGE:628310 5'
3002	13335	26383	1.53	6.0E-02	AA188730.1	EST_HUMAN	z978a04.r1 Stratagene HeLa cell s3 937215 Homo sapiens cDNA clone IMAGE:628310 5'
3301	18475	29498	2.07	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' and similar to tissue-specific protein
3301	18475	29497	2.07	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma IV Homo sapiens cDNA 5' and similar to tissue-specific protein
3725	16886		0.76	6.0E-02	BE884443.2	EST_HUMAN	601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
5514	18712		1.01	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011199-013-604 BT0253 Homo sapiens cDNA
6345	19515	32872	1	6.0E-02	AB07537.1	EST_HUMAN	w48h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.11 L1 L1 repetitive element;
7127	18553	31487	2.86	6.0E-02	5174688	NT	Homo sapiens stimulated trans-acting factor (60 kDa) (STAF50) mRNA
7127	18553	31488	2.86	6.0E-02	5174688	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7338	20418	33880	2.37	6.0E-02	BF382349.1	EST_HUMAN	601615274F2 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:4049228 5'
7857	20912	34417	1.78	6.0E-02	AI204276.1	EST_HUMAN	qf58p08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754199 3'
8617	21697		0.46	6.0E-02	11466495	NT	Reclinomonas americana mitochondrion, complete genome
9472	22529	36092	1.28	6.0E-02	AI623167.1	EST_HUMAN	is78a08.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237362 3'
9472	22529	36093	1.28	6.0E-02	AI623167.1	EST_HUMAN	is78a08.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2237362 3'
9506	22661	36233	2	6.0E-02	AJ245395.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9506	22661	36234	2	6.0E-02	AJ245395.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
10109	23147	36746	0.72	6.0E-02	AA309797.1	EST_HUMAN	EST180854 Jurkat T-cells V Homo sapiens cDNA 5' and similar to similar to heat shock protein 1, 60 kDa-like



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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10109	23147	36747	0.72	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to heat shock protein 1, 60 kDa-like
11618	24669		1.42	6.0E-02	AA128386.1	EST_HUMAN	zn87c08.1 Stratagene lung carcinoma 837219 Homo sapiens cDNA clone IMAGE:565166 5' similar to gb:269181 60S RIBOSOMAL PROTEIN L31 (HUMAN);
12921	25608		5.12	6.0E-02	AI809273.1	EST_HUMAN	wf69j03.x1 Soares_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:060298
239	13481	28489	5.88	5.9E-02	AW934719.1	EST_HUMAN	O60298 KIAA0551 PROTEIN;
3048	16224	28246	2.77	5.9E-02	AF190269.1	NT	RC1-DT0001-290100-012-010 DT0001 Homo sapiens cDNA
4864	17997		0.77	5.9E-02	AF166111.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
8817	21898	35435	2	6.9E-02	8055249	NT	Duck parvovirus strain 90-2193 capsid protein (VP3) gene, partial cds
8650	21093		0.87	5.9E-02	BF242748.1	EST_HUMAN	Mus musculus Iroquois related homeobox 5 (Drosophila) (Irx5), mRNA
11026	24104		7.39	5.9E-02	6678970	NT	60187760F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105994 5'
11835	24824		1.35	5.9E-02	BF575339.1	EST_HUMAN	Mus musculus foliata-like (Fell), mRNA
11850	24839		1.37	6.9E-02	AJ240733.1	EST_HUMAN	60207654F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243834 5'
856	14129		6	5.8E-02	D80110.1	NT	Gallus gallus HKC9 telomere junction
1893	14845	27929	0.87	5.8E-02	D61768	SWISSPROT	Thiobacillus ferrooxidans merC, merA genes and URF-1
3753	16814	29917	1.68	5.9E-02	AE001776.1	NT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
4474	17614	30893	6.79	5.8E-02	AW051927.1	EST_HUMAN	Thermotoga maritima section 87 of 136 of the complete genome
4474	17614	30594	6.79	5.8E-02	AW051927.1	EST_HUMAN	wx24602.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4659	17804	30792	4.64	5.8E-02	AI247505.1	EST_HUMAN	wx24602.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4698	17804	30783	4.84	5.8E-02	AI247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_TNFRS1_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4698	17831		2.1	5.8E-02	AF096284.1	NT	qh56f01.x1 Soares_fetal_liver_spleen_TNFRS1_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
7855	20910	34414	2.78	5.8E-02	M99150.1	NT	gb:M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
7855	20910	34415	2.78	5.8E-02	M99150.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
8866	21045	35479	0.61	5.8E-02	AL163283.2	NT	Human polymorphic microsatellite DNA
12365	25251		1.65	5.8E-02	AF220177.1	NT	Human polymorphic microsatellite DNA
12681	26180		4.55	5.8E-02	AA604269.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
3123	16299	28312	1.14	5.7E-02	AI031844.1	EST_HUMAN	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
3139	16315	29328	1.09	5.7E-02	AF119117.1	NT	no75et11.st NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:112684 3'
3902	17061	30060	2.3	5.7E-02	AW686791.1	EST_HUMAN	ou63b05.st NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP-C37A2.2
4807	17841		0.95	5.7E-02	M95099.1	NT	CE086111;
							Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
							EST378865 IMAGE resequences, MAGI Homo sapiens cDNA
							Bos taurus lysozyme gene (cow 3), complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6000	19185		0.87	5.7E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7630	20699	34175	0.88	5.7E-02	BE871911.1	EST_HUMAN	601447837F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851885 5'
7630	20699	34176	0.88	5.7E-02	BE871911.1	EST_HUMAN	601447837F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3851885 5'
7710	20775	34260	0.72	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
7710	20775	34261	0.72	5.7E-02	D78003.1	NT	Xenopus laevis mRNA for fourth component of complement, complete cds
8349	21430	34954	1.45	5.7E-02	AJ286090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv9.2 gene)
10055	23093	36695	0.82	5.7E-02	6681280	NT	Mus musculus ec2 oncogene (Ec2), mRNA
11464	24523	38193	3.14	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC.cn18b09 random
11464	24523	38194	3.14	5.7E-02	AI752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC.cn18b09 random
11630	24710		1.68	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12586	25989		19.03	5.7E-02	D50320.1	NT	Pig DNA for SPAK-2, complete cds
12769	25512		2.17	5.7E-02	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12853	26042		3.04	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
13012	28169		5.21	5.7E-02	AF281280.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
13171	25759	31929	1.18	5.7E-02	R48513.1	EST_HUMAN	Xf6cd10.s1 Scarsa breast 2Nbt-Bst Homo sapiens cDNA clone IMAGE:183523 3' similar to contains L1 repetitive element
1556	14709	27789	1.1	5.6E-02	AF094455.1	NT	Hydrocotyle rotundifolia ribosomal protein L16 (rpl16) gene, intron; chloroplast gene for chloroplast product
2362	15463		1.95	5.6E-02	BE804308.1	EST_HUMAN	601494378F2 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898610 5'
4763	17988	30878	1.37	5.6E-02	AB013100.1	NT	Lyopersion esculentum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4818	17951	30836	1.31	5.6E-02	AA280599.1	EST_HUMAN	zs45c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700419 3'
6799	19954	33354	5.87	5.6E-02	AW172708.1	EST_HUMAN	Xf02c10.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2656050 3' similar to TR:O94979 O94979 KIAA0908 PROTEIN
7031	20167	33689	1.02	5.6E-02	AA868182.1	EST_HUMAN	od47f12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element
7301	20363	33842	3.3	5.6E-02	BE080001.1	EST_HUMAN	QVO-BN0147-280400-214-g07 BN0147 Homo sapiens cDNA
8010	21060	34372	1.32	5.6E-02	A1183883.1	EST_HUMAN	q464g11.x1 Scarsa testis_NHT Homo sapiens cDNA clone IMAGE:1734308 3'
9002	22081	35823	2.52	5.6E-02	BE542683.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453278 5'
9002	22081	35824	2.52	5.6E-02	BE542683.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453278 5'
10017	23055	36651	1.18	5.6E-02	AA482864.1	EST_HUMAN	nt49c07.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859 LAMINA ASSOCIATED POLYPEPTIDE 1C

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11883	24851		2.42	5.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2720	15838	28048	7.33	5.6E-02	X97889.1	NT	H sapiens gene encoding La autoantigen
3286	18460	29481	3.33	5.5E-02	6755501	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4332	17475	30459	0.98	5.5E-02	L41561.1	NT	Gallid herpesvirus mRNA fragment
5776	18958	32272	3.49	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
6149	18988	32272	4.32	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7535	20608	34083	1.65	5.5E-02	6755902	NT	Mus musculus tufalin 1 (Tuf1), mRNA
8311	21383	34917	0.87	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
8311	21383	34918	0.87	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
9855	22895	36478	0.78	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9855	22895	36477	0.78	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9951	22890	36583	1.24	5.6E-02	U69492.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
							Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB)>
11271	24339	37977	6.31	5.5E-02	U09771.1	NT	Oryza sativa tbb3-1 gene for putative Bowman Birk trypsin inhibitor
3084	18280		0.85	5.4E-02	AJ277488.1	NT	RC5-BT0559-140200-012-C03 BT0559 Homo sapiens cDNA
3508	18476		8.19	5.4E-02	BE073468.1	EST_HUMAN	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
4020	17177	30186	0.91	5.4E-02	U85806.1	NT	Bacillus subtilis complete genome (section 13 of 21); from 2355281 to 2613730
8316	21388		1.18	5.4E-02	Z99118.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
9271	22347	35897	0.51	5.4E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10938	24020	37653	1.86	5.4E-02	U20780.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11453	24513	38180	1.36	5.4E-02	BF371289.1	EST_HUMAN	RC6-FN0112-180700-021-D08 FN0112 Homo sapiens cDNA
11453	24513	38181	1.36	5.4E-02	BF371289.1	EST_HUMAN	RC6-FN0112-180700-021-D08 FN0112 Homo sapiens cDNA
12463	26930		3.72	5.4E-02	U44894.1	NT	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1078	14244	27300	1.55	5.3E-02	AW391248.1	EST_HUMAN	QVO-ST0213-021299-082-a09 ST0213 Homo sapiens cDNA
1078	14244	27301	1.55	5.3E-02	AW391248.1	EST_HUMAN	QVO-ST0213-021299-082-a09 ST0213 Homo sapiens cDNA
1535	14698	27768	20.57	5.3E-02	T94760.1	EST_HUMAN	ye3712.1 Stragene lung (8937210) Homo sapiens cDNA clone IMAGE:118951 5' similar to gb:K01506
2566	15631	28316	3.22	5.3E-02	AJ276408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN);
3008	16184	29207	0.97	5.3E-02	M59417.1	NT	Pseudomonas putida tfgS gene
3008	16184	29208	0.97	5.3E-02	M59417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3221	16395	29408	4.83	5.3E-02	AJ276408.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
5200	18321	31280	7.98	5.3E-02	M80463.1	NT	Pseudomonas putida tfgS gene
							Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5434	18634	31612	2.39	6.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
5434	18634	31613	2.39	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6228	19403	32753	1.14	5.3E-02	M85289.1	NT	Human heparan sulfatase proteoglycan (HSPG2) mRNA, complete cds
7024	20160	33580	4.02	5.3E-02	8895413	NT	Lymphocystis disease virus 1, complete genome
7241	20325	33769	1.37	5.3E-02	U32832.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7617	20590		2.3	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mice, mRNA], 4053 nt
8061	21073	34585	0.68	5.3E-02	P38742	SWISSPROT	HYPOTHETICAL 130.0 KD PROTEIN IN SNF6-SPO11 INTERGENIC REGION
8600	21681		0.68	5.3E-02	U10098.1	NT	Mus musculus 128/Sv cys21n C (cst8) gene, complete cds
9325	22401	35954	1.73	5.3E-02	X03127.1	NT	Podospira anserina mitochondrial epsilon-gen DNA
10462	23497		0.61	5.3E-02	Y07807.1	NT	D. rerio mRNA for xp-23 POU gene, splice variant (neurula, 9-10 hpf and postembryogenesis, 20-28 hpf)
10538	23573	37180	0.79	5.3E-02	X68432.1	NT	B. rerio pailc mRNA for transcription factor
13173	25761	31831	1.55	5.3E-02	AF276815.1	NT	Branchiostoma floridae homeodomain-containing protein Hox13 (Hox13) gene, exon 2 and partial cds
2368	15489		64.04	5.2E-02	5031903	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3183	18358	28363	2.39	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3183	18358	28384	2.39	5.2E-02	AJ277681.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4050	17206	30218	0.8	5.2E-02	AF238101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds
4393	17536	30515	3.31	5.2E-02	U07132.1	NT	Human steroid hormone receptor Ner-1 mRNA, complete cds
5287	18406	31373	0.66	5.2E-02	AB035201.1	NT	Rattus norvegicus mRNA for thyroglobulin, complete cds
6040	19223	32545	0.64	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6233	19408		0.84	5.2E-02	AB030965.1	EST_HUMAN	wj80e04.x1 NCI_OGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MIER15.b1 MER15 repetitive element
7424	20601	33972	1.23	5.2E-02	P36322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8389	21470		2.39	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8931	22971	36560	2.16	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
8931	22971	36561	2.16	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
12725	25483		1.6	5.2E-02	Q03030	SWISSPROT	OXA1/OACETATE DECARBOXYLASE ALPHACHAIN
2437	15565		0.88	5.1E-02	AL134071.1	EST_HUMAN	DKFZp847D073_r1 647 (synonym: hibr1) Homo sapiens cDNA clone DKFZp847D073 5'
5181	18283	31248	0.89	5.1E-02	BE957423.2	EST_HUMAN	601663565R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838361 3'
5251	18372		0.66	5.1E-02	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
5349	18462		0.74	5.1E-02	U72397.1	NT	Bacteriophage 80 alpha holin and amidase genes, complete cds
6812	19966	33370	0.78	5.1E-02	AF280369.1	NT	HIV-1 patient 98 from Italy protease (pol) gene, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6997	18518	31608	1.73	5.1E-02	BF378625.1	EST_HUMAN	QVO-UM0051-250800-350-b08 UM0051 Homo sapiens cDNA
8447	21528	35055	0.82	5.1E-02	M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT1) gene, complete cds
8447	21528	35058	0.82	5.1E-02	M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT1) gene, complete cds
8542	21623	35160	1.42	5.1E-02	AJ131906.1	NT	Spodoptera littoralis mRNA for 3-dehydrodysfome 3beta-reductase
8086	22165	35710	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9086	22165	35711	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
10014	23052	36846	4.27	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Ssf1 homolog (SSD1) gene, complete cds
10384	23418	37026	1.9	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
11068	24143	37778	1.81	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
11068	24143	37779	1.81	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
12736	25487	26721	2.8	5.0E-02	AF098004.1	NT	Cucumis melo polygalacturonase precursor (MFG3) mRNA, complete cds
495	13690	27452	2.82	5.0E-02	Z99104.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1231	14390	27452	2.82	5.0E-02	Z99104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
2047	15188	28299	5.08	5.0E-02	P02810	SWISSPROT	SALVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-FPIF-S) (PROTEIN A/PROTEIN C) [CONTAINS: PEPTIDE P-C]
2879	14182	27244	10.68	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3418	16587		1.36	5.0E-02	7305510	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA
3684	16847		1.01	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 87 of 163 of the complete genome
3775	16936	28942	5.9	5.0E-02	U12769.2	NT	Arthersea pernyi period clock protein homolog mRNA, complete cds
4841	18071		1.05	5.0E-02	P40232	SWISSPROT	CASEIN KINASE II BETA CHAIN (CK II)
8258	19432	32776	0.84	5.0E-02	AF096284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
8438	19603		1.28	5.0E-02	AJ242825.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7128	18554	31469	0.89	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
7709	20774	34259	10.04	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
7913	20884		0.67	5.0E-02	AW062464.1	EST_HUMAN	MRO-CT0084-100899-002-g10 C10084 Homo sapiens cDNA
10403	23436	37046	1.37	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fis3) mRNA, complete cds
10566	23888		0.65	5.0E-02	BF213260.1	EST_HUMAN	801844753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4070101 5'
11782	24772	39469	2.26	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 160 of the complete genome
12229	26004		4.7	5.0E-02	Q04047	SWISSPROT	NO-QN-TRANSIENT A PROTEIN
231	13452		11.82	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds
380	13588	28623	4.18	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
380	13588	28624	4.18	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
2837	18114	29126	0.71	4.9E-02	U32686.1	NT	Zea mays phytoene synthase (Y1) gene, complete cds
3360	16532	29546	1.85	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIN A TROPHY PROTEIN)

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3650	18823		0.85	4.8E-02	AA188940.1	EST_HUMAN	zq48a12.s1 Stratagene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:632926 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
3681	18844	26851	0.78	4.8E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3681	18844	26852	0.78	4.8E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4984	18053	31069	2.64	4.8E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
4984	18053	31070	2.64	4.8E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
5488	18885	31702	1.62	4.8E-02	L00122.1	NT	Rat elastase II gene, exon 6
5488	18885	31703	1.62	4.8E-02	L00122.1	NT	Rat elastase II gene, exon 6
7292	20374	33831	1.79	4.8E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8815	21894		1.07	4.8E-02	AE002308.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8942	22021		0.61	4.8E-02	BE931532.1	EST_HUMAN	MRQ-HT0408-170800-003-a08 HT0408 Homo sapiens cDNA
8954	22033	36676	0.97	4.8E-02	AL161569.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10500	23535	37145	0.54	4.8E-02	P10532	SWISSPROT	TRANSCRIPTION FACTOR E3
10802	23835	37459	1.57	4.8E-02	L41161.1	NT	Mus musculus SM22 alpha gene, exon 1
10802	23835	37460	1.57	4.8E-02	L41161.1	NT	Mus musculus SM22 alpha gene, exon 1
11687	24686	38378	3.46	4.8E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12957	25624		3.23	4.8E-02	M19394.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
340	13552	26582	1.19	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
341	13552	26582	2.61	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
501	13696	26726	11.53	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2347	16478	26610	2.08	4.8E-02	W51983.1	EST_HUMAN	z44b02.s1 Soares, serous, fibroblastic NBHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to
3280	18454	29478	1.79	4.8E-02	X17144.1	NT	gb:W30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
4793	17928		1.06	4.8E-02	Z64280.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
5237	18359	31328	0.68	4.8E-02	U91914.1	NT	S. sacra gene for skeletal muscle myosin receptor
8332	21414	34940	1.41	4.8E-02	AW388497.1	NT	Streptococcus constellatus D-erythrin D-erythrinase gene, partial cds
8329	22405	35957	1.01	4.8E-02	AJ001398.1	EST_HUMAN	MR2-ST0126-221089-012-b02 ST0126 Homo sapiens cDNA
8329	22405	35957	1.01	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9329	22405	35957	1.01	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
11219	24288	37928	1.84	4.8E-02	X61236.1	NT	S. cerevisiae NUM1 gene, involved in nuclear migration control
11219	24288	37928	1.84	4.8E-02	X61236.1	NT	S. cerevisiae NUM1 gene, involved in nuclear migration control
12511	25350		1.48	4.8E-02	6932893	NT	Streptococcus thermophilus bacteriophage Sf19, complete genome
5122	18248	31214	0.74	4.7E-02	6931261	NT	Rattus norvegicus Nestin (Nes), mRNA

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6989	20197	33623	3.34	4.7E-02	W01153.1	EST_HUMAN	y27109.r1 Soares melanocyte 2Nbl-H1 Homo sapiens cDNA clone IMAGE:281017 5' similar to contains Alu repetitive element
7025	20161	33581	0.69	4.7E-02	BF686025.1	EST_HUMAN	602143554F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4304772 5'
7025	20161	33582	0.69	4.7E-02	BF686025.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
7058	20111	33527	1.71	4.7E-02	M62752.1	NT	Rat statin-related protein (s1) gene, complete CDS
8446	21628	35053	9.44	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
9154	22332	35777	1.31	4.7E-02	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
9178	22354		2.97	4.7E-02	AB026978.1	NT	Gallus gallus Wpkci-8 gene, complete cds
9428	22502	36068	7.75	4.7E-02	X16543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
9936	22975		0.7	4.7E-02	A1873042.1	EST_HUMAN	we79c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
11852	24841	38535	1.43	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11852	24841	38536	1.43	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
12446	26182		4.31	4.7E-02	AV648521.1	EST_HUMAN	AV648521 G1C Homo sapiens cDNA clone GLOBKD02 3'
281	13489	28531	0.69	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
758	13939	28984	2.89	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1320	14478		1.49	4.6E-02	A1014255.1	EST_HUMAN	am60d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TRP:P90533
1390	14544	27620	5.39	4.6E-02	AV727059.1	EST_HUMAN	P90533 LIMA ;contains element LTR1 repetitive element ;
2557	15682	28807	2.34	4.6E-02	AW236023.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCBWC01 5'
2868	13499	28531	1.78	4.6E-02	BE153583.1	EST_HUMAN	G12849 G-RICH SEQUENCE FACTOR-1 ;
3073	16249	29270	0.64	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3410	16249	29270	0.69	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3585	16249	29270	0.84	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4239	17385		0.82	4.6E-02	AF220385.1	NT	Mus musculus nucleolar RNA helicase HGU (dax21) gene, complete cds
5852	18042	32348	1.67	4.6E-02	AF076982.1	NT	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (Gnrl2) gene, complete cds
6359	19529	32887	3.67	4.6E-02	X61824.1	NT	C. reinhardtii atp2 (atpB) mRNA
6359	19529	32888	3.67	4.6E-02	X61824.1	NT	C. reinhardtii atp2 (atpB) mRNA
6938	20251	33987	1.41	4.6E-02	A1149574.1	EST_HUMAN	gc6006.x1 Soares_placenta_8tc8weeks_2NblHP8tc8w Homo sapiens cDNA clone IMAGE:1713971 3' similar to contains L1.13 L1 repetitive element ;
8007	21057	34569	0.63	4.6E-02	5978720	NT	Rattus norvegicus Cathepsin H (Cath), mRNA
8856	21095	35472	3.81	4.6E-02	BE154008.1	EST_HUMAN	PM0-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
11699	24887	38377	3.39	4.6E-02	AA913328.1	EST_HUMAN	0127109.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13078	25708		3.14	4.6E-02	X57808.1	NT	Human germline immunoglobulin lambda light chain gene
480	13655	26693	2.24	4.5E-02	P22448	SWISSPROT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1245	14404	27465	1.52	4.5E-02	AF005730.1	NT	Marburg virus strain MS Africa/Johannesburg/1976/Ozolin VP35 gene, complete cds
1245	14404	27466	1.62	4.6E-02	AF005730.1	NT	Marburg virus strain MS Africa/Johannesburg/1976/Ozolin VP35 gene, complete cds
1847	14993	28095	4.83	4.5E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2177	15312	28440	2.2	4.5E-02	AE003964.1	NT	Xyella fastidiosa, section 110 of 220 of the complete genome
3817	16977	29981	5.04	4.5E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6360	19530	32889	1.63	4.5E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6838	19785	33184	0.84	4.5E-02	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
7018	20154	33574	0.59	4.5E-02	L28487.1	NT	Methanococcus marisnigri carbon monoxide dehydrogenase large subunit (cdh1A) gene, carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
7018	20154	33575	0.59	4.5E-02	L28487.1	NT	Methanococcus marisnigri carbon monoxide dehydrogenase large subunit (cdh1A) gene, carbon monoxide dehydrogenase small subunit (cdh1B) gene, complete cds
8587	21688	35207	2.24	4.5E-02	AF036884.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
10155	23162	36788	4.2	4.5E-02	AA325216.1	EST_HUMAN	EST28167 Cerebellum II Homo sapiens cDNA 5' and similar to neuro-D4 protein
10305	23340	36945	0.47	4.5E-02	X95508.1	NT	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
10421	23458	37061	0.78	4.5E-02	AB000470.1	NT	A. europaeum mRNA for legumin-like protein
12442	26313	32089	2.61	4.5E-02	11418013	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12891	26051	31684	3.78	4.6E-02	AA191097.1	EST_HUMAN	Homo sapiens ret finger protein-like 3 (RFFL3), mRNA
227	13449		4.35	4.4E-02	BE92733.1	EST_HUMAN	zq43111.1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5'
1050	14216	27273	0.77	4.4E-02	L19295.1	NT	601652164F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
2163	15289		6.82	4.4E-02	P31588	SWISSPROT	Drosophila melanogaster extracellular (EXD) mRNA, complete cds
2559	15884	28809	1.81	4.4E-02	AW875475.1	EST_HUMAN	HYPOTHETICAL PROTEIN (ORF 2280)
3730	16891	29895	1.68	4.4E-02	AF159160.1	NT	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
4760	17885	30866	1.33	4.4E-02	AF109907.1	NT	Mycoplasma xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4750	17885	30867	1.33	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7287	20350	33802	0.59	4.4E-02	AF095824.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7287	20350	33803	0.59	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8952	22031	35572	2.34	4.4E-02	AA736959.1	EST_HUMAN	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
11328	24389	38034	2.64	4.4E-02	AF080669.1	NT	ntw13nd3.s1 NCL CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
							Hepatitis E virus strain HEV-US2 polypeptide (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds



Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11477	24536	38206	3.08	4.4E-02	AA498739.1	EST_HUMAN	ae3304.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897831 5'
12158	25126		4.55	4.4E-02	AB040328.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
12347	28192		1.65	4.4E-02	BF241246.1	EST_HUMAN	601878746F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107418 5'
602	19882	27034	7.25	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2634	15757	28871	1.55	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBAOH08 5'
3818	16682	29693	8.18	4.3E-02	AF163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3749	16910		1.21	4.3E-02	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6825	19785	33172	4.94	4.3E-02	P30427	SWISSPROT	PLECTIN
6825	19785	33173	4.94	4.3E-02	P30427	SWISSPROT	PLECTIN
6871	20023	33433	0.8	4.3E-02	AA652268.1	EST_HUMAN	ns59c12.s1 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:1188886
8711	21791	35327	0.69	4.3E-02	AF283359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
9001	22080	35622	1.32	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
12412	25291		1.32	4.3E-02	X55322.1	NT	H.sapiens NCAM mRNA for neural cell adhesion molecule
845	14023	27081	1.74	4.2E-02	AL138077.2	EST_HUMAN	Campylobacter jejuni NCTC11168 complete genome, segment 4/8
889	14085		2.4	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
918	14094	27159	1.51	4.2E-02	AW003645.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
1768	14807		1.37	4.2E-02	AL445068.1	NT	L1 RETROPOSOM, ORF2 MRNA contains L1.13 L1 L1 repetitive element ;
1818	14868	28080	0.69	4.2E-02	P23091	SWISSPROT	Thermoplasma acidophilum complete genome, segment 4/5
3784	18915	28918	1.66	4.2E-02	P23091	SWISSPROT	TRANSFORMING PROTEIN MAF
4855	17898	30982	0.59	4.2E-02	BF342995.1	EST_HUMAN	TRANSFORMING PROTEIN MAF
							60207105F1 NCL CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4162072 5'
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5735	18928	32224	0.74	4.2E-02	AF280107.1	NT	4 (CYP3A4) and cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5735	18928	32225	0.74	4.2E-02	AF280107.1	NT	4 (CYP3A4) and cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7122	18548	31460	0.61	4.2E-02	BE268285.1	EST_HUMAN	601124566F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2883318 5'
7695	20760	34244	4.35	4.2E-02	AF216752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7717	20781	34267	0.61	4.2E-02	AV730347.1	EST_HUMAN	AV730347 HTF Homo sapiens cDNA clone HTFAVH04 5'
9010	22089	35631	3.82	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10367	23402	37013	1.46	4.2E-02	Q16850	SWISSPROT	T-BRAIN-1 PROTEIN (T-BRAIN-1) (TBR-1) (TES-56)

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Table 4  
Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11295	24361	38002	1.52	4.2E-02	AA976118.1	EST_HUMAN	on33b11.g1 NCI CGAP_Lu5 Homo sapiens cDNA IMAGE:1558461 3' similar to gb:M65290
11587	24640	38320	2.83	4.2E-02	BE815822.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN);
11587	24640	38321	2.83	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-410 BN0174 Homo sapiens cDNA
11795	24786	38483	1.52	4.2E-02	AF176458.1	NT	PM3-BN0174-250500-009-410 BN0174 Homo sapiens cDNA
12729	26109		6.84	4.2E-02	AI983494.1	EST_HUMAN	PRRS isolate PRRSV38 envelope glycoprotein gene, complete cds
13076	25705		1.17	4.2E-02	D14711.1	NT	wt48g10.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
523	13716	26743	1.85	4.1E-02	AF200629.1	NT	Slaphylococcus aureus HSP10 and HSP60 genes
2741	15859	28970	1.06	4.1E-02	AE002330.2	NT	Homo sapiens HPS1 gene, intron 5
4005	17162	30168	0.61	4.1E-02	BE297236.1	EST_HUMAN	Chlamydia muridarum, section 60 of 85 of the complete genome
4005	17162	30169	0.61	4.1E-02	BE297236.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
4595	17732		0.61	4.1E-02	AW893484.1	EST_HUMAN	601177907F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3533353 5'
5229	18351		0.61	4.1E-02	X85880.1	NT	QV1-NN0012-180400-164-166 NN0012 Homo sapiens cDNA
5759	18851	32263	1.06	4.1E-02	BE251894.1	EST_HUMAN	L monocytogenes type 3 partial lap gene (strain 443)
5759	18851	32264	1.06	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343858 5'
7022	20168		0.98	4.1E-02	X75881.1	NT	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343858 5'
7248	20331	33778	1.39	4.1E-02	AE002132.1	NT	A. thaliana mRNA for plasma membrane intrinsic protein 1a
7682	20747	34228	1.79	4.1E-02	7662347	NT	Uraeplasma urealyticum section 33 of 59 of the complete genome
7778	20834	34325	20.08	4.1E-02	L02110.1	NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA
7842	20992	34502	2.81	4.1E-02	AF026198.1	NT	Mus musculus proviral retroviral insertion in the cGMP-phosphodiesterase (rd beta PDE) gene, intron 1, with the proviral insert encompassing the env pseudogene (3' end) and 3' LTR
8402	21483	35011	0.74	4.1E-02	P97857	SWISSPROT	Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit; complete cds
8945	21924	35462	0.79	4.1E-02	P34887	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
9355	22430	35988	0.87	4.1E-02	AA372398.1	EST_HUMAN	MOTIFS 1) (ADAMTS-1) (ADAM-TS1)
13112	26110	31668	9.61	4.1E-02	AJ271909.1	NT	GUTIGLE COLLAGEN 34
3316	18489	29507	3.65	4.0E-02	AB040904.1	NT	EST842291 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3900	17059	30058	1.09	4.0E-02	L11910.1	NT	Brassica napus glh gene for plastid glutamine synthetase, exons 1-12
5495	18694	31710	5.31	4.0E-02	AF280107.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
							Human retinoblastoma susceptibility gene exons 1-27, complete cds
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6343	19513	32870	0.98	4.0E-02	BF110434.1	EST_HUMAN	7n52h07.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3588380 3' similar to TR:O75288 O75286
7867	20921	34428	5.89	4.0E-02	L28898.1	NT	R29124_1.; Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (subnp) mRNA, complete cds
7929	20979		0.71	4.0E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
7943	20963	34503	0.8	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7943	20993	34504	0.8	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7980	21029	34543	0.61	4.0E-02	AF288153.1	NT	Homo sapiens erythrocyte topomodulin (E-TMOD) gene, exon 7
8914	21993	35532	2.52	4.0E-02	P08640	SWISSPROT	GLUCOAMYLASE S1S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN
9844	22884		0.63	4.0E-02	BF078976.1	EST_HUMAN	GLUCOHYDROLASE
9869	22809	36485	2.46	4.0E-02	AJ000941.1	NT	60215384F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4284724 5'
10180	23227		1.08	4.0E-02	D43949.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thid:fumarate reductase subunit A
12073	25054		1.52	4.0E-02	AJ001018.1	NT	Human mRNA for KIAA0082 gene, partial cds
12333	25909	31859	18.34	4.0E-02	AJ001058.1	NT	Kluyveromyces fragilis gene for Cat+ ATPase
1144	14309	27366	2.79	3.9E-02	BF516149.1	EST_HUMAN	Ovis aries mRNA for acetyl-coA carboxylase
1375	14530	27603	2.15	3.9E-02	P41047	SWISSPROT	UIH-BW1-enx-h08-0-JL.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
2016	15168	28281	3.22	3.9E-02	AJ403388.1	NT	FAS ANTIGEN LIGAND
2769	15884		1.97	3.9E-02		NT	Mmusculus DNA for desmin-binding fragment DesD7
5246	18367	31334	0.67	3.9E-02	AW392417.1	EST_HUMAN	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC)
5279	18398	31366	0.9	3.9E-02	8924019	NT	mRNA
5279	18398	31367	0.9	3.9E-02	8924019	NT	RC6-ST0258-171199-021-C09 S10258 Homo sapiens cDNA
5849	19039	32348	1	3.9E-02	BE068841.1	EST_HUMAN	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5977	19162	32482	0.65	3.9E-02	BF675203.1	EST_HUMAN	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
7203	20068	33478	0.97	3.9E-02	BE271437.1	EST_HUMAN	601648974F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933642 5'
8023	21108	34623	1.44	3.9E-02	BF239613.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274810 5'
8260	21332	34849	0.6	3.9E-02	AJ229041.1	NT	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
8250	21332	34850	0.6	3.9E-02	AJ229041.1	NT	601908848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
11695	21071	34562	1.58	3.9E-02	P48778	SWISSPROT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
12184	26059		3.54	3.9E-02	AB042553.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
							ANTIGEN GOR
							Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12908	25595		2.35	3.9E-02	U68081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, Mus musculus chromosome X contig8; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnx28orf
13036	25979		64.89	3.6E-02	ALD49866.2	NT	Human protein C gene, complete cds
5558	18754	31792	0.8	3.8E-02	M11228.1	NT	HOMEOBOX PROTEIN HOXB4 (HOX-2.6)
6212	19387	32736	1.04	3.8E-02	P10284	SWISSPROT	Human sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
7471	20946	34018	1.72	3.8E-02	6005700	NT	Human von Willebrand factor gene, exons 23 through 34
8854	21943		1.51	3.8E-02	M60875.1	NT	Human sapiens PRO0514 protein (PRO0514), mRNA
10789	23822	37446	0.64	3.8E-02	7662563	NT	Human sapiens PELOTA (PELOTA) gene, complete cds
10888	23872	37603	1.71	3.8E-02	AF143952.2	NT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1016	14187	27248	4.05	3.7E-02	P19137	SWISSPROT	wr5608.x1 NCL CGAP Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2310	15442	28577	6.19	3.7E-02	A1984803.1	EST_HUMAN	Homo sapiens mRNA for KIAA0718 protein, partial cds
2845	16768	28883	0.97	3.7E-02	AB018261.1	NT	EOMESODERMIN
3115	16291	28306	1.13	3.7E-02	P78944	SWISSPROT	601896233F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4125584 5'
3117	16293	29307	4.33	3.7E-02	BF312863.1	EST_HUMAN	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnma3), mRNA
3543	16708		0.91	3.7E-02	6880541	NT	Aeropyrum pernix genomic DNA, section 67
7228	28218		0.95	3.7E-02	AF000063.1	NT	Xylella fastidiosa, section 121 of 229 of the complete genome
7869	20923	34430	0.81	3.7E-02	AE003975.1	NT	at55c09.a1 Soares parathyroid tumor NbhHPA Homo sapiens cDNA clone 1360912 3'
10219	23255		1.01	3.7E-02	AA782516.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12227	25178	38837	7.41	3.7E-02	BF124974.1	EST_HUMAN	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
12851	25945	31764	3.71	3.7E-02	11418392	NT	Odontella sinensis chloroplast, complete genome
13059	25699		1.23	3.7E-02	11467432	NT	H. vulgare Ss1 gene for sucrose synthase
3744	16905	28909	0.82	3.6E-02	X73221.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
3752	16913	29916	0.9	3.6E-02	AL096806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5313	18430	31400	0.67	3.6E-02	AL066810.1	NT	C-glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5543	18740	31758	0.61	3.6E-02	X59403.1	NT	C-glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5543	18740	31774	0.61	3.6E-02	X59403.1	NT	

Single Exon Probes Expressed in Placenta

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5617	18811	31890	0.66	3.6E-02	AF181722.1	NT	Homo sapiens RUPAS (RU2) mRNA, complete cds
6848	19599	33408	4.48	3.6E-02	AW1945516.1	EST_HUMAN	CM2-EN0019-110500-192-510 EN0013 Homo sapiens cDNA
6848	19599	33407	4.48	3.6E-02	AW1945516.1	EST_HUMAN	CM2-EN0019-110500-192-510 EN0013 Homo sapiens cDNA
7234	20318	33761	1.79	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Oxy precursor (sgp2) gene, complete cds
7458	20534	34009	2.89	3.6E-02	AA714521.1	EST_HUMAN	nm20a05.s1 NCL CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_rna2
7811	20866	34380	0.84	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
9591	22846	38216	2.18	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9591	22846	38217	2.16	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9812	22852	38431	0.84	3.6E-02	BF347688.1	EST_HUMAN	602020453F1 NCL CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4158118 5'
11456	24516	38183	1.48	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
11456	24516	38184	1.48	3.6E-02	BF131609.1	EST_HUMAN	601820416F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052570 5'
918	14093	27158	0.88	3.5E-02	U09506.1	NT	Drosophila melanogaster tigrin mRNA, complete cds
1033	14202	27260	2.43	3.5E-02	AF283417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1595	14748	27831	1.4	3.5E-02	BF078085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1595	14748	27832	1.4	3.5E-02	BF078085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4329	17472	30457	1.83	3.5E-02	AE001773.1	NT	Thermotoga maritima section 85 of 138 of the complete genome
4435	17676	30556	1.11	3.5E-02	P53780	SWISSPROT	CYSTATIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6351	18521	32878	1.76	3.6E-02	J01238.1	NT	Maize actin 1 gene (MAc1), complete cds
8165	21247		0.91	3.5E-02	H29951.1	EST_HUMAN	jp44a03.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190256 5' similar to contains Alu repetitive element;
8924	21903	35443	2.93	3.5E-02	BE968970.1	EST_HUMAN	601844701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929737 3'
10224	23260	36848	0.84	3.5E-02	X76642.1	NT	Lactis MG1363 grpE and dnaK genes
10270	23305	36902	0.61	3.5E-02	BE561042.1	EST_HUMAN	601344661F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11785	24775	38471	1.79	3.6E-02	AW861641.1	EST_HUMAN	PM1-CT0328-291289-002-H03 CT0328 Homo sapiens cDNA
11785	24775	38472	1.79	3.6E-02	AW861641.1	EST_HUMAN	PM1-CT0328-291289-002-H03 CT0328 Homo sapiens cDNA
12878	25583		1.31	3.5E-02	AF009683.1	NT	Homo sapiens T cell receptor beta locus, TORBV85P to TORBV71S2A2 region
12955	25991		2.71	3.5E-02	BE276948.1	EST_HUMAN	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3513833 5'
592	13783	26802	47.28	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
592	13783	26803	47.29	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
593	13783	26802	3.28	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds

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Probe Seq ID NO:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
593	13783	26803	3.26	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1076	14242	27288	2.67	3.4E-02	AW274020.1	EST_HUMAN	xx26d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1233	14392		5.43	3.4E-02	11346460	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2465	15592	28717	1.7	3.4E-02	T57160.1	EST_HUMAN	yo20e06.r1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:61250 5' similar to contains MER28 repetitive element
3517	16683	29694	1.5	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21O008
3876	17034	30032	0.81	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-060700-011-410 FN0155 Homo sapiens cDNA
4030	17186	30196	3.72	3.4E-02	AW784952.1	EST_HUMAN	RC8-LJ0015-210200-021-A10 UM0015 Homo sapiens cDNA
4720	17855	30838	2.77	3.4E-02	X59789.1	NT	Musculus S-antigen gene promoter region
5172	18294		1.9	3.4E-02	Q26457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5189	18311	31277	1.81	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6983	18612	31604	4.68	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8456	21537		3.16	3.4E-02	AI869629.1	EST_HUMAN	w19604.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2433031 3'
8947	22028	35567	1.18	3.4E-02	AA694886.1	EST_HUMAN	nu70108.s1 NCI_CGAP_A1M7 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element contains element MER25 MER25 repetitive element ;
9118	22187		5.28	3.4E-02	AA194306.1	EST_HUMAN	zq04f11.e1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017429 G1017425
9980	23018		0.68	3.4E-02	A082719.1	EST_HUMAN	IPISGKPLPKVTLSDRGVPLKATMRNFTEITAEINLTKESVTADAGRYEITAAANSSTGTTKAFINIVLDRPG
363	13591		6.8	3.3E-02	AA395735.1	EST_HUMAN	PPT GPVVISDITEESVTLKWEPPKYDGSQVTVYLLKRETSIAVWTEVSATVARTMMKVMKL ... ;
1193	14355	27413	12.43	3.3E-02	AB035887.1	NT	o290108.x1 Soares_papillary tumor_NbHPA Homo sapiens cDNA clone IMAGE:1083519 3'
1689	14821	27804	1.23	3.3E-02	AF110783.1	NT	z176e08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1778	14927		1.37	3.3E-02	AE000700.1	NT	Cricetus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
2149	15285		2.02	3.3E-02	R09112.1	EST_HUMAN	Homo sapiens skeletal muscle LIM-protein1 (FHL-1) gene, complete cds
3445	16613	29631	0.86	3.3E-02	H02389.1	EST_HUMAN	Aquifex aeolicus coction 32 of 109 of the complete genome
4293	17726	27804	3.74	3.3E-02	AF110783.1	NT	y126c09.r1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
4599	17821	30709	2.24	3.3E-02	BF245905.1	EST_HUMAN	y35f02.r1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:150771 5'
6560	19722	33089	26.73	3.3E-02	BF245905.1	EST_HUMAN	Homo sapiens skeletal muscle LIM-protein1 (FHL-1) gene, complete cds
6560	19722	33100	25.73	3.3E-02	BF245905.1	EST_HUMAN	Mus musculus tumor rejection antigen gp93 (Trat), mRNA
7677	20742	34223	0.63	3.3E-02	AF12162.1	NT	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
8523	22588	36157	0.74	3.3E-02	BF115621.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
8523	22598	36158	0.74	3.3E-02	BF115621.1	EST_HUMAN	Nicotiana plumbaginifolia molybdopterin synthase sulphuryase (crx3) gene, partial cds
							7m92d04.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'
							7m92d04.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3562423 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9824	22678	36248	0.67	3.3E-02	AA488202.1	EST_HUMAN	ad0809.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70844_cds1
9824	22679	36249	0.57	3.3E-02	AA488202.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN)
11383	24444	38104	3.28	3.3E-02	BF681107.1	EST_HUMAN	ad0809.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70844_cds1
12428	25303		3.1	3.3E-02	T66546.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN)
12557	25378		1.8	3.3E-02	AF289885.1	NT	602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332487 5'
12581	25398		1.85	3.3E-02	MB1890.1	NT	ye4911.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121101 5'
134	13360	26394	1.78	3.2E-02	AJ002005.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
1150	14314	27370	6.32	3.2E-02	AF098275.1	NT	Human Interleukin 11 (IL11) gene, complete mRNA
1150	14314	27371	6.32	3.2E-02	AF098275.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1812	14851	28054	1.08	3.2E-02	AF128894.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2187	15322		1.09	3.2E-02	P28986	SWISSPROT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2802	13360	26394	0.87	3.2E-02	AJ002005.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
3204	16378	28389	13.21	3.2E-02	BE867353.1	EST_HUMAN	LARGE TEGUMENT PROTEIN
3806	16966	29970	0.94	3.2E-02	AL163203.2	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
4334	17477		16.42	3.2E-02	X94768.1	NT	601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848727 5'
4890	18020	31005	3.85	3.2E-02	AF114182.1	NT	Homo sapiens chromosome 21 segment HS21C003
5310	18427	31397	0.83	3.2E-02	AW850159.1	EST_HUMAN	H.sapiens RP3 gene (XLRP gene 3)
5652	18846	32127	1.49	3.2E-02	X68709.1	NT	Saxifraga nidifica maturated (maik) gene, chloroplast gene encoding chloroplast protein, partial cds
5652	18846	32128	1.49	3.2E-02	X68709.1	NT	IL3-C10219-271069-022-C04 CT0219 Homo sapiens cDNA
5653	19812	33200	2.4	3.2E-02	M32437.1	NT	S.griseocarneum whiG-Stv gene
6656	19815		30.91	3.2E-02	T89397.1	EST_HUMAN	S.griseocarneum whiG-Stv gene
6743	19869	33290	3.7	3.2E-02	AF173845.1	NT	Ratipolyomavirus left junction in cell line W98.14
7938	20989	34439	0.92	3.2E-02	11424049	NT	yc33h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
8496	21577	35113	8.04	3.2E-02	6880585	NT	Alu repetitive element; contains LTR1 repetitive element ;
9141	22220		0.87	3.2E-02	AF109718.1	NT	Saginus oedipus tissue kallikrein gene, complete cds
9426	22500	36065	1.2	3.2E-02	AI278971.1	EST_HUMAN	Homo sapiens cytochrome P460, subfamily IIB (phenobarbital-inducible) (CYP2B), mRNA
9428	22500	36066	1.2	3.2E-02	AI278971.1	EST_HUMAN	Mus musculus kinesin family member 3c (Kif3c), mRNA
10262	23297		4.51	3.2E-02	AA719785.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
10568	23601	37207	1.11	3.2E-02	U96762.1	NT	qm17b04.x1 NCI_OGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
							qm17b04.x1 NCI_OGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
							zg54b12.s1 Soares pineal gland_N3HP3 Homo sapiens cDNA clone IMAGE:397151 3' similar to
							gb:U08441 CYTOCHROME C OXIDASE/POLYPEPTIDE III (HUMAN);
							Macaca mulatta chondrokinin receptor CCR5 mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1289	14445		1.92	3.1E-02	4503418	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1333	14490	27569	1.46	3.1E-02	P18845	SWISSPROT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1940	15083	28184	1.28	3.1E-02	6871664	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
5378	18580	31449	1.29	3.1E-02	U78104.1	NT	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
5476	18675		2.6	3.1E-02	AA278478.1	EST_HUMAN	z81606.t1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
5764	18956	32259	0.77	3.1E-02	BF687742.1	EST_HUMAN	602068763F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065789 5'
8122	21204		0.68	3.1E-02	AV696098.1	EST_HUMAN	601658878R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886291 3'
9142	22221	35764	0.48	3.1E-02	BE965092.2	EST_HUMAN	601658878R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886291 3'
9339	22415	35988	0.48	3.1E-02	AI87202.1	EST_HUMAN	601658878R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886291 3'
10237	23272	36864	2.87	3.1E-02	AF034779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1652	14905		2.41	3.0E-02	AF187125.1	NT	Polyketides synthase cytochrome oxidase I gene, partial cds; mitochondrial product
2652	15775	29989	1.08	3.0E-02	AA402242.1	EST_HUMAN	z83903.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
3743	16904	29808	2.82	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3839	16998		0.83	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0286-150200-040-e09 ST0296 Homo sapiens cDNA
4058	17214		0.94	3.0E-02	AA364003.1	EST_HUMAN	ESTT74530 Pineal gland II Homo sapiens cDNA 5' end
5164	18288	31260	8.17	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5184	18288	31251	8.17	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5507	18706		3.21	3.0E-02	AB046783.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6384	19553	32910	0.67	3.0E-02	N99615.1	EST_HUMAN	z839a10.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element;
6384	19553	32911	0.67	3.0E-02	N99615.1	EST_HUMAN	z839a10.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element;
6929	20244	33677	2.87	3.0E-02	AJ242906.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS) gene
7047	20100	33516	2.9	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7047	20100	33517	2.9	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7218	20083	33497	1.82	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7218	20083	33498	1.82	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7380	20458	33921	1.22	3.0E-02	M66524.1	NT	Human dystrophin gene
8317	21389		0.48	3.0E-02	BF678706.1	EST_HUMAN	602154364F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295854 5'
8821	21800	35439	0.65	3.0E-02	BE512870.1	EST_HUMAN	601171628F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3645047 5'
8842	21821	35469	0.74	3.0E-02	BF353889.1	EST_HUMAN	IL5-HT0704-290600-108-c04 HT0704 Homo sapiens cDNA



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## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8893	22072		1.93	3.0E-02	AF275654.1	NT	Omlthorhynchus anathinus coagulation factor X mRNA, complete cds
10677	23711	37318	2.03	3.0E-02	AE001797.1	NT	Thermotoga maritima section 109 of 136 of the complete genome
10770	23803	37426	0.47	3.0E-02	Z21211.1	EST_HUMAN	HSAAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11508	24586	39243	2.28	3.0E-02	M81367.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11889	24974	38878	7.11	3.0E-02	AA483218.1	EST_HUMAN	ne87604.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:511263
12536	28168	31556	1.95	3.0E-02	R32019.1	EST_HUMAN	yh83cd04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3'
12943	28621		11.62	3.0E-02	AW895565.1	EST_HUMAN	QV4-NN0036-270400-187-h05 NN0038 Homo sapiens cDNA
12989	28161		4.97	3.0E-02	AF048887.1	NT	Rattus norvegicus UDP-Galglucosylceramide beta-1,4-galactosyltransferase mRNA, complete cds
3650	16813	28826	0.9	2.8E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
4039	17185	30208	0.81	2.8E-02	H72805.1	EST_HUMAN	yv07e10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
6188	19364	32712	1.39	2.9E-02	AF060221.1	NT	Sus scrofa dooxyribonuclease II mRNA, complete cds
6421	19590	32855	0.58	2.9E-02	BF032233.1	EST_HUMAN	801452691F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3856598 5'
7398	20476	33943	9.95	2.9E-02	BE271437.1	EST_HUMAN	801140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7584	20659	34133	0.65	2.9E-02	D28214.1	EST_HUMAN	HUMNK282 Human epidermal keratinocyte Homo sapiens cDNA clone 282
8187	21269	34793	0.82	2.9E-02	AF129276.1	NT	Buohnera aphidicola natural-host Schlechtendalia chinensis glucanase-6-phosphate dehydrogenase (gnd) gene, partial cds
8187	21269	34794	0.82	2.9E-02	AF129276.1	NT	Buohnera aphidicola natural-host Schlechtendalia chinensis glucanase-6-phosphate dehydrogenase (gnd) gene, partial cds
8859	22899	36482	2.14	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
9859	22899	36483	2.14	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
10078	23116	37196	0.63	2.8E-02	AP000064.1	EST_HUMAN	EST388708 MAGC resequences, MAGN Homo sapiens cDNA
10553	23688	37196	1.25	2.9E-02	AP000064.1	NT	Aeropyrum pernix genome DNA, section 717
11303	18813	28826	1.44	2.8E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12538	26057		1.35	2.8E-02	AU135817.1	EST_HUMAN	AU135817 PLACE1 Homo sapiens cDNA clone PLACE1002982 5'
579	13771		0.76	2.8E-02	AW970163.1	EST_HUMAN	EST382234 MAGC resequences, MAGK Homo sapiens cDNA
3453	16820	29639	1.2	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3453	16820	29640	1.2	2.8E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
4430	15770		0.76	2.8E-02	8393761	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5805	18800	31888	11	2.8E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948087 5'
6948	20261	33698	1.08	2.8E-02	178960.1	EST_HUMAN	y421b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108555 5'
8523	21804	35142	1.67	2.8E-02	AJ005820.1	NT	Craterostigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1)
9219	22297	35840	0.75	2.8E-02	AA280782.1	EST_HUMAN	zs59c08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711488 5'
9408	22483	36047	1.41	2.8E-02	AF187872.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8513	22578	36144	0.76	2.8E-02	AE001062.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
8574	22636	36207	0.47	2.8E-02	J05109.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds
8574	22636	36208	0.47	2.8E-02	J05109.1	NT	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds
							Human gamma T-cell receptor beta chain (Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S3A2T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
4518	14671	27153	0.66	2.7E-02	U66059.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
3518	16694	29895	1.99	2.7E-02	AL161494.2	NT	Y86H12.1 Soares, multiple_sclerosis_2N6HMSP Homo sapiens cDNA clone IMAGE:280487 5'
4319	17462	30447	1.83	2.7E-02	N47258.1	EST_HUMAN	Y86H12.1 Soares, multiple_sclerosis_2N6HMSP Homo sapiens cDNA clone IMAGE:280487 5'
4319	17462	30448	1.93	2.7E-02	N47258.1	EST_HUMAN	60186481F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083075 5'
5382	16565	31432	0.6	2.7E-02	BF245672.1	EST_HUMAN	Y33d09.1 Soares fetal liver spleen (NFLS) Homo sapiens cDNA clone IMAGE:128657 5' similar to SP-JC2264 JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6557	18755	31703	1.43	2.7E-02	R12245.1	EST_HUMAN	T.aestivum pTTH20 mRNA for wheat type V thionin
6022	19205	32525	0.69	2.7E-02	X97580.1	NT	A.bisporus pgkA gene
6734	19890		1.02	2.7E-02	X97580.1	NT	contains Alu repetitive element;
7213	20078	33491	1.92	2.7E-02	AA983571.1	EST_HUMAN	transmembrane secretory component [human, leukocytes, Genomic, 657 nt, segment 4 of 11]
8549	21630		1.36	2.7E-02	AI377036.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
8816	21895	35434	0.55	2.7E-02	S43442.1	NT	IL3-CT0219-280100-062-C09 C10219 Homo sapiens cDNA
685	13776	26786	2.52	2.6E-02	AL163282.2	NT	ab02b02.e1 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:839595 3'
1399	14553		0.99	2.6E-02	AW850515.1	EST_HUMAN	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2439	15567	26694	2.6	2.6E-02	AA490021.1	EST_HUMAN	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
2441	15669	26696	4.45	2.6E-02		NT	Mus musculus MHC class III region RD gene, partial cds; B1, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and snRNP genes, complete cds; G7A gene, partial cds; and unknown genes
2441	15669	26697	4.45	2.6E-02	6754241	NT	
					6754241	NT	
2982	16158		2.07	2.6E-02	AF108906.1	NT	Chicken dactylin-1 mRNA, complete cds
5025	18154	31131	3.89	2.6E-02	L12032.1	NT	Delonoxys radiodurans R1 section 151 of 229 of the complete chromosome 1
5176	18298	31261	1.22	2.6E-02	AE002014.1	NT	Q15041 HYPOTHETICAL PROTEIN KIAA0069 ;
5203	18324	31293	2.54	2.6E-02	AW241154.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
6011	19185		2.94	2.6E-02	AL161563.2	NT	qg27f11.x1 NCJ CGAP Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
6349	19519		6.85	2.6E-02	AI206030.1	EST_HUMAN	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895678 3'
6555	19717	33083	2	2.6E-02	BE621748.1	EST_HUMAN	
8988	20194	33619	0.83	2.6E-02	Z69064.1	NT	Vaccinia virus ORF1L, strain Wyeth

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6866	20194	33620	0.83	2.6E-02	Z99084.1	NT	Vaccinia virus ORF1L, strain Wyeth
7050	20103	33520	5.63	2.6E-02	6981271	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
7449	20520	33999	0.65	2.6E-02	P21894	SWISSPROT	ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)
8703	21783	35316	0.73	2.6E-02	AA860946.1	EST_HUMAN	al2204.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1406719.3'
9550	22702	36268	1.24	2.6E-02	11432020	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
9915	22965	36541	0.78	2.6E-02	AF114952.1	NT	Saccharomyces dairensensis NRRL Y-12839(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9915	22965	36542	0.78	2.6E-02	AF114952.1	NT	Saccharomyces dairensensis NRRL Y-12839(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene encoding mitochondrial protein, complete cds
10814	23648	37257	5.37	2.6E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11670	24747	38547	1.59	2.6E-02	AA279951.1	EST_HUMAN	zs84c02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162.5'
11861	24949	39547	1.35	2.6E-02	AW500547.1	EST_HUMAN	UI-HF-BND-ak-e-10-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077468.5'
12460	28150	31563	1.43	2.6E-02	BF343827.1	EST_HUMAN	602015501F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4160944.6'
12583	23392		1.32	2.6E-02	11422836	NT	Homo sapiens hypothetical protein FLJ10724 (FLJ10724), mRNA
12947	25658		1.39	2.6E-02	R43678.1	EST_HUMAN	yc86f07.s1 Scores Infant brain 1N1B Homo sapiens cDNA clone IMAGE:22845.3' similar to contains DBR repetitive element;
545	13738	28762	1.75	2.5E-02	AI793130.1	EST_HUMAN	cn26f06.y6 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1557827.5'
545	13738	28763	1.75	2.5E-02	AI793130.1	EST_HUMAN	cn26f06.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827.5'
832	14010	27068	9.64	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950865.3'
832	14068	27133	5.83	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950865.3'
2821	15935		2.53	2.5E-02	U12871.1	NT	Rattus norvegicus rapahlin-3A mRNA, complete cds
3021	16197	28219	2.95	2.5E-02	X89697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
3021	16197	28220	2.95	2.5E-02	X89697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4156	18468	30302	0.82	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-at12 NN0128 Homo sapiens cDNA
4156	18468	30303	0.92	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-at12 NN0128 Homo sapiens cDNA
4322	17486	30450	4.86	2.5E-02	AW592114.1	EST_HUMAN	ht36h08.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834015.3'
5830	18021	32327	0.72	2.5E-02	AI732776.1	EST_HUMAN	z883c10.x6 Scores ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:810354.3'
6322	19494		4.88	2.5E-02	BE670128.1	EST_HUMAN	7c30a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008.3' similar to contains L1.t1 L1 repetitive element;
6336	19508		3.72	2.5E-02	BE746888.1	EST_HUMAN	601579393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928064.6'
6456	19633	32894	0.8	2.5E-02	L29029.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7843	20898	34400	1.72	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4213406.5'
7843	20898	34401	1.72	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4213406.5'
8008	21058	34570	0.64	2.5E-02	AF129458.1	NT	Chlamydomonas reinhardtii class II DNA phyclyase (PHR2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8167	21249	34768	0.5	2.5E-02	BE252469.1	EST_HUMAN	60110829F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344278 5'
9025	22104	35845	0.92	2.5E-02	Q91713	SWISSPROT	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
9184	22242	35785	0.57	2.5E-02	AW025821.1	EST_HUMAN	w008c10.x1 NCL_CGAP_G09 Homo sapiens cDNA clone IMAGE:2516370 3'
10271	23306		0.63	2.5E-02	X71303.1	NT	D. radiatum 28S ribosomal RNA, D2 domain
10910	23843	37466	0.65	2.5E-02	A147615.1	EST_HUMAN	gb22a08.x1 Soares_pregnant_uterus_NbHfU Homo sapiens cDNA clone IMAGE:1699982 3'
11048	24125	37759	1.71	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
11048	24125	37760	1.71	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 48.7 KD PROTEIN C19G10.05 IN CHROMOSOME 1
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (A1alpha) and major histocompatibility protein class II beta chain (I2beta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-lp
11120	24182		2.93	2.5E-02	AF050157.1	NT	Homo sapiens gene for LECT2, complete cds
12065	25046		1.87	2.5E-02	AB007546.1	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC83634), mRNA
12419	26072		2.17	2.5E-02	11420078	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAP3K13), mRNA
12621	25934		1.29	2.5E-02	11433220	NT	Dictyostelium discoideum putative protein kinase MkcA (mkcA) gene, complete cds
12718	25476		1.83	2.5E-02	U60169.1	NT	601652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
12760	25497	32032	1.58	2.5E-02	BE973927.1	EST_HUMAN	tc72c07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2070158 3'
178	13401	26431	1.44	2.4E-02	A137892.1	EST_HUMAN	y73f11.1 Soares fetal liver spleen (NFLS) Homo sapiens cDNA clone IMAGE:211149 5'
1828	14780	27665	1.89	2.4E-02	H65984.1	EST_HUMAN	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2102	16054	28363	1.38	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
2102	16054	28364	1.38	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4488	17628	30609	1.69	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
6344	10614	32871	0.86	2.4E-02	W86690.1	EST_HUMAN	zf63h04.s1 Soares_fetal_liver_spleen (NFLS_S1) Homo sapiens cDNA clone IMAGE:416791 3'
7370	20449	33912	1.2	2.4E-02	Z20573.1	EST_HUMAN	H3AAAGKXV T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7386	20464	33928	1.11	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7386	20464	33928	1.11	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
8074	21156		0.76	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0186-230300-019-H05 ST0186 Homo sapiens cDNA
8128	21211		0.97	2.4E-02	M16780.1	NT	Human retrotransposon 3' long terminal repeat
8836	21716		0.57	2.4E-02	H78376.1	EST_HUMAN	yv12c05.s1 Soares_fetal_liver_spleen (NFLS_S1) Homo sapiens cDNA clone IMAGE:233576 3' similar to contains Alu repetitive element; contains A3R repetitive element
8728	21808	35344	11.99	2.4E-02	N69442.1	EST_HUMAN	zaf35g11.s1 Soares_fetal_liver_spleen (NFLS_S1) Homo sapiens cDNA clone IMAGE:294596 3' similar to gb K02909 RATSR7K Rat (RNA); contains A3R.b1 A3R repetitive element
9187	22285	35806	0.78	2.4E-02	AE001125.1	NT	Borrelia burgdorferi (section 11 of 70) of the complete genome
							z191c08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb J04422 ISLET AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR
9211	22289	35931	0.81	2.4E-02	AA825680.1	EST_HUMAN	XTR repetitive element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8893	22833	38516	0.55	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopterin synthase sulphurylase (cnx5) gene, complete cds
8893	22833	38517	0.55	2.4E-02	AF124160.1	NT	Arabidopsis thaliana molybdopterin synthase sulphurylase (cnx5) gene, complete cds
10011	23049	38843	2.75	2.4E-02	AV692864.1	EST_HUMAN	AV692894 GKC Homo sapiens cDNA clone GK0DSC03 5'
10186	23223	38817	2.82	2.4E-02	AA493894.1	EST_HUMAN	h07b12.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:343583 similar to contains Alu repetitive element/contains element PTRS repetitive element
10839	23872		0.5	2.4E-02	BE387111.1	EST_HUMAN	601274982F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615902 5'
11874	24862	38557	2.45	2.4E-02	AF109506.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; emRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds, and unknown genes
11874	24862	38558	2.45	2.4E-02	AF109505.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds, and unknown genes
12210	25163		3.98	2.4E-02	9627909	NT	Bacteriophage b1L97, complete genome
12362	25260	32116	4.45	2.4E-02	8753635	NT	Mus musculus DnB homolog 1 (E. coli) (Dnbl1), mRNA
12478	25330	32055	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds
12478	25330	32098	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds
12668	25445		10.87	2.4E-02	AB008569.1	NT	Ceenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
12697	25464		1.28	2.4E-02	N42980.1	EST_HUMAN	W03a08.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:270610 5'
12883	25000	31853	1.25	2.4E-02	AA179693.1	EST_HUMAN	z13h01.r1 Stratiene fetal retina 937202 Homo sapiens cDNA clone IMAGE:603361 5'
1921	16064		6.25	2.3E-02	W05340.1	EST_HUMAN	z084g08.r1 Soares_fetal_lung_NbHL10W Homo sapiens cDNA clone IMAGE:299294 5'
1938	15078		16.25	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT8 (INT8) gene, exon 4
2065	15205	28321	0.99	2.3E-02	AW787355.1	EST_HUMAN	CM2-UM0038-290400-172-b11 UM0038 Homo sapiens cDNA
2428	15554	28681	2.68	2.3E-02	Z74283.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
3773	16934	28940	7.02	2.3E-02	Z20377.1	EST_HUMAN	HSAAACADH.P. Human foetal Brain Whole tissue Homo sapiens cDNA
3807	16867		0.67	2.3E-02	L23429.1	NT	Canis beta-galactosidase-binding lectin (LGA) mRNA, 3' end
4287	17412	30398	1.17	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4287	17412	30399	1.17	2.3E-02	L24789.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4540	17678	30860	1.08	2.3E-02	AW89107.1	EST_HUMAN	CM4-NN0080-290400-180-b04 NN0080 Homo sapiens cDNA
4571	17709	30869	0.6	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010800-318-g07 MT0118 Homo sapiens cDNA
4571	17709	30890	0.6	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010800-318-g07 MT0118 Homo sapiens cDNA
4572	18468	30691	1.2	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770671 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4572	18489	30632	1.2	2.3E-02	AW593693.1	EST_HUMAN	xs25008.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2770671 3'
4717	17852	30835	3.01	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4717	17852	30836	3.01	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
5144	18287	31237	0.9	2.3E-02	AW844307.1	EST_HUMAN	RC2-CN0051-280100-011-407 CN0051 Homo sapiens cDNA
5285	18384	31349	0.82	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5285	18384	31350	0.82	2.3E-02	AF257110.1	NT	Rattus norvegicus guanine nucleotide binding protein gamma subunit 11 mRNA, complete cds
5491	18590	31707	3.86	2.3E-02	U86303.1	NT	Caulobacter crescentius topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pcob) homolog gene, partial cds
6365	19335	32894	0.82	2.3E-02	BF106484.1	EST_HUMAN	501822921R1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042829 3'
6753	19911	33308	4	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7119	18545	31456	0.89	2.3E-02	BE141475.1	EST_HUMAN	MRO-HT0080-011069-002-208 HT0080 Homo sapiens cDNA
7619	20689	34164	0.63	2.3E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8060	21149	34681	4.52	2.3E-02	U63610.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
8667	21747	35285	1.12	2.3E-02	AJ298705.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8667	21747	35286	1.12	2.3E-02	AJ298705.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8894	21973	35509	0.75	2.3E-02	AI685380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
8894	21973	35510	0.75	2.3E-02	AI685380.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9338	22414	35967	0.84	2.3E-02	P41896	SWISSPROT	HYPOTHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
10063	23101	36704	0.94	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C
10236	23271	36862	1.44	2.3E-02	AE000189.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10236	23271	36863	1.44	2.3E-02	AE000189.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
11022	24101	37739	2.38	2.3E-02	P08840	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
12338	25919		3.61	2.3E-02	BE278331.1	EST_HUMAN	601178958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3948567 5'
12801	25835	32011	1.78	2.3E-02	BF528462.1	EST_HUMAN	602043828F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181454 5'
12801	25835	32012	1.78	2.3E-02	BF528462.1	EST_HUMAN	602043828F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4181454 5'
12819	25604	31974	2.47	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12875	26195		1.88	2.3E-02	U11077.1	NT	Dicystostellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
756	19337	26982	3.59	2.2E-02	AF018267.1	NT	Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1786	14935		1.79	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1800	14949	28042	2.94	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
1800	14949	28043	2.94	2.2E-02	P07313	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2072	15212	28328	2.17	2.2E-02	Z82001.1	NT	S.pneumoniae popA gene and open reading frames
3521	18887		2.03	2.2E-02	AA577785.1	EST_HUMAN	m24e04.e1 NCI_OGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3736	18897		4.09	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3956	17114	30119	0.98	2.2E-02	AW601317.1	EST_HUMAN	PM0-BT0340-170100-004-003 BT0340 Homo sapiens cDNA
4028	17185	30185	0.89	2.2E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
5177	18289	31262	1.37	2.2E-02	Z73597.1	NT	S.cerevisiae chromosome XVI reading frame ORF YPL241c
7398	20474	33941	3.43	2.2E-02	AV699721.1	EST_HUMAN	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
8568	21647	35188	1.41	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8568	21647	35188	1.41	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9009	22088	36630	0.82	2.2E-02	X79488.1	NT	P.vulgata alpha tub 2 mRNA
9856	22898	36478	0.46	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9858	22898	36479	0.46	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9888	22928	36511	2.73	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9888	22928	36512	2.73	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10409	23444		1.25	2.2E-02	6878140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
12825	25421		6.8	2.2E-02	AA503553.1	EST_HUMAN	ne47h07.s1 NCI_OGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element
432	13627		4.48	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
462	13657		6.62	2.1E-02	AF029728.1	NT	Dicystosellum discoideum histidine kinase C (dhkc) mRNA, complete cds
1292	14448	27514	6.65	2.1E-02	U72073.1	NT	Bacillus subtilis cdkLM cluster, CdkK (cdkK), CdkL (cdkL), and spore coat protein CdkM (cdkM) genes, complete cds
1418	14571	27644	1.31	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1418	14571	27648	1.31	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1823	14872	28065	0.87	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1823	14872	28068	0.87	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
1823	14872	28067	0.97	2.1E-02	P02438	SWISSPROT	KERATIN, HIGH-SULFUR MATRIX PROTEIN, B2A
2019	15159	28764	0.97	2.1E-02	AF190899.1	NT	Tegula aureodonta major acrosomal protein precursor (TMAP) mRNA, complete cds
2092	15232	28354	1.16	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-411 BT0546 Homo sapiens cDNA
2092	15232	28355	1.16	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-411 BT0546 Homo sapiens cDNA
2877	13980	27032	3.12	2.1E-02	N29268.1	EST_HUMAN	y43h07.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:264541 5'
3674	16837	29847	1.01	2.1E-02	AA461271.1	EST_HUMAN	z68b09.r1 Soares fetal_Nb2HF8_9y Homo sapiens cDNA clone IMAGE:766121 5'
4249	17395	30384	0.68	2.1E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4427	17587	30548	0.89	2.1E-02	BF343655.1	EST_HUMAN	602016306F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4151181 5'
4567	17705	30685	2.14	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
4577	17714	30698	1.64	2.1E-02	AI768127.1	EST_HUMAN	wg81d11.XI Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4831	17804	30953	5.95	2.1E-02	Y08501.1	NT	A. thaliana mitochondrial genome, part A
4852	17985	30973	0.76	2.1E-02	AA065737.1	EST_HUMAN	eg55gt12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
4940	18070	31048	0.89	2.1E-02	AI823432.1	EST_HUMAN	wh54a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
5316	18432	31402	0.91	2.1E-02	BF026405.1	EST_HUMAN	601671411F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954410 5'
5756	18948	32250	0.6	2.1E-02	AW378529.1	EST_HUMAN	CN4-HT0244-11189-040-105 HT0244 Homo sapiens cDNA
7212	20077	33490	0.73	2.1E-02	BF086189.1	EST_HUMAN	QV3-GN0059-120900-329-at2 GN0059 Homo sapiens cDNA
8716	21796	35333	0.66	2.1E-02	9790238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
9703	22752	36322	0.54	2.1E-02	AA884288.1	EST_HUMAN	am83e07.e1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element; contains element MER11 repetitive element;
9831	22871	36453	2.49	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9831	22871	36454	2.49	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10189	23226	36820	1.15	2.1E-02	L29324.1	NT	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes
10266	23301	36899	0.75	2.1E-02	AA884288.1	EST_HUMAN	am83e07.e1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element; contains element MER11 repetitive element;
10856	23869	37508	0.49	2.1E-02	AP001619.1	NT	Bacillus halodurans genomic DNA, section 13/14
11787	24777	38474	1.48	2.1E-02	6754255	NT	Mus musculus heat shock protein, 74 kDa, A (Hsp28a), mRNA
12063	28044	38752	1.42	2.1E-02	AW844320.1	EST_HUMAN	RC4-CN0050-130200-012-104_1 CN0050 Homo sapiens cDNA
12602	18493		11.16	2.1E-02	Y19213.1	NT	Homo sapiens putative psin-HA pseudogene for hair keratin, exons 2 to 7
12647	26916	31862	1.22	2.1E-02	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
13091	25712	31938	3.82	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmeA precursor (omeA) gene, complete cds
19	13257	26257	1.28	2.0E-02	BF002892.1	EST_HUMAN	7c51c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3308998 3' similar to contains MER1.13
20	13258	26258	14.96	2.0E-02	AW595655.1	EST_HUMAN	MER1 repetitive element;
269	13488	26518	5.03	2.0E-02	6753635	NT	QV4-NN0038-270400-187-105 NN0038 Homo sapiens cDNA
306	13622	26558	2.95	2.0E-02	AA455338.1	EST_HUMAN	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
821	14000	27064	3.63	2.0E-02	6753635	NT	aa15b10.1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:813307 5'
1111	14278	27333	0.98	2.0E-02	AL096805.1	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
1226	14386	27448	0.91	2.0E-02	8922391	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1 (p38.33) of Homo sapiens
							Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1228	14386	27449	0.91	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1922	15065	28168	1.84	2.0E-02	8922463	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1922	15065	28168	1.84	2.0E-02	8922463	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2850	15973		2.09	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3148	13257	26257	1.56	2.0E-02	BF002832.1	EST_HUMAN	7q51c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3308998 3' similar to contains MER1.13
3213	16387		1.13	2.0E-02	7309474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
3289	16473		1.99	2.0E-02	AF085688.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
4113	17267	30287	1.57	2.0E-02	M18096.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' and
5219	18341		0.74	2.0E-02	AI271895.1	EST_HUMAN	qj83e03.x1 NCI_CGAP_K143 Homo sapiens cDNA clone IMAGE:1866076 3'
6018	18201	32520	0.59	2.0E-02	L35321.2	NT	Dictyostellium discoideum class VII unconventional myosin (myoI) gene, complete cds
7723	20787	34275	0.95	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt. position (4/7)
7723	20787	34276	0.95	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt. position (4/7)
10081	23119		2.39	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
10570	23605	37210	1.84	2.0E-02	AI640342.1	EST_HUMAN	wa17b02.x1 NCI_CGAP_K611 Homo sapiens cDNA clone IMAGE:2288315 3'
10879	23964	37592	1.95	2.0E-02	Z73868.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162
11653	24732	38423	1.91	2.0E-02	D88184.1	NT	Equus caballus DNA for 17alpha-hydroxysteroid 17,20-lyase, complete cds
11978	24983	38684	2.04	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
11978	24983	38685	2.04	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12149	18469	31535	1.8	2.0E-02	AA455538.1	EST_HUMAN	est15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
12844	15973		2.26	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
13186	25711		5.63	2.0E-02	T80037.1	EST_HUMAN	y004c09.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:24875 5'
711	13993	26929	2.42	1.9E-02	AA572764.1	EST_HUMAN	nt19a07.e1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914198 similar to contains L1.11 L1
2097	15237	28358	4.85	1.9E-02	AL163303.2	NT	repetitive element
2097	15237	28358	4.85	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2970	16146	29164	9.16	1.9E-02	AA713856.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
3018	16194	29217	1.92	1.9E-02	AV648699.1	EST_HUMAN	nm04105.e1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
3332	16505		0.72	1.9E-02	AB033611.1	NT	AV848699 GLC Homo sapiens cDNA clone GLCBLH07 3'
3699	16860		1.12	1.9E-02	N52250.1	EST_HUMAN	Utricularia latipolles mitochondrial gene for cytochrome b, complete cds
3783	16954		8.1	1.9E-02	BE738088.1	EST_HUMAN	yz28502.e1 Soares multiple sclerosis 2N8HMS Homo sapiens cDNA clone IMAGE:284331 3'
3808	16968	29971	0.83	1.9E-02	AI301183.1	EST_HUMAN	601572892F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
							q04c07.x1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1897260 3' similar to contains Alu repetitive element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4158	17309	30305	1.3	1.9E-02	AF141940.1	NT	Mycoplasma litans VihA1 precursor (vhaA1) and VihA2 precursor (vhaA2) genes, partial cds
4310	17453	30440	1.58	1.9E-02	P08081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4310	17453	30441	1.58	1.9E-02	P08081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4683	17708	30785	2.79	1.9E-02	AI452998.1	EST_HUMAN	448d04.x1 Soares_NSF_F8_9W_OT_PA_F_S1 Homo sapiens cDNA clone IMAGE:2144531 3' similar to contains Alu repetitive element;
5125	15701	28822	4.22	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5431	18831	31609	0.98	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TOR gamma 1 and gamma 3 gene clusters
5585	18780	31825	1.25	1.9E-02	L47572.1	NT	Meleagris gallopavo paraxonase-2 (PON2) mRNA, complete cds
5808	18037		0.93	1.9E-02	AB019507.1	NT	Drosophila kaneoki gene for glycyl-3-phosphate dehydrogenase, complete cds
7250	20333	33780	1.1	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7250	20333	33781	1.1	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8769	21848		1.33	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 3/7
9532	22597	36169	1.21	1.9E-02	BF316129.1	EST_HUMAN	501896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
8914	22854	36540	0.87	1.9E-02	L10114.1	NT	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
10251	23293	36882	1.24	1.9E-02	BF89832.1	EST_HUMAN	501852365F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'
10458	29493	37104	0.87	1.9E-02	D64001.1	NT	Synechococcus sp. PCC8803 complete genome, 20/27, 2539000-2844794
11021	24100	37738	1.91	1.9E-02	AF008938.1	NT	Vibrio cholerae V86 phage putative replicative protein gene, complete cds
12372	28824	31865	4.41	1.9E-02	AF101065.1	NT	Hirudo medicinalis Intermediate filament glialin mRNA, complete cds
13008	28890		1.46	1.9E-02	L11098.1	NT	Candida albicans lambda Csa3/5 fragment
358	13567	26505	1.57	1.8E-02	AW771104.1	EST_HUMAN	hn52a08.x1 NCJ CGAP Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element
703	13886	26918	1.81	1.8E-02	BF308122.1	EST_HUMAN	MER29 repetitive element;
1188	14348	27406	1.43	1.8E-02	X17684.1	NT	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
1467	14821	27704	1.38	1.8E-02	AF243382.1	NT	H. francisci mRNA for myelin basic protein (MBP)
2743	15860	28972	1.74	1.8E-02	AE004544.1	NT	Drosophila melanogaster cytoplasmic protein encore (enc) mRNA, complete cds
3282	18458		0.94	1.8E-02	AI805829.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3983	17160	30156	1.09	1.8E-02	AW879122.1	EST_HUMAN	te52a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090286 3'
3983	17160	30157	1.09	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4197	17347		1.01	1.8E-02	AA851446.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4550	17688	30669	1.52	1.8E-02	AW936363.1	EST_HUMAN	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406836 3'
5069	18197	31171	2.02	1.8E-02	G60810	SWISSPROT	QV4-DT0021-301289-071-b11 DT0021 Homo sapiens cDNA
6949	20262	33700	4.44	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
7824	20594	34170	2.3	1.8E-02	BF125690.1	EST_HUMAN	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5'REGION
7650	20694	34170	0.61	1.8E-02	BF125690.1	EST_HUMAN	601763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'
							601763268F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026280 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8322	21404	34931	0.88	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds
8683	21743	35283	0.46	1.8E-02	AW805327.1	EST_HUMAN	QV2-NN1073-220400-159-h09 NN1073 Homo sapiens cDNA
8710	21780	35326	0.76	1.8E-02	6678943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
8803	22742	36311	0.57	1.8E-02	BF241924.1	EST_HUMAN	601877028F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9693	22742	36312	0.57	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9842	22882		2.23	1.8E-02	AA897543.1	EST_HUMAN	aj92089.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1304921 3' similar to gb:L11672 ZINC
10268	23303	35900	1.7	1.8E-02	BE778274.1	EST_HUMAN	FINGER PROTEIN 91 (HUMAN);
10431	23466	37072	1.28	1.8E-02	X96933.1	NT	601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866963 5'
11721	23907	37630	1.76	1.8E-02	AB002337.2	NT	L-stagnalis mRNA for myomodulin neuro-peptide precursor
11721	23907	37631	1.76	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11912	24899	36802	1.55	1.8E-02	AP000006.1	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11926	24912	36813	2.45	1.8E-02	U62749.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (87)
13086	25894		1.78	1.8E-02	AF202180.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
929	14104	27187	1.34	1.7E-02	BE394869.1	EST_HUMAN	Plasmodium falciparum erythrocyte membrane-associated giant protein antigen 332 (Ag332) gene, partial cds
1831	14979	28075	2.12	1.7E-02	AW573183.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632160 5'
1831	14979	28076	2.12	1.7E-02	AW573183.1	EST_HUMAN	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.t1 L1 repetitive element
1920	15063		2.85	1.7E-02	AL163204.2	NT	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.t1 L1 repetitive element
2181	15316		13.13	1.7E-02	AB004816.1	NT	Homo sapiens chromosome 21 segment HS21G004
2705	15823		1.36	1.7E-02	7657495	NT	Oryzologus cuniculus mRNA for miltaugmin29, complete cds
3062	16236	29259	0.89	1.7E-02	AI147815.1	EST_HUMAN	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
3602	16769		4.84	1.7E-02	AW827368.1	EST_HUMAN	qb22a08.x1 Soares_prenatal_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3718	16877		0.83	1.7E-02	P04929	SWISSPROT	hm45a04.x1 NCL_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element
4284	17429		1.23	1.7E-02	AA69818.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
4317	17460		2.02	1.7E-02	R02606.1	EST_HUMAN	ac18f04.s1 Stralagene ovary (#837217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element
4576	17713	30697	0.74	1.7E-02	AI305279.1	EST_HUMAN	y88008.f1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124547 5'
4649	17785	30768	1.32	1.7E-02	AW573183.1	EST_HUMAN	qm08g07.x1 NCL_CGAP_LUS Homo sapiens cDNA clone IMAGE:1861276 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);
							hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.t1 L1 repetitive element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4836	17869	30957	1.91	1.7E-02	V00941.1	NT	Messenger RNA for anglerfish ( <i>Lophius americanus</i> ) somatostatin II
4934	18064		5.98	1.7E-02	A015076.1	EST_HUMAN	ov61e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
6253	19427	32773	1.69	1.7E-02	A1769247.1	EST_HUMAN	wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_31 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
6709	19887	33256	1.23	1.7E-02	A038280.1	EST_HUMAN	ov85h03.x1 Soares_Tetal_liver_spleen_1NF1S_S1 Homo sapiens cDNA clone IMAGE:1672061 3'
7195	20060	33471	1.26	1.7E-02	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7353	20432	33894	1.9	1.7E-02	8400716	NT	Homo sapiens nebulin (NEB), mRNA
7513	20587	34060	1.08	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7513	20587	34061	1.08	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7821	20972		1.71	1.7E-02	A010770.1	NT	Homo sapiens hyperion gene, exons 1-50
9536	21078	34591	0.89	1.7E-02	U21854.1	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
9000	22940	36526	1.28	1.7E-02	AL040554.1	EST_HUMAN	DKFZp434f0314_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434f0314 5'
12093	25073	38780	1.68	1.7E-02	5902007	NT	Homo sapiens serum constituent protein (MSE66), mRNA
12881	26111	31687	2.35	1.7E-02	AW903482.1	EST_HUMAN	CM4-NN1030-040400-130-068 NN1030 Homo sapiens cDNA
13166	25757	31928	1.46	1.7E-02	AAB46926.1	EST_HUMAN	ce08d04.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385287 similar to contains element MSR1 repetitive element;
524	13717		4.05	1.8E-02	AL021829.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 13/162
1689	14841	27926	1.37	1.6E-02	Y18889.1	NT	Treponema mallophilum flaB2, flaB3 and fliD genes for flagellin subunit proteins and CAP protein homologue
2323	15455	28588	1.81	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2323	15455	28587	1.81	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2831	15764	28869	0.97	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQ1 gene
2708	15826	28941	1.75	1.6E-02	AA484872.1	EST_HUMAN	ne81d06.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2758	15875		1.01	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3614	16778	29793	5.33	1.6E-02	AW850852.1	EST_HUMAN	IL3-CT0218-160200-063-C07 CT0219 Homo sapiens cDNA
4291	17436		1.96	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fae-binding protein, BING1, lapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4415	17599	30543	2.04	1.6E-02	AW875407.1	EST_HUMAN	QV2-PT0012-140100-030-07 PT0012 Homo sapiens cDNA
5367	18570	31438	0.56	1.6E-02	AJ281385.1	EST_HUMAN	qu42b09.x1 NCL_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:1967417 3'
5741	18934	32234	1.42	1.6E-02	6671716	NT	Mus musculus CD5 antigen (Cd5), mRNA
8780	19935	33331	2.16	1.6E-02	AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
7071	20124	33539	1.14	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7071	20124	33540	1.14	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7888	20940	34448	0.88	1.8E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8312	21384	34919	0.74	1.8E-02	AJ277692.1	NT	Homo sapiens partial TUB gene for tubby (house) homolog and LMO1 gene for LIM domain only 1 protein
8372	21453		3.37	1.0E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
10248	23281		2.97	1.8E-02	AF079784.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10633	23687	37278	1.61	1.8E-02	AA572818.1	EST_HUMAN	n19g03.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914280 similar to SW:TELO_RABIT P29294 TELOKIN. [1]
10633	23687	37277	1.61	1.8E-02	AA572818.1	EST_HUMAN	n19g03.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:914280 similar to SW:TELO_RABIT P29294 TELOKIN. [1]
11149	25908	37848	2.9	1.8E-02	Z84828.1	NT	G.gallus microsatellite DNA (LE10260 (T101111))
11488	24547	38219	2.11	1.8E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11488	24547	38220	2.11	1.8E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11801	24791	39488	2.16	1.8E-02	AJ373558.1	EST_HUMAN	q286t10.x1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:2042442 3'
12348	18455	28586	3.49	1.8E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
12348	18455	28587	3.49	1.8E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
770	13951		9.38	1.5E-02	8923734	NT	Homo sapiens transcription factor (HSA130394), mRNA
2209	15343	28469	3.58	1.5E-02	N39521.1	EST_HUMAN	y27b07 at Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243926 3'
2244	15377	28505	1.6	1.5E-02	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
3128	16304	28317	1.04	1.5E-02	AJ008216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3128	16304	28318	1.04	1.5E-02	AJ008216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3818	16378	29382	1.14	1.5E-02	BF092842.1	EST_HUMAN	MR4-TN0115-080000-201-b12 TN0115 Homo sapiens cDNA
4590	17727	30710	0.72	1.5E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
6423	19692	32957	2.07	1.5E-02	Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7472	20847		1.69	1.5E-02	11487282	NT	Cyanophora paradoxa cyanellin, complete genome
7561	20833	34108	1.57	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
8058	21141	34680	1.38	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8065	21147	34688	3.06	1.5E-02	11417739	NT	Homo sapiens vdy1-tRNA synthetase 2 (VAHS2), mRNA
9030	22109	36660	1.42	1.5E-02	BF345554.1	EST_HUMAN	602019135F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4164804 5'
9868	22630		0.68	1.5E-02	AF096774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9770	22768	36337	1.59	1.5E-02	D44608.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
10016	23054	36649	1.3	1.5E-02	R32687.1	EST_HUMAN	yf54b10.r1 Soares placenta NB2-IP Homo sapiens cDNA clone IMAGE:133531 5'
10016	23054	36650	1.3	1.5E-02	R32687.1	EST_HUMAN	yf54b10.r1 Soares placenta NB2-IP Homo sapiens cDNA clone IMAGE:133531 5'
10850	23883	37514	0.46	1.5E-02	T92188.1	EST_HUMAN	yf1710.s1 Stragene lung (H337210) Homo sapiens cDNA clone IMAGE:118027 3'
11056	24133		1.78	1.5E-02	D28547.1	NT	Rice gene for thiodoxin h, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11442	24503	38171	2.21	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
12576	25970		2.38	1.5E-02	AW750384.1	EST_HUMAN	RC4-GN0049-140100-011-c11 GN0049 Homo sapiens cDNA
430	13626		1.54	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 58 of 84 of the complete genome
1142	14307	27363	3.81	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC61225), mRNA
1285	14441		2.12	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 183 of the complete genome
1326	14483		2.49	1.4E-02	U67778.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
3284	18458	28478	1.83	1.4E-02	AF160969.2	NT	Bifidobacterium longum Na+/H+ antiporter (ihdB), cytosine deaminase, and alpha-galactosidase (aglL) genes, complete cds; and N-acetylglucosaminylxylase repressor protein (negCxyR) gene, partial cds
3485	18653	28658	1.23	1.4E-02	AW074212.1	EST_HUMAN	xb09d09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3'
3573	18738	28753	6.9	1.4E-02	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3573	18738	28754	6.9	1.4E-02	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3508	18772	28787	0.75	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3748	18907	28911	12.14	1.4E-02	6898918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-B), mRNA
4612	17749	30729	9.97	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGG Homo sapiens cDNA
4612	17749	30730	9.97	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGG resequences, MAGG Homo sapiens cDNA
4998	18127	31102	8.22	1.4E-02	BE793142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4998	18127	31103	6.22	1.4E-02	BE793142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
5911	28210		0.74	1.4E-02	X91338.1	NT	H. sapiens LaSS-B pseudogene 3
6545	19707	33083	4.52	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.st NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element
6545	19707	33084	4.52	1.4E-02	AA559030.1	EST_HUMAN	nl11c04.st NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element
8333	21415		1.55	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 88/182
9059	22178	35722	1.44	1.4E-02	M81702.1	NT	Candida boidinii melhydrol oxidase (AOD1) gene, complete cds
9366	22431	35989	1.41	1.4E-02	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9600	22855	36227	1.68	1.4E-02	BE544581.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3484241 5'
10780	23813		0.89	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
12588	25194	38358	8.85	1.4E-02	X80459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12640	25430		1.84	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12859	25825		1.46	1.4E-02	11428968	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
13075	25704		1.51	1.4E-02	AF238059.2	NT	Rheum x cultorum NADH dehydrogenase subunit F (ndhF) gene, partial cds; chloroplast gene for chloroplast product

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1913	15059		1.19	1.3E-02	BE739263.1	EST_HUMAN	601569462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826335 5'
2010	15150	28254	2.13	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2512	15639	28769	0.88	1.3E-02	AE002445.1	NT	Nisseria meningitidis serogroup B strain MC58 section 87 of 206 of the complete genome
3285	16459	29479	2.41	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3285	16459	29480	2.41	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
4076	17232		1.22	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
5275	18394		3.02	1.3E-02	D26547.1	NT	Rice gene for thioesterase, complete cds
5360	18563	31478	1.61	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnxq28orf
5360	18563	31479	1.61	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnxq28orf
6293	19466	32819	1.2	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p14 (btf2p14) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
6327	19499	32856	1.05	1.3E-02	M62962.1	NT	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7101	18528	31481	1.3	1.3E-02	AL161548.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7101	18528	31482	1.3	1.3E-02	AL161548.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7752	20812	34303	4.9	1.3E-02	AI031593.1	EST_HUMAN	ex08g05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element
8678	21768	35294	1.67	1.3E-02	AF166961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10411	23448	37051	1.89	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10485	23520	37129	0.85	1.3E-02	AE001804.1	NT	Chlamydia trachomatis section 31 of 67 of the complete genome
11239	24308	37944	3.35	1.3E-02	AW288563.1	EST_HUMAN	x34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
11239	24308	37945	3.35	1.3E-02	AW288563.1	EST_HUMAN	x34e03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
12845	26127		1.7	1.3E-02	Z69117.1	NT	Bacillus subtilis complete genome (section 14 of 21), from 2598451 to 2812870
12753	25499		2.56	1.3E-02	9633069	NT	Human herpesvirus 6B, complete genome
12965	25885		30.16	1.3E-02	AF162238.1	NT	Homo sapiens V1b vesopressin receptor (VPR3) gene, complete cds
219	13441		0.82	1.2E-02	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
366	13676	26606	4.38	1.2E-02	AA05269.1	EST_HUMAN	z85g01.1 Soares retina N244HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element
465	13660	26696	1.43	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR53 REGION
767	13938	26983	2.67	1.2E-02	AI183522.1	EST_HUMAN	q68e12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1734870 3' similar to contains L1.t1 L1 repetitive element
2246	15378	28507	2.03	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013

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2514	15840	28762	1.02	1.2E-02	AW172350.1	EST_HUMAN	X37609.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2701	15840	28762	1.43	1.2E-02	AW172350.1	EST_HUMAN	X37609.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3170	16346		7.3	1.2E-02	AA075418.1	EST_HUMAN	Zm88e03.t1 Strabagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5'
3359	16531	29545	2.05	1.2E-02	R62805.1	EST_HUMAN	Y41108.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
3362	16534	29548	0.59	1.2E-02	A1688694.1	EST_HUMAN	ZB86a07.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:308552 3' similar to contains element MER22 repetitive element;
5035	18163	31139	2.02	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5154	18276		1.97	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CpUbiq1 mRNA, partial cds
5185	18317	31288	1.31	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5871	19081	32368	1.78	1.2E-02	D78689.1	NT	Rana rugosa mRNA for calcitriol, complete cds
6243	19417	32765	0.72	1.2E-02	AF045555.1	NT	Homo sapiens vbscr1 (WBSCR1) and vbscr5 (WBSCR6) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7147	20282	33724	8.67	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7443	20520	33993	1.42	1.2E-02	H02197.1	EST_HUMAN	Y34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'
7465	20540	34014	8.54	1.2E-02	AV732053.1	EST_HUMAN	AV732053 HTF Homo sapiens cDNA clone HTFBJC09 5'
7729	20791	34280	0.66	1.2E-02	BF216950.1	EST_HUMAN	601882949F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095253 5'
8188	21268	34792	2.3	1.2E-02	Q11205	SWISSPROT	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4-B)
8321	21403	34929	0.56	1.2E-02	R68831.1	EST_HUMAN	Y43706.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8321	21403	34930	0.56	1.2E-02	R68831.1	EST_HUMAN	Y43706.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:142019 3'
8386	21467	34983	1.22	1.2E-02	AF193812.1	NT	Homo sapiens fringe protein mRNA, partial cds
8386	21467	34984	1.22	1.2E-02	AF193812.1	NT	Homo sapiens fringe protein mRNA, partial cds
8091	22170		1	1.2E-02	T76887.1	EST_HUMAN	Y47208.s1 Soares fetal liver spleen 1NFS1Homo sapiens cDNA clone IMAGE:113774 3'
9839	22879	36461	2.54	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
9872	22812	36497	1.24	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
12757	25986		1.16	1.2E-02	P17139	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
12974	26834		6.24	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TF-ujwara) Homo sapiens cDNA clone GEN-557G08 5'
1298	14454	27520	1.22	1.1E-02	AA070364.1	EST_HUMAN	Zm88e11.s1 Strabagene neuroepithelium (#537231) Homo sapiens cDNA clone IMAGE:530924 3'
1743	14882	27986	1.48	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1743	14892	27987	1.48	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2086	15236	28357	5.35	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153808 5'



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2942	18119		5.31	1.1E-02	N99523.1	EST_HUMAN	zr40e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295040 5'
3612	16776	26792	3.59	1.1E-02	AI653508.1	EST_HUMAN	lc95b10.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW_XPF_HUMAN
4222	17370		0.86	1.1E-02	AW813798.1	EST_HUMAN	Q92989 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4951	18081	31037	1.27	1.1E-02	AL046393.2	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
							DKFZ588E0924_s1 586 (synonym: hnt1) Homo sapiens cDNA clone DKFZ588E0924
6277	19461	32800	0.89	1.1E-02	U69480.1	NT	Bacillus subtilis SpoVK (spoVK), YnaA (ynaA), YnaB (ynbA), YnaC (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynbA), YnaC (ynbB), YnaD (ynbD), YnaE (ynbE), YnaF (ynbF), YnaG (ynbG), YnaH (ynbH), YnaI (ynbI), YnaJ (ynbJ), xylan beta-1,4-xylosyl>
7773	20830	34321	2.19	1.1E-02	BE149811.1	EST_HUMAN	RC1-HT0258-100300-016-h07 HT0258 Homo sapiens cDNA
7989	21039	34561	1.25	1.1E-02	9631294	NT	Melanoplus sanguinipes entomopoxvirus, complete genome
8461	21532	35061	0.46	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8451	21532	35062	0.46	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8841	21620	35456	0.89	1.1E-02	AW898160.1	EST_HUMAN	QV3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA
8022	22101	35641	0.7	1.1E-02	CO4803.1	EST_HUMAN	C04803 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHC4040
9103	22162	35727	7.44	1.1E-02	Q81982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
10133	23171	36769	2.02	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.r1 Stratagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:549328 5'
10269	23334	36939	4.06	1.1E-02	AA314665.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line H1 Homo sapiens cDNA 5' end
11224	24283	37634	2.41	1.1E-02	11435608	NT	Homo sapiens T-box 5 (TBX5), mRNA
12165	25152		4.01	1.1E-02	AA688239.1	EST_HUMAN	ab77111.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
7	13245	26247	8.82	1.0E-02	AW848120.1	EST_HUMAN	Alu repetitive element
1552	14706	27785	0.97	1.0E-02	AW368128.1	EST_HUMAN	MR3-CT0176-111099-003-a10 CT0176 Homo sapiens cDNA
2898	15761		1.71	1.0E-02	AA806389.1	EST_HUMAN	CM2-HT0177-041059-017-H12 HT0177 Homo sapiens cDNA
3159	16334	28344	2.88	1.0E-02	BE835558.1	EST_HUMAN	cc22h08.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
3336	18509	29525	1.24	1.0E-02	BE968998.1	EST_HUMAN	RC0-FN0025-250500-021-402 FN0025 Homo sapiens cDNA
3598	18762		0.7	1.0E-02	AW845621.1	EST_HUMAN	601849967R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933889 3'
3988	17143	30148	0.85	1.0E-02	AI065086.1	EST_HUMAN	MRO-CT0060-081099-003-h10 CT0060 Homo sapiens cDNA
4002	17159	30165	0.59	1.0E-02	AI163302.2	NT	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
4899	18029	31017	5	1.0E-02	6753521	NT	Homo sapiens chromosome 21 segment HS21C102
4869	18088	31074	4.14	1.0E-02	R66567.1	EST_HUMAN	Mus musculus corticotropin releasing hormone receptor 2 (chr2), mRNA
5116	18243	31208	0.83	1.0E-02	AL161593.2	NT	Y954h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:199533 5'
5242	18364	31332	1.66	1.0E-02	P06599	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, cDNA fragment No. 89
5632	18729	31745	0.81	1.0E-02	H52891.1	EST_HUMAN	EXTENSIN PRECURSOR
							yj36h11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235941 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5865	18055	32382	0.88	1.0E-02	AF303888.1	NT	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2
6242	19416	32764	1.28	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (Sy2) gene, complete cds
6310	19482	32836	2.78	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0386-070100-201-h01 BT0356 Homo sapiens cDNA
6310	19482	32837	2.78	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0386-070100-201-h01 BT0356 Homo sapiens cDNA
6901	20216	33846	1.69	1.0E-02	Z29842.1	NT	Z.mays U3snRNA pseudogene
9593	22648	36218	6.34	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
9593	22648	36220	6.34	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
11542	24598		2.12	1.0E-02	AF157559.1	NT	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11579	24828		1.7	1.0E-02	A1417981.1	EST_HUMAN	tg55h07.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2112733 3' similar to gb:X15183_cds1 HEAT SHOCK PROTEIN HSP 90-ALPHA (HUMAN); contains Alu repetitive element; contains element MER5 repetitive element;
11649	24728	38420	1.95	1.0E-02	AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
12278	26206		1.76	1.0E-02	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 82 (SAP 82) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
12339	26941	31782	3.68	1.0E-02	AW65521.1	EST_HUMAN	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
12355	26002		4.31	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12764	25974		1.4	1.0E-02	AJ278505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12949	26080		2.91	1.0E-02	X62854.1	NT	H.sapiens gene for Me491/CD83 antigen
916	14091	27156	5.69	9.0E-03	A1796126.1	EST_HUMAN	wh42109.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element MER22 MER22 repetitive element;
1293	14449		1.66	9.0E-03	BE781889.1	EST_HUMAN	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2469	15595	28721	2.84	9.0E-03	AL161590.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2971	16147	29165	0.81	9.0E-03	A1251744.1	EST_HUMAN	qh80f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
2971	16147	29166	0.81	9.0E-03	A1251744.1	EST_HUMAN	qh80f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3758	18819	28921	0.66	9.0E-03	J05194.1	NT	S.acidocaldarius thermophilin gene, complete cds
5931	19117		1.19	9.0E-03	A1809792.1	EST_HUMAN	wf77f04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3'
6788	19822		4.01	9.0E-03	BE746988.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'
7623	20693	34169	0.81	9.0E-03	A1242219.1	EST_HUMAN	qh87c12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853974 3'
7640	20709	34188	0.91	9.0E-03	8922570	NT	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
8059	21142		0.8	9.0E-03	AL039591.1	EST_HUMAN	DKFZp434L0412_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0412 5'
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8443	21524		0.54	9.0E-03	AF223391.1	NT	
10050	23089	36690	0.54	9.0E-03	P28011	SWISSPROT	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M290 IEL ANTIGEN)
10063	23104	36707	1.47	9.0E-03	P28808	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11232	24301		1.68	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
11851	24937	38638	1.31	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
11951	24937	38639	1.31	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
12494	26208		2.07	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291289-001-e09 HT0452 Homo sapiens cDNA
12722	26200		37.58	9.0E-03	BE343385.1	EST_HUMAN	hw17b08.x1 NCL CGAP Lu24 Homo sapiens cDNA IMAGE:3183181 3'
12638	25558	32016	1.21	9.0E-03	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
13074	25703		17.9	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291289-001-e09 HT0452 Homo sapiens cDNA
514	13708		3.15	8.0E-03	AA723007.1	EST_HUMAN	2h30e03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413590 3' similar to contains Alu repetitive element:
1013	14185	27246	12.89	8.0E-03	AF106656.1	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
2226	16363	28486	1.87	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2617	15741	28853	3.05	8.0E-03	P10266	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
3442	18610	28628	1.02	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3768	18927	28930	1.81	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3768	18927	28931	1.81	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4372	17615	30495	1.15	8.0E-03	BE840049.1	EST_HUMAN	QV6-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4502	17642	30627	5.73	8.0E-03	BF363327.1	EST_HUMAN	GM4-NN0119-300800-223-805 NN0119 Homo sapiens cDNA
4839	17872	30561	0.63	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLFI PROTEIN
4839	17972	30982	0.63	8.0E-03	P03181	SWISSPROT	HYPOTHETICAL BHLFI PROTEIN
6271	18390	31358	0.94	8.0E-03	AU140281.1	EST_HUMAN	AU140281 PLACE2 Homo sapiens cDNA clone PLAGE2000223 5'
5840	18834	31911	2.8	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lipase, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
6328	25823	32857	1.27	8.0E-03	AF000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt position (2/7)
6889	20041	33450	4.4	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE YANA
7068	20112		1.08	8.0E-03	V01109.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7357	20438	33898	1.43	8.0E-03	M17197.1	NT	A. californica (marine gastropod mollusc) neurotrophin gene (bag cell), exon 1, 5' end
7714	20779		1.8	8.0E-03	AB038287.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
9084	22163	35707	0.64	8.0E-03	P98160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
9111	22180	35734	3.93	8.0E-03	AW808692.1	EST_HUMAN	PRECURSOR (HSPG) (PERLECAN) (PLC)
9180	22268	35801	0.88	8.0E-03		NT	MR1-ST0111-111199-011-H08 ST0111 Homo sapiens cDNA
10154	23191		4.76	8.0E-03	BE086509.1	EST_HUMAN	Mus musculus fusion 2 (human) (Fus2), mRNA GV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11005	24084	37721	2.01	8.0E-03	BE789441.1	EST_HUMAN	601475619F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878405 5'
11231	24300		2.78	8.0E-03	Z49852.1	NT	S.cerevisiae chromosome X reading frame ORF YJR152w
11683	24742	38433	1.30	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
11663	24742	38434	1.39	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
12015	24689	38701	4.37	8.0E-03	AF064589.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
12205	25159		1.89	8.0E-03	M68035.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
12252	25191		7.14	8.0E-03	AB038161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
13145	25959		1.18	8.0E-03	A1277808.1	EST_HUMAN	qir58c09.x1 Soares_plecanta_8cdwneka_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1892752 3'
712	13894	26930	12.35	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
712	13894	26931	12.35	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
989	14170	27231	3.28	7.0E-03	AF243376.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1140	14305	27381	3.55	7.0E-03	AV731712.1	EST_HUMAN	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1395	14549		1.03	7.0E-03	Q61060	SWISSPROT	FORKHEAD BOX PROTEIN D3 (HNF3FH) TRANSCRIPTION FACTOR GENESIS (HEPATOCYTE
1428	14590	27653	3.39	7.0E-03	AA688298.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HFN-2)
1532	14685	27764	3.28	7.0E-03	AW303599.1	EST_HUMAN	ab78b09.s1 Siralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
2332	16060	28598	2	7.0E-03	P04929	SWISSPROT	xv21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
2695	15815		0.88	7.0E-03	AW772132.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3848	18811	28824	0.65	7.0E-03	A1150273.1	EST_HUMAN	hm87n07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3032989 3' similar to contains Alu repetitive element
3863	17023	30022	0.71	7.0E-03	AW444463.1	EST_HUMAN	gf34f02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
3914	17073	30071	1.13	7.0E-03	AF196344.1	NT	U1-H-B13-ekb-c-10-0-U1.s1 NCI_CGAP_Sut55 Homo sapiens cDNA clone IMAGE:2733691 3'
4128	17023	30022	0.77	7.0E-03	AW444463.1	EST_HUMAN	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4721	17859		0.98	7.0E-03	AW630888.1	EST_HUMAN	U1-H-B13-ekb-c-10-0-U1.s1 NCI_CGAP_Sut55 Homo sapiens cDNA clone IMAGE:2733691 3'
5103	18231		6.54	7.0E-03	AL163278.2	NT	h88a05.y1 NCI_CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2889938 5'
5940	19126		0.72	7.0E-03	H71106.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
6238	25921		4.42	7.0E-03	AW887059.1	EST_HUMAN	y82g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to gb:U14723 CLUSTERIN PRECURSOR (HUMAN);
8444	18811	32974	1.67	7.0E-03	W68251.1	EST_HUMAN	RC1-CT0286-050-000-018-c08 CT02866 Homo sapiens cDNA
6567	18826	33213	2.92	7.0E-03	AA327129.1	EST_HUMAN	z633f10.r1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:342475 5'

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## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6885	19853	33243	1.05	7.0E-03	BE657385.1	EST_HUMAN	7634b10.x1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
7228	20133	33550	1.93	7.0E-03	BE928133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 38408_2; contains TAR1.12 TAR1 TAR1 repetitive element;
7689	20754	34238	4.76	7.0E-03	Z35838.1	NT	CM2-CT0478-230800-347-511 CT0478 Homo sapiens cDNA
7689	20754	34239	4.76	7.0E-03	Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
8031	21114	34632	0.59	7.0E-03	AJ229043.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
8031	21114	34633	0.59	7.0E-03	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8302	21384	34905	2.48	7.0E-03	BE175667.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8813	21892	35433	0.58	7.0E-03	AF281074.1	NT	RC5-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
8997	22652		0.64	7.0E-03	AF111168.2	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
							Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
							Homo sapiens fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains
9794	22834	36414	0.68	7.0E-03	N52378.1	EST_HUMAN	y49c10.a1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains
9821	22961	36548	2.72	7.0E-03	P48982	SWISSPROT	Alu repetitive element;
9821	22961	36549	2.72	7.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10513	23548		1.34	7.0E-03	AV687379.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10704	23737		0.82	7.0E-03	AI799734.1	EST_HUMAN	AV687379 GK Homo sapiens cDNA clone GKCAFC07 5'
10800	23833	37456	0.47	7.0E-03	BE154643.1	EST_HUMAN	wc37609.x1 NCL CGAP_P728 Homo sapiens cDNA clone IMAGE:2320840 3'
11065	24141	37776	2.41	7.0E-03	AB008852.1	NT	PM3-HT0344-181169-002-g06 HT0344 Homo sapiens cDNA
11140	24212	37838	1.66	7.0E-03	AJ004862.1	NT	Bos taurus mRNA for NDP52, complete cds
11140	24212	37839	1.55	7.0E-03	AJ004862.1	NT	Homo sapiens partial MUC8B gene, exon 1:29
							Homo sapiens partial MUC8B gene, exon 1:29
12792	28189		1.95	7.0E-03	H94065.1	EST_HUMAN	yv16h01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains
12800	28534		1.46	7.0E-03	BE283253.1	EST_HUMAN	Alu repetitive element;
12808	28601		1.78	7.0E-03	Y17455.1	NT	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
13058	28188		1.68	7.0E-03	AL183300.2	NT	Homo sapiens LSF2 gene, penultimate exon
1269	14427	27494	8.76	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens chromosome 21 segment H521C100
1269	14427	27495	8.76	6.0E-03	AW511148.1	EST_HUMAN	hcd2a05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
2831	15846	28054	0.94	6.0E-03	AF112374.1	EST_HUMAN	SW:PXR_HUMAN 076469 ORPHAN NUCLEAR RECEPTOR PXR;
2856	16133	28147	3.28	6.0E-03	AA759135.1	EST_HUMAN	hcd2a05.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
2856	16133	28148	3.28	6.0E-03	AA759135.1	EST_HUMAN	SW:PXR_HUMAN 076469 ORPHAN NUCLEAR RECEPTOR PXR;
3318	18491		2.27	6.0E-03	HT5990.1	EST_HUMAN	Danio rerio odorant receptor gene cluster
							an78e11.s1 Soares testis_NHT Homo sapiens cDNA clone 1321772 3'
							an78e11.s1 Soares testis_NHT Homo sapiens cDNA clone 1321772 3'
							y77h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3378	16550		0.63	6.0E-03	AF180338.1	NT	Ndorcus ep. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3469	16636	28655	1.26	6.0E-03	U08880.1	NT	Fugu rubripes zinc finger protein, isletocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3469	16636	28655	1.26	6.0E-03	U08880.1	NT	Fugu rubripes zinc finger protein, isletocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3638	16800		1.11	6.0E-03	W37985.1	EST_HUMAN	zfp13a11.1 Scarses, parathyroid tumor, NblHPA Homo sapiens cDNA clone IMAGE:322172 5'
3760	16911	28914	3.73	6.0E-03	BF510986.1	EST_HUMAN	U1-H-B14-apm-c-06-0-J1.s1 NCL CGAP_S188 Homo sapiens cDNA clone IMAGE:3087754 3'
3877	17036	30034	1.31	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (G6p), mRNA
4032	17188	30199	0.6	6.0E-03	AW847284.1	EST_HUMAN	RCO-CT0204-240999-021-b10 CT0204 Homo sapiens cDNA
4087	17223		1.26	6.0E-03	BE250108.1	EST_HUMAN	600942904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859513 5'
4484	17624		1.54	6.0E-03	AJ016833.1	EST_HUMAN	ov33011.x1 Scarses, testis, NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4817	17850	30635	7.9	6.0E-03	AA324242.1	EST_HUMAN	EST217116 Cerebellum II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
5305	18422	31392	0.6	6.0E-03	AA889972.1	EST_HUMAN	g95g09.s1 Scarses, parathyroid tumor, NblHPA Homo sapiens cDNA clone IMAGE:1404268 3'
6281	25822	32803	0.66	6.0E-03	6627521	NT	Variable virus, complete genome
6566	20269	33707	0.8	6.0E-03	O14994	SWISSPROT	SYNAPSIN III
6994	18513	31505	0.97	6.0E-03	BE253748.1	EST_HUMAN	601112363F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7389	20477	33944	0.65	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' end
7389	20477	33945	0.65	6.0E-03	AA299442.1	EST_HUMAN	EST11949 Uterus tumor I Homo sapiens cDNA 5' and
7624	20879	34380	0.8	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-18 and complete cds
8042	21125	34646	6.71	6.0E-03	AJ033980.1	EST_HUMAN	ov1304.x1 Scarses, parathyroid tumor, NblHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element;
8161	21243	34763	2.76	6.0E-03	AW799337.1	EST_HUMAN	RCO-JM0051-210300-032-g02 UM0051 Homo sapiens cDNA
8238	21318		1.65	6.0E-03	BF038188.1	EST_HUMAN	601454915F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3858626 5'
9764	22692	36282	7.03	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
10249	23284		2.49	6.0E-03	AJ432661.1	EST_HUMAN	i22a02.x1 NCL CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
10365	23400	37011	0.75	6.0E-03	AJ011849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A;
10603	23638		0.91	6.0E-03	AF084555.1	NT	Bacillus subtilis fmd gene
10615	23649	37258	0.64	6.0E-03	X68366.1	NT	Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10661	23695		0.54	6.0E-03	AF245505.1	NT	M.thermoformicicum complete plasmid pFV1 DNA
10983	24062	37697	1.56	6.0E-03	AW962184.1	EST_HUMAN	Homo sapiens adican mRNA, complete cds
11049	24126		1.84	6.0E-03	11545814	NT	EST374237 MAGE sequences, MAGG Homo sapiens cDNA
							Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11228	24297		4.1	6.0E-03	U14556.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
11229	24298	37808	2.66	6.0E-03	BE737895.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
12321	26232		2.04	6.0E-03	AF010498.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
12425	26896		1.3	6.0E-03	BF671185.1	EST_HUMAN	602151024F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292212 5'
12451	28926		4.65	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450295 (section 39 of 146) of the complete genome
12532	25893		2.49	6.0E-03	U03790.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12590	26397		1.63	6.0E-03	Q62209	SWISSPROT	SYNAPTOMEMAL COMPLEX PROTEIN 1(SOP-1 PROTEIN)
12944	26622		2.41	6.0E-03	AJ245460.1	NT	Brassica napus slg gene for S-locus glycoprotein, cultivar T2
13095	26018		1.81	6.0E-03	X74807.1	NT	R.nervigicus VEGP2 gene
13147	25746		1.19	6.0E-03	BF110298.1	EST_HUMAN	7c3b1.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568564 3'
686	13871	26903	1.59	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
686	13871	26904	1.59	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
687	13871	26903	3.08	6.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
687	13871	26904	3.08	6.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF; aminocacyl-IRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1136	14301	27367	1.47	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase RH3
1601	14754		1.08	6.0E-03	AI188977.1	EST_HUMAN	q079d05.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1735689 3'
2748	16863	28974	2.43	5.0E-03	AB033008.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
3208	16381	28392	3.87	5.0E-03	T87623.1	EST_HUMAN	y881f09.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:22395 3'
3223	16397		2.72	6.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3235	16409	29423	1.17	5.0E-03	R71794.1	EST_HUMAN	y88g02.s1 Soares breast 2NBHst Homo sapiens cDNA clone IMAGE:1556668 3'
3351	16523		0.84	6.0E-03	AJ297357.1	NT	Homo sapiens partial UMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
3790	16951	28957	6.28	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (penB) gene, complete cds
3854	17014	30014	0.81	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4079	17235		1.64	5.0E-03	AA299875.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4241	17387	30374	0.85	5.0E-03	AJ002125.1	NT	Natrix domestica Zfx type gene
4421	17662	30548	0.71	5.0E-03	H78355.1	EST_HUMAN	y079g10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:240068 5'
4423	17014	30014	0.76	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4731	17886	30848	0.92	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4841	17974	30864	1.56	5.0E-03	AI752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
5286	18405		1.9	5.0E-03	4758747	NT	Homo sapiens myosin-binding protein C, fast-type (MYBPC2) mRNA
5916	19104	32417	5.4	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
							PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
6169	19345	32691	2.82	5.0E-03	O00507	SWISSPROT	Chlamydomonas reinhardtii AR39, section 92 of 94 of the complete genome
6204	19379		0.88	5.0E-03	AE002234.2	NT	60094458471 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2660871 3'
6726	19882		7.34	5.0E-03	BE300091.1	EST_HUMAN	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
6988	18505	31520	7.22	5.0E-03	AB025024.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7185	20050		0.85	5.0E-03	AB038267.1	NT	Mus musculus dynein, exon, heavy chain 11 (Dnaho11), mRNA
7237	20321	33765	0.61	5.0E-03	6753651	NT	EST T03012 Fetal brain, Stratagene (cat#93c206) Homo sapiens cDNA clone HFBOR93 similar to EST containing Alu repeat
7654	20722	34198	0.7	5.0E-03	T05124.1	EST_HUMAN	RC3-CT0255-031089-011-407 CT0255 Homo sapiens cDNA
7774	20831		1.21	5.0E-03	AW854327.1	EST_HUMAN	Homo sapiens MASL1 mRNA, complete cds
7944	20894	34505	7.18	5.0E-03	AB076818.1	NT	RC8-CT0281-081189-011-A05 CT0281 Homo sapiens cDNA
8415	21498	35027	0.81	5.0E-03	AW855907.1	EST_HUMAN	RC8-CT0281-081189-011-A05 CT0281 Homo sapiens cDNA
8415	21499	35028	0.81	5.0E-03	AW855907.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8433	21514	35045	1.99	5.0E-03	P48982	SWISSPROT	Mouse complement receptor (CR2) mRNA, 3' end
8811	21890		5.83	5.0E-03	M01132.1	NT	Escherichia coli genomic DNA, (19.1 - 19.4) min
8907	22086	35628	1.21	5.0E-03	D90723.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
9140	22219	35763	0.52	5.0E-03	M25090.1	NT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cde
10044	23082	36684	1.03	5.0E-03	L21710.1	NT	RCO-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
10176	23213	36805	0.74	5.0E-03	AW821898.1	EST_HUMAN	n48h10.s1 NCI CGAP P18 Homo sapiens cDNA clone IMAGE:895587
10360	23395	37008	0.58	5.0E-03	AA533143.1	EST_HUMAN	Homo sapiens PRO0471 protein (PRO0471), mRNA
10639	23574	37181	0.47	5.0E-03	7662567	NT	ag49c10.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126280 3'
10696	23729		0.47	5.0E-03	AA653281.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
10959	24040		4.78	5.0E-03	T19586.1	EST_HUMAN	xn59g05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:26980-40 3' similar to contains L1 L2 L1 repetitive element;
11181	24250	37884	2.39	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:26980-40 3' similar to contains L1 L2 L1 repetitive element;
11181	24250	37885	2.39	5.0E-03	AW170334.1	EST_HUMAN	contains L1 L2 L1 repetitive element;
11297	24363	38004	1.78	5.0E-03	T48153.1	EST_HUMAN	y09c04.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70688 6'



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
11615	24666		3.41	5.0E-03	BE048055.1	EST_HUMAN	tz4604.y1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291622 5'
12070	26051	38759	1.4	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12070	26051	38760	1.4	5.0E-03	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12457	26144		11.85	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12618	26414		21.79	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
12718	25478		2.03	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12760	25504		1.94	5.0E-03	AA455597.1	EST_HUMAN	SW:DXA2_MOUSE P14885 PROBABLE DIPHEENOL OXIDASE A2 COMPONENT ;
12802	25935		5.99	5.0E-03	BF672332.1	EST_HUMAN	60207774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
13002	25651	31951	2.68	5.0E-03	AW449108.1	EST_HUMAN	U1H-B13-ak4-4-08-0-U1.s1 NCL_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2734215 3'
242	13484	26493	1.54	4.0E-03	AW500196.1	EST_HUMAN	U1HF-BNO-akc-h-04-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078831 5'
331	13545	26575	1.75	4.0E-03	R46482.1	EST_HUMAN	y651e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
459	13651	26889	1.96	4.0E-03	P54675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PI3K)
618	13803	26825	4.37	4.0E-03	AA698339.1	EST_HUMAN	on75912.s1 Soares NFL_T_GBC ST Homo sapiens cDNA clone IMAGE:1562568 3'
900	14075	27142	1.65	4.0E-03	R46482.1	EST_HUMAN	y651e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
934	14109		2.85	4.0E-03	AW749101.1	EST_HUMAN	RCS-BT0339-110100-012-01 BT0333 Homo sapiens cDNA
1174	14337	27393	34.08	4.0E-03	AA069777.1	EST_HUMAN	2181e08.r1 Strategene colon (R637204) Homo sapiens cDNA clone IMAGE:510988 5'
1198	14358	27417	1.83	4.0E-03	AW794740.1	EST_HUMAN	RCS-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1331	14486	27559	1.48	4.0E-03	AA284374.1	EST_HUMAN	z559a01.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1783	14832	28028	2.68	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and oligodendrocyte associated protein AT1-46 mRNA, complete cds
2076	16215	28334	17.33	4.0E-03	AA058777.1	EST_HUMAN	z181e08.r1 Strategene colon (R637204) Homo sapiens cDNA clone IMAGE:510988 5'
2321	16453		2.08	4.0E-03	BE470556.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2352	15483	28815	1.53	4.0E-03	AW784740.1	EST_HUMAN	RCS-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
2639	15762	28875	1.95	4.0E-03	U62111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2639	15762	28876	1.95	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2755	15872	28980	2.97	4.0E-03	AJ277355.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2755	15872	28981	2.97	4.0E-03	AJ277355.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2761	15877	28984	0.87	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3297	16471	29491	1.08	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-H08 HT0340 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3297	19471	29492	1.09	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151299-003-108 HTD340 Homo sapiens cDNA
3619	16783	29798	0.83	4.0E-03	AW188426.1	EST_HUMAN	X9804.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3619	16783	29798	0.83	4.0E-03	AW188426.1	EST_HUMAN	X9804.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2665279 3'
3714	16875	29880	0.84	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
4021	16875	29880	0.85	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
4040	17186	30207	0.72	4.0E-03	AF060868.1	NT	Mus musculus tumor susceptibility protein 101 (tsg101) gene, complete cds
4102	17256		2.18	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
5339	18452	31420	0.98	4.0E-03	AW500547.1	EST_HUMAN	UHF-BNO-alk-10-0-JL1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077486 5'
5380	18592	31564	1.58	4.0E-03	AF005859.1	NT	Drosophila melanogaster engr2D7 (enr2D7) mRNA, complete cds
5515	18713	31726	27.24	4.0E-03	AF169826.1	NT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5914	19102	32416	3.1	4.0E-03	P04196	SWISSPROT	(HPRG)
5918	19106	32418	1.8	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-LABELLED TROPHOBLASTIC ANTIGEN PRECURSOR
6003	19188	32507	0.8	4.0E-03	AL133871.1	EST_HUMAN	DKFZp7611014.g1.761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7611014 6'
6209	19384		4.18	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
6363	19533	32892	0.97	4.0E-03	AW590572.1	EST_HUMAN	hg45c07.x1 NCI_CGAP_G03 Homo sapiens cDNA clone IMAGE:2948652 3'
6439	19606	32959	1.76	4.0E-03	BE548453.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6809	19983	33387	1.07	4.0E-03	AA813222.1	EST_HUMAN	el32111.e1 Soares_testis_NHT Homo sapiens cDNA clone 1392045 3'
6914	20229	33682	1.41	4.0E-03	U78408.1	NT	Lycopodium esculentum knotted 3 protein (TKn3) mRNA, complete cds
7217	20082	33495	1.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7217	20082	33496	1.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7348	20428	33889	3.73	4.0E-03	Q02617	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
7589	20560	34136	0.86	4.0E-03	AI681483.1	EST_HUMAN	b37g12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7591	20682	34138	0.62	4.0E-03	BE670170.1	EST_HUMAN	7631b02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7693	20758		0.85	4.0E-03	X92109.1	NT	H. sapiens hcgIX gene
8128	21210	34731	0.57	4.0E-03	Q9TT92	SWISSPROT	ADAMTS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
8238	21320	34838	4.61	4.0E-03	AF111944.1	NT	Drosophila discoidium AX4 development protein DG1122 (DG1122) gene, partial cds
8398	21479	35008	2	4.0E-03	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
8665	21745	35284	0.67	4.0E-03	AF139827.1	NT	Plasmodium falciparum replication factor C subunit 1 (rfc1) gene, complete cds
8761	21840	35381	0.51	4.0E-03	Y12555.1	NT	Homo sapiens P2X7 gene, exon 12 and 13
8911	21990	35529	7.06	4.0E-03	AI553983.1	EST_HUMAN	hs49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element
9090	22169		3.24	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9100	22179	35723	3.78	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9825	22865	36447	0.47	4.0E-03	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9825	22865	36448	0.47	4.0E-03	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10131	23169	36768	0.63	4.0E-03	H30684.1	EST_HUMAN	yp42g12.1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:180150 5'
10587	23622	37226	1.35	4.0E-03	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
11283	24349	37886	1.38	4.0E-03	4759101	NT	Homo sapiens splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot, Drosophila homolog) (SFRS8) mRNA
11394	24455	38117	5	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
12072	25053	38762	1.57	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
12434	26163		5.84	4.0E-03	BE815173.1	EST_HUMAN	FMA-BN07138-180600-002-508 BN0138 Homo sapiens cDNA
12457	25321		1.35	4.0E-03	BE288280.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12641	25367		1.95	4.0E-03	AW504273.1	EST_HUMAN	U1-HF-BN0-alp-p-04-0-JLr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12814	25543		3.33	4.0E-03	BF224125.1	EST_HUMAN	7q74c08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains Alu repetitive element; contains element MER31 repetitive element
12858	26053		2.18	4.0E-03	AW614596.1	EST_HUMAN	hT02c07.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2853632 3' similar to contains element LTR5 repetitive element
12871	25581		1.34	4.0E-03	AW819141.1	EST_HUMAN	RC3-ST0281-240400-015-103 ST0281 Homo sapiens cDNA
13202	25784	31918	1.23	4.0E-03	11436953	NT	Homo sapiens Grib2-associated binder 2 (KIAA0571), mRNA
382	13590	26626	1.25	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
802	14077	27143	4.87	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1694	14846	27930	3.65	3.0E-03	AA468110.1	EST_HUMAN	nc73c03.s1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element
2367	15498		6.37	3.0E-03	Z32521.1	NT	S.cereale (cv. Helio) mRNA for ribosephosphate isomerase
2368	15499	28624	1.14	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2368	15499	28625	1.14	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
3058	16232		0.77	3.0E-03	Y08006.1	NT	Arabidopsis thaliana rps16t gene
3162	16327	26338	3.65	3.0E-03	BE379286.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'
3220	16394	29405	2.63	3.0E-03	AW802687.1	EST_HUMAN	IL2-UM0076-240300-056-003 UM0076 Homo sapiens cDNA
3504	16871	26881	2.16	3.0E-03	U34505.1	NT	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exon 1 and 2
3513	16879		7.5	3.0E-03	Y12500.1	NT	C.elegans camde gene
4086	17241	30248	7.76	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4086	17241	30249	7.76	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4147	17299	30291	1.67	3.0E-03	AI792278.1	EST_HUMAN	en04f09.y6 Gassler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4515	17654	30642	5.53	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4841	17777	30759	4.82	3.0E-03	AI536141.1	EST_HUMAN	xu8.P10.H3 conorm Homo sapiens cDNA 3'

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## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4858	17861	30978	0.89	3.0E-03	AL118067.1	EST_HUMAN	DKFZp781B0712_1 1761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp781B0712 5'
4955	19085	31061	2.05	3.0E-03	AJ732754.1	EST_HUMAN	ab18a08.x5 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
4978	18107	31083	5.53	3.0E-03	BE787946.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5255	18375	31341	0.9	3.0E-03	4509414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GAT1) mRNA
5255	18375	31342	0.9	3.0E-03	4509414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GAT1) mRNA
5282	18381	31347	1.75	3.0E-03	AI188880.1	EST_HUMAN	SW-AP17_MOUSE Q00380 CLATHRIN COAT ASSEMBLY PROTEIN AP17, contains MSR1,2 MER22 repetitive element
5380	18582	31451	3.35	3.0E-03	8922499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5673	18867	32163	1.09	3.0E-03	AJ249981.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5744	18837	32237	0.83	3.0E-03	U35323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 (Lmp2) gene, complete cds
6683	19841	33231	9.72	3.0E-03	AA456701.1	EST_HUMAN	bet3f10.r1 Soares_NhrM/Pu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7168	20301	33744	0.75	3.0E-03	D37877.1	NT	Fugu rubripes mRNA for sodium channel alpha subunit, partial cds
7354	20433	33895	1.38	3.0E-03	AJ011419.1	NT	Kluyveromyces marxianus pep3 gene for purine-cytosine permease
7691	20758	34241	3.71	3.0E-03	AB021738.1	NT	Onza sativa gene for bZIP protein, complete cds
8124	21208	34726	0.9	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8124	21206	34727	0.9	3.0E-03	BF333058.1	EST_HUMAN	RCO-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8350	21431	34955	1.4	3.0E-03	N92680.1	EST_HUMAN	2527504.s1 Soares_parathyroid_tumor_NhrIPA Homo sapiens cDNA clone IMAGE:304783 3'
8490	21571	35108	0.47	3.0E-03	AI866028.1	EST_HUMAN	wf24d09.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2429841 3'
8510	21591		0.63	3.0E-03	M63498.1	NT	S.cerevisiae UGA35 gene, complete cds
8655	21735	35276	1.34	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8678	21759	35295	1.5	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
8786	21865		1.45	3.0E-03	Q8QM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
9192	22270		10.8	3.0E-03	AW613774.1	EST_HUMAN	h18d010.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869131 3' similar to contains L1,1 L1 repetitive element
9245	22322	35866	4.28	3.0E-03	AL161389.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
9289	22845	35896	0.98	3.0E-03	AJ016731.1	EST_HUMAN	ov03d12.x1 NCL_CGAP_K18 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_rnat
9280	22358	35908	0.53	3.0E-03	BF336078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);
9509	22564		0.78	3.0E-03	D90901.1	NT	602036980F1 NCL_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4183938 5'
9648	21089	34804	0.77	3.0E-03	BE154670.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
9836	22878		0.58	3.0E-03	P03355	SWISSPROT	PM3-HT0344-071289-003-d07 HT0344 Homo sapiens cDNA POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]

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## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9908	22948		6.61	3.0E-03	P08672	SWISSPROT	CIRCUMSPOROZITE PROTEIN PRECURSOR (CS)
10090	23137	38798	2.31	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
10200	23237	36827	1.44	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
10344	23378	36990	3.89	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
11085	24159		2.87	3.0E-03	5803028	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
11458	20756	34241	1.45	3.0E-03	AB021798.1	NT	Oryza sativa gene for bZIP protein, complete cds
11722	23908	37532	1.47	3.0E-03	P22531	SWISSPROT	SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930)
11732	23918	37543	1.9	3.0E-03	AF268285.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11770	24762	38487	2.52	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11770	24762	38458	2.52	3.0E-03	AF094481.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11849	24838	38532	1.35	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
12077	25057		1.46	3.0E-03	AW294812.1	EST_HUMAN	U1-H-B12-ah1-d08-Q-U1 st NCI CGAP_Sut4 Homo sapiens cDNA clone IMAGE:2726842 3'
12193	25948		1.62	3.0E-03	AI525056.1	EST_HUMAN	promoter-5.E07.r b1 tumor Homo sapiens cDNA 5'
12235	26179	38346	1.24	3.0E-03	AA993154.1	EST_HUMAN	α77b10.st Scores, total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1.3 MER28 repetitive element ;
12298	26090		1.76	3.0E-03	AB009668.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
12481	26333	32057	1.23	3.0E-03	AJ295282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
520	13721	26746	0.87	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
528	13721	26747	0.87	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
808	16023		11.88	2.0E-03	T70874.1	EST_HUMAN	α115h03.11 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108341 5'
1394	14548	27624	2.08	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1397	14551	27626	1.42	2.0E-03	AA691805.1	EST_HUMAN	nu86101.s1 NCI CGAP_A1v1 Homo sapiens cDNA clone IMAGE:1217593
1408	14580	27634	20.85	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRG2 (DRG2) gene, complete cds
1519	14872	27754	1.1	2.0E-03	P46508	SWISSPROT	PLATELET-ENDOTHELIAL TETRASPAN/ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1546	14898	27776	2.26	2.0E-03	4557838	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1546	14898	27777	2.26	2.0E-03	4557838	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1621	14773		6.17	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR
1811	14960	28053	1.27	2.0E-03	AA450138.1	EST_HUMAN	zw42a10.r.1 Scores, total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:789114 5'
1828	15071		1.09	2.0E-03	BE144908.1	EST_HUMAN	CM2-HT0183-081099-018-d03 HT0183 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2051	15192	28305	1.59	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2324	15456	28588	0.97	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2647	15770		4.83	2.0E-03	AW137782.1	EST_HUMAN	UHH-B11-ad-g-10-0-UJ.s1 NCI_OGAP_Sut3 Homo sapiens cDNA clone IMAGE:2717010 3'
3503	16670	29680	4.92	2.0E-03	AA450138.1	EST_HUMAN	z42a10.r1 Soares fetal_fetus_Nb2HF8_9vi Homo sapiens cDNA clone IMAGE:789114 5'
3510	16676	29686	0.96	2.0E-03	BF568955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3768	16917	29919	5.48	2.0E-03	XB7344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
4062	17218	30226	0.62	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4229	17376	30364	2.39	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4280	17435	30423	1.02	2.0E-03	AA178983.1	EST_HUMAN	zp13h01.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:605361 5'
4336	17479		13.93	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4632	17670		1.99	2.0E-03	L35078.1	NT	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4547	17686		1.22	2.0E-03	AW297380.1	EST_HUMAN	UHH-BW0-ell-g-03-0-UJ.s1 NCI_OGAP_Sut3 Homo sapiens cDNA clone IMAGE:2730413 3'
4551	17689	30670	1.05	2.0E-03	AI064746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4668	17803	30780	2.11	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4668	17803	30781	2.11	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4828	17981	30949	1.02	2.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
4832	17965		1.57	2.0E-03	R87773.1	EST_HUMAN	yx45e02.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
4862	18091	31067	1.07	2.0E-03	P11000	SWISSPROT	WALL-ASSOCIATED PROTEIN PRECURSOR
5132	18257	31223	0.84	2.0E-03	AF003528.1	NT	Homo sapiens X-linked arylidolite ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5604	18789	31849	1.57	2.0E-03	BF241410.1	EST_HUMAN	60187688F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5745	18810	32238	1.83	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5828	19019	32325	2.08	2.0E-03	U63711.1	NT	Xenopus laevis xafilin mRNA, complete cds
8236	19411	32758	3.83	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
8236	19411	32759	3.93	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6476	19543	33004	2.28	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6476	19543	33005	2.28	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
6478	19646	33007	7.55	2.0E-03	BF308187.1	EST_HUMAN	601867434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6514	19879	33049	2.16	2.0E-03	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6515	19880	33050	0.75	2.0E-03	AV709075.1	EST_HUMAN	AV709075 ADC Homo sapiens cDNA clone ADCAEF09 5'
6544	19708	33082	1.45	2.0E-03	X94451.1	NT	Lacculium mRNA for lya4-mRNA synthetase (LyeRS)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6736	19892		1.36	2.0E-03	AI991089.1	EST_HUMAN	wu36h09.x1 Soares_Deckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' cimilar to SW_RL29_HUMAN P47914 60S RIBOSOMAL PROTEIN L29; contains element MSR1 repetitive element;
6775	19930	33326	0.7	2.0E-03	AA677631.1	EST_HUMAN	2f3a1.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430652 3'
7098	18525	31517	1.35	2.0E-03	AB038502.1	NT	Ceanorhabditis elegans mRNA for galectin LEC-11, complete cds
7231	20136	33564	3.3	2.0E-03	BE067986.1	EST_HUMAN	GM4-BT0366-061298-054-401 BT0366 Homo sapiens cDNA
7294	20376	33833	0.65	2.0E-03	AI298883.1	EST_HUMAN	gm69411.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1866885 3'
7444	20521	33994	0.8	2.0E-03	T86599.1	EST_HUMAN	yd77g10.r1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:114306 5'
7794	20850	34342	1.41	2.0E-03	P07364	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8241	21323	34840	2.97	2.0E-03	AW592004.1	EST_HUMAN	h637b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834035 3' similar to TR-Q60976 Q60976 JERKY.;
8412	21493	35023	5.49	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares_melanocyte_2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element;
8412	21493	35024	5.49	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares_melanocyte_2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element;
8459	21640	35069	0.84	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C8G9.05 IN CHROMOSOME 1
8481	21662	35097	1.09	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8538	21617	35163	1.04	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain; factor-1 (RPF-1), mRNA
8538	21617	35164	1.04	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain; factor-1 (RPF-1), mRNA
8561	21642	35181	1.03	2.0E-03	AU136679.1	EST_HUMAN	AU136679 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
8614	21694		0.9	2.0E-03	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8966	19018	32323	0.79	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
8966	19018	32324	0.79	2.0E-03	AW796111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9441	22815	36079	1.07	2.0E-03	AF224569.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9726	22781	36362	0.71	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:194296 3'
9726	22791	36363	0.71	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:194296 3'
9758	22898	36264	3.33	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GNEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRA-CELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
9868	22908	36493	1.22	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9868	22908	36494	1.22	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9924	22964	36552	0.6	2.0E-03	AF087732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9824	22864	36553	0.6	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
10119	23157	36755	0.86	2.0E-03	AW884289.1	EST_HUMAN	QV3-OT0084-060400-144-001 OT0084 Homo sapiens cDNA
10248	23283		6.26	2.0E-03	AA251376.1	EST_HUMAN	Zs10a06.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:684754 3'
10628	23692	37270	0.49	2.0E-03	BF367366.1	EST_HUMAN	MF2-GN0030-140900-001-005 GN0030 Homo sapiens cDNA
11263	24334		2.14	2.0E-03	M86524.1	NT	Human dystrophin gene
11778	20850	34342	3.79	2.0E-03	P07354	SWISSPROT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11836	24825		2.36	2.0E-03	BF330909.1	EST_HUMAN	RC3-BT0333-310800-115-004 BT0333 Homo sapiens cDNA
11844	24833	36526	9.64	2.0E-03	Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
12180	25140		3.37	2.0E-03	AI625745.1	EST_HUMAN	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ;
12198	25155	36853	4.31	2.0E-03	AF157516.2	NT	Homo sapiens SEL1L (SEL1L) gene, partial cds
12222	25171	36836	1.71	2.0E-03	AI084325.1	EST_HUMAN	oy43g06.s1 Soares_parathyroid_tumor_Nb1PA Homo sapiens cDNA clone IMAGE:1668634 3' similar to
12245	18467		4.86	2.0E-03	AJ245167.1	NT	TR:P87535 P87535 P3-PLA1 PRECURSOR ;
12462	28140		4	2.0E-03	AV697968.1	EST_HUMAN	Camelus dromedarius crip19 gene for immunoglobulin heavy chain variable region
12561	26383	32039	1.29	2.0E-03	Y00508.1	NT	AV697968 GKC Homo sapiens cDNA clone GKCGX005 5'
							H. sapiens M1 gene for muscarinic acetylcholine receptor
12897	26594		1.38	2.0E-03	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G8b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
13090	25927		2.46	2.0E-03	AV697966.1	EST_HUMAN	AV697966 GKC Homo sapiens cDNA clone GKCGX005 5'
432	13648	26684	1.38	1.0E-03	H95471.1	EST_HUMAN	y08c08.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
862	14029	27091	1.55	1.0E-03	AI720263.1	EST_HUMAN	es70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
852	14029	27092	1.55	1.0E-03	AI720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOL-COA HYDRATASE ;
1119	14284	27339	2.61	1.0E-03	AI865788.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOL-COA HYDRATASE ;
1139	14304	27360	1.61	1.0E-03	AI854572.1	EST_HUMAN	wk86a10.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
1192	14354	27412	0.85	1.0E-03	AI692616.1	EST_HUMAN	wk86a10.x1 NCI CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551242 3'
2084	15224	28348	3.42	1.0E-03	P47808	SWISSPROT	wk86a01.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element;
2222	15356	28486	9.52	1.0E-03	AJ131016.1	NT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMYM1)
3044	16220	29241	1.37	1.0E-03	AB033117.1	NT	Homo sapiens SCL gene locus
3280	16434	29451	2.81	1.0E-03	P18915	SWISSPROT	Homo sapiens mRNA for KIAA1291 protein, partial cds
							CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)



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## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3260	18434	29452	2.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3374	16546	29560	0.75	1.0E-03	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3632	16766	29813	0.94	1.0E-03	U68081.1	NT	Human MUC2 gene, promoter region
3632	16766	29814	0.94	1.0E-03	U68081.1	NT	Human MUC2 gene, promoter region
3755	16916		1.43	1.0E-03	AB044400.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4034	17190	30200	0.88	1.0E-03	AW170562.1	EST_HUMAN	Xt63d07.x1 Soares_NHCCc_cervical_tumor Homo sapiens cDNA clone IMAGE:2698381 3' similar to contains TAR1.11 TAR1 repetitive element;
4044	17200	30211	0.81	1.0E-03	Z49849.1	NT	S.cerevisiae chromosome X reading frame ORF YJR149w
4566	17694	30673	2.34	1.0E-03	BE839162.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4598	17735	30715	4.89	1.0E-03	BE248536.1	EST_HUMAN	TCBAP1D4609 Pediatric pre-B cell acute lymphoblastic leukemia Baylar-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4609
4785	17920	30908	0.81	1.0E-03	U29449.1	NT	Casohabiditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4945	18076	31050	2.54	1.0E-03	A1073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4945	18076	31051	2.54	1.0E-03	A1073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4948	18076		6	1.0E-03	BE164067.1	EST_HUMAN	PM0-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5188	18310	31276	15.5	1.0E-03	O48409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5324	18437	31407	4.73	1.0E-03	BE219340.1	EST_HUMAN	hV51602.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176955 3'
5423	18624	31600	2	1.0E-03	AA280951.1	EST_HUMAN	zs44f01.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5518	18716	31730	3.57	1.0E-03	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5572	18769	31809	1.84	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5572	18768	31810	1.84	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5690	18884	32176	0.95	1.0E-03	BE796491.1	EST_HUMAN	60158841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5'
5696	18890	32181	1.77	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5751	18943	32244	0.8	1.0E-03	N41974.1	EST_HUMAN	yy07h06.r1 Soares melanocyte 2Nb5HM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element
5751	18943	32245	0.8	1.0E-03	N41974.1	EST_HUMAN	yy07h06.r1 Soares melanocyte 2Nb5HM Homo sapiens cDNA clone IMAGE:270587 5' similar to contains element MER6 repetitive element
6033	19216		0.99	1.0E-03	BF541639.1	EST_HUMAN	602558042F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066907 5'
6144	19322		2.75	1.0E-03	X07699.1	NT	Mouse nucleolin gene
6164	19360	32708	0.85	1.0E-03	BE983939.2	EST_HUMAN	601657816R1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3675693 3'
6321	19493		8.77	1.0E-03	11626176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6464	19631	32992	1.11	1.0E-03	T57761.1	EST_HUMAN	yy93a11.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:115772 5'
6539	19702		1.68	1.0E-03	AW902585.1	EST_HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6895	20046	33455	1.41	1.0E-03	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
7302	20384	33843	2.81	1.0E-03	D16826.1	NT	Human gene for fourth somatostatin receptor subtype
7656	20724		1.12	1.0E-03	AJ226042.1	NT	Homo sapiens 959 kb contig between AVL1 and CBR1 on chromosome 21q22, segment 2/3
7817	20872	34370	1.98	1.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
7885	20937	34443	3.44	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7934	20984	34492	0.79	1.0E-03	BE880044.1	EST_HUMAN	601491081F1 NIH_MGC, 69 Homo sapiens cDNA clone IMAGE:3883276 5'
8073	21155	34674	0.66	1.0E-03	AF274581.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
8136	21218	34739	5.02	1.0E-03	AJ251973.1	NT	Homo sapiens partial steelfin-1 gene
8337	21418	34944	1.95	1.0E-03	AA122270.1	EST_HUMAN	z197c09 s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1,11 L1 repetitive element;
8438	21519	35048	2.35	1.0E-03	AF153980.1	NT	Homo sapiens exostosin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8625	21705	35241	0.75	1.0E-03	U29397.1	NT	Rattus norvegicus plasma membrane Ca2+-ATPase isoform 3 (PMCA3) gene, 5' flanking region
9144	22223		1.48	1.0E-03	Y11204.1	NT	V. carteri gene encoding vdxoxpsin
9170	22248	35791	0.65	1.0E-03	AW840353.1	EST_HUMAN	CM3-LT0079-170200-092-e07 LT0079 Homo sapiens cDNA
9281	22357		0.65	1.0E-03	U62111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
9319	22395	35947	3.89	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9319	22395	35948	3.89	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9786	22836		0.47	1.0E-03	AJ247482.1	EST_HUMAN	gbtM97388 TATA-BINDING PROTEIN-ASSOCIATED PHOSPHOPROTEIN (HUMAN);
9807	22847	36424	2.06	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9807	22847	36425	2.06	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
10025	23063	36660	0.89	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG-40) (DERMATAN SULFATE
10366	23401	37012	9.37	1.0E-03	AF003529.1	NT	PROTEOGLYCAN-II (DSPG)
10372	23407		0.75	1.0E-03	AF097485.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10322	23557	37165	1.08	1.0E-03	AJ024350.1	EST_HUMAN	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10923	23856	37478	0.5	1.0E-03	AE004762.1	NT	ov75108.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:184873 3' similar to contains MER39.b1
10923	23856	37479	0.5	1.0E-03	AE004762.1	NT	Pseudomonas aeruginosa PA01, section 323 of 629 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10830	23853		0.53	1.0E-03	AA709202.1	EST_HUMAN	ag93112.s1 Stratigene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:1142083 3' similar to contains Alu repetitive element:
10902	23986	37617	2.01	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0278-181099-011-a09 CT0278 Homo sapiens cDNA
10902	23986	37618	2.01	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0278-181099-011-a09 CT0278 Homo sapiens cDNA
10989	24068	37702	2.46	1.0E-03	BE170859.1	EST_HUMAN	QV3-HT0543-220300-130-a03 HT0543 Homo sapiens cDNA
11062	24138		2.03	1.0E-03	AI583847.1	EST_HUMAN	h73612.x1 NCL_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246448 3' similar to TR:Q26195 Q26195 PVA1 GENE:
11425	24486		2.83	1.0E-03	AV759949.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 6'
11858	24846	38543	2.17	1.0E-03	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
11858	24846	38544	2.17	1.0E-03	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
11824	24910	38611	1.53	1.0E-03	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY)
11824	24910	38612	1.53	1.0E-03	P13002	SWISSPROT	(TRANSCRIPTION FACTOR NTF-1)
12176	25156	38831	5.51	1.0E-03	BE894488.1	EST_HUMAN	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY)
12679	26118		7.37	1.0E-03	AI347355.1	EST_HUMAN	(TRANSCRIPTION FACTOR NTF-1)
12812	26142	31551	3.83	1.0E-03	BE780572.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12889	25560		1.17	1.0E-03	11405934	NT	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:2083013 3' similar to contains Alu repetitive element:
6327	18440	31409	0.7	9.0E-04	P08548	SWISSPROT	601468878F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3912035 5'
5789	18969		2.06	9.0E-04	P08727	SWISSPROT	Nicotiana tabacum chloroplast, complete genome
6388	19557		0.59	9.0E-04	AJ006346.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6815	19775	33166	1.27	9.0E-04	P02381	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6843	22883		1.46	9.0E-04	AB037203.1	NT	Homo sapiens KVLQ11 gene
1517	14670		1.07	8.0E-04	X86469.1	NT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
4298	17439		4.4	8.0E-04	P08547	SWISSPROT	Glycylthiza glabra GgbAS1 mRNA for beta-amylin synthase, complete cds
4987	18017	31002	2.5	8.0E-04	U29185.1	NT	Xlaevis mRNA for C4SR protein
11412	24473		2.59	8.0E-04	AA770984.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11576	24631		1.87	8.0E-04	AI571089.1	EST_HUMAN	Homo sapiens prion protein (PrP) gene, complete cds
1874	16018	28127	1.11	7.0E-04	L41825.1	NT	z24c10.s1 Soares_fetal_heart_NbHH18W Homo sapiens cDNA clone IMAGE:377874 3'
2472	15599	28724	1.45	7.0E-04	U29185.1	NT	b85a08.x1 NCL_CGAP_U2 Homo sapiens cDNA clone IMAGE:2176310 3'
2778	15894	28004	1.33	7.0E-04	AL163210.2	NT	Homo sapiens CYP17 gene, 5' end
3353	16525	29540	1.4	7.0E-04	4886170	NT	Homo sapiens prion protein (PrP) gene, complete cds
							Homo sapiens chromosome 21 segment HS21C010
							Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA

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6221	19396	32745	0.93	7.0E-04	AA518212.1	EST_HUMAN	ng85g12.st NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:599718 similar to contains L1.b3 L1 L1
6642	19801		2.33	7.0E-04	AI769331.1	EST_HUMAN	repetitive element ;
7376	20455		0.72	7.0E-04	AK024446.1	NT	wg35f09.xt Soares NSF F8 9W_OT_PA_P_ST Homo sapiens cDNA clone IMAGE:2367209 3'
10008	23046	36639	0.65	7.0E-04	P13497	SWISSPROT	Homo sapiens mRNA for FLJ00335 protein, partial cds
10008	23046	36640	0.65	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11865	24853		1.7	7.0E-04	U76027.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11865	24881	38578	3.76	7.0E-04	Z40561.1	EST_HUMAN	Homo sapiens Brulon's tyrosine Kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
12723	25491		6.28	7.0E-04	BE077941.1	EST_HUMAN	(L44L) and FTP3 (FTP3) genes, complete cds
13007	25650		2.68	7.0E-04	R17336.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
13038	25682		5.43	7.0E-04	6005935	NT	CM1-BT0814-110300-142-b12 BT0814 Homo sapiens cDNA
2760	16876		0.97	8.0E-04	BF341380.1	EST_HUMAN	Xp13-c08.t1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:32298 5'
4069	17226	30232	1.84	8.0E-04	AI862525.1	EST_HUMAN	Homo sapiens Retina-derived POL-domain factor-1 (RPF-1), mRNA
4201	17350	30341	0.85	8.0E-04	K01315.1	NT	602013339.F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4140287 6'
4201	17350	30342	0.85	8.0E-04	K01315.1	NT	wj15a11.xt NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402878 3'
4301	17444	30430	3.91	8.0E-04	U45983.1	EST_HUMAN	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4565	17703	30683	0.89	8.0E-04	BE173435.1	EST_HUMAN	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4565	17703	30684	0.89	8.0E-04	BE173435.1	EST_HUMAN	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
8050	21133		4.68	8.0E-04	P46408	SWISSPROT	RC2-HT0560-190200-011-109 HT0560 Homo sapiens cDNA
8205	21287		0.51	8.0E-04	H92947.1	EST_HUMAN	RC2-HT0560-190200-011-109 HT0560 Homo sapiens cDNA
10185	23222		3.26	8.0E-04	AL048507.2	EST_HUMAN	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
10215	23261		0.53	8.0E-04	AI858288.1	EST_HUMAN	y84c11.c1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone IMAGE:231858 3' similar to contains LOR1 repetitive element ;
10285	23320	36922	2.29	8.0E-04	BE005850.1	EST_HUMAN	DKFZ568M2024_r1 588 (synonym: hute1) Homo sapiens cDNA clone DKFZp568M2024
10547	23582		0.84	8.0E-04	AF287478.1	NT	wi35g02.xt NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2426830 3'
11774	24766	38462	2.07	8.0E-04	AJ228042.1	EST_HUMAN	RC2-BN0120-260400-012-h11 BN0120 Homo sapiens cDNA
11868	24864	38549	2.47	8.0E-04	AW013847.1	EST_HUMAN	Lytechinus variegatus embryonic blastocoel extracellular matrix protein precursor (ECM3) mRNA, complete cds
11937	24923		1.82	8.0E-04	Q01768	SWISSPROT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
12663	26007		3.31	8.0E-04	AW390618.1	EST_HUMAN	U1-H-B10-aab-e-09-0-U1.s1 NCI_CGAP_Sut1 Homo sapiens cDNA clone IMAGE:2708825 3'
13226	25797		14.14	8.0E-04	AI817088.1	EST_HUMAN	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P16)
668	13864	26882	7.86	5.0E-04	O10341	SWISSPROT	RC1-HT0269-261189-012-408 HT0269 Homo sapiens cDNA
							wj76g11.xt NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element ;
							HYPOTHETICAL 29.3 KD PROTEIN (ORF92)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1531	14684		2.03	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-e07 CT0225 Homo sapiens cDNA
3500	16667	29677	1.6	5.0E-04	AA548931.1	EST_HUMAN	nk27et1.s1 NCJ_CGAP_Co11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element
3809	16969	28972	0.94	5.0E-04	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5589	18784	31830	2.51	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6785	19821	33317	7.06	5.0E-04	AA156080.1	EST_HUMAN	z333b08.r1 Stratagene colon (#337204) Homo sapiens cDNA clone IMAGE:588683 5'
7534	20807	34082	9.01	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
8143	21225	34745	5.99	5.0E-04	AI189392.1	EST_HUMAN	qdt1306.x1 Scars_placenta_8to9weeks_2NhpHP8u9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602.cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element
8498	21679	35115	0.95	5.0E-04	AA814519.1	EST_HUMAN	cb96e02.s1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339228 3' similar to contains element MER22 repetitive element
9477	22534	35098	1.67	5.0E-04	AA846545.1	EST_HUMAN	af56n03.s1 Scars_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'
9871	22713	36281	0.58	5.0E-04	N83765.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
8718	22783	36354	0.84	5.0E-04	P29126	SWISSPROT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR
8908	22849	36428	4.78	5.0E-04	AW270938.1	EST_HUMAN	xs06e02.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'
10484	23619		0.6	5.0E-04	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
11220	24289		1.9	5.0E-04	AL048607.2	EST_HUMAN	DKFZp566M2024_J1 585 (synonym: hule1) Homo sapiens cDNA clone DKFZp566M2024
12012	18784	31830	15	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
12301	25936		2.39	5.0E-04	AA588513.1	EST_HUMAN	ntf5h02.s1 NCJ_CGAP_P1 Homo sapiens cDNA clone IMAGE:913875
12872	26981		1.33	5.0E-04	U63834.1	NT	Human KIT protein and alternatively spliced KIT protein (KIT) gene, complete cds
403	13600		0.75	4.0E-04	BF241482.1	EST_HUMAN	601876534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
690	13874	26607	1.36	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
870	14046	27111	1.55	4.0E-04	AI720263.1	EST_HUMAN	es70508.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
870	14046	27112	1.55	4.0E-04	AI720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE ;
1493	14946	27728	5.68	4.0E-04	AW753356.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE ;
2148	15284	28410	1.87	4.0E-04	AL163278.2	NT	RCS-CT0254-130100-023-401 CT0254 Homo sapiens cDNA
2202	15337		1.1	4.0E-04	AL048704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078 DKFZp434D059_J1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D059 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2691	15811	28927	2.04	4.0E-04	Q98815	SWISSPROT	SERPIN-2 (SILK GUM PROTEIN 2)
3233	18407	28420	2.78	4.0E-04	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3397	16567	28583	0.60	4.0E-04	A1720283.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
3443	16811	28629	0.6	4.0E-04	AV696624.1	EST_HUMAN	O13825 AU-BINDING PROTEIN ENOYL-CoA HYDRATASE. ;
4443	17583	30581	3.24	4.0E-04	AA576331.1	EST_HUMAN	AV696624 GKC Homo sapiens cDNA clone GKCFH07 5'
4443	17583	30582	3.24	4.0E-04	AA576331.1	EST_HUMAN	h10a10.s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL
4669	17785	30781	2.33	4.0E-04	AA086324.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5199	18320	31289	3.82	4.0E-04	BE560860.1	EST_HUMAN	h10a10.s1 NCL CGAP_Co1 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL
7418	20498	33965	1.55	4.0E-04	P48442	SWISSPROT	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
7705	20770		0.85	4.0E-04	AL161588.2	NT	z161c08.s1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:3978910 5'
7898	20948	34466	0.9	4.0E-04	AU122079.1	EST_HUMAN	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:264142 5'
8733	21813	35348	3.64	4.0E-04	BF240712.1	EST_HUMAN	y39e12.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:1644341 3'
8741	21820	35354	1.68	4.0E-04	N25507.1	EST_HUMAN	ov87h03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3'
9892	22932	36516	3.37	4.0E-04	A1025699.1	EST_HUMAN	Mus musculus neuropilin-2 (e17) mRNA, alternatively spliced, complete cds
10045	23083		1.12	4.0E-04	AF022855.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
12691	26808		1.56	4.0E-04	AF254822.1	NT	DKFZp761J221.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221.1
160	13385	26415	3.21	3.0E-04	AL119426.1	EST_HUMAN	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
200	13423	26454	1.7	3.0E-04	P49259	SWISSPROT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
903	14078	27144	1.63	3.0E-04	U83891.1	NT	q22d03.y1 NCL CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2028187 5'
1886	16030	28137	1.7	3.0E-04	AI262100.1	EST_HUMAN	h23a02.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2118082 3'
1901	16044		0.87	3.0E-04	AI986674.1	EST_HUMAN	INTERNALIN B PRECURSOR
3383	16554	28568	4.35	3.0E-04	P28147	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4071	17227	30234	4.84	3.0E-04	P49448	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 1/2
4167	17317		1.36	3.0E-04	AJ271735.1	NT	RC9-HT0014-310599-028 HT0014 Homo sapiens cDNA
4205	17354		1.06	3.0E-04	BE140608.1	EST_HUMAN	MR0-HT0241-030200-008-e01 HT0241 Homo sapiens cDNA
4635	17771		1.16	3.0E-04	BE148546.1	EST_HUMAN	PM0-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
4937	18067		5.2	3.0E-04	BE183778.1	EST_HUMAN	QV3-DT0045-221289-046-d09 DT0045 Homo sapiens cDNA
5004	18133	31107	0.65	3.0E-04	AW937723.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
6271	19445		5.68	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C078
6959	20187	33611	1.54	3.0E-04	AL163278.2	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7130	18556	31471	0.67	3.0E-04	AW893981.1	EST_HUMAN	RC4-NN0027-060400-011-508 NN0027 Homo sapiens cDNA
7765	20824	34316	0.73	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8454	21535	35065	2.18	3.0E-04	P22807	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
10124	23182	36760	1.26	3.0E-04	AA454055.1	EST_HUMAN	zz48d08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:785471 5' similar to gb:M62762
10381	23418	37025	0.46	3.0E-04	AI892193.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);
10876	23710	37318	1.98	3.0E-04	AA781201.1	EST_HUMAN	w76a11.x1 Soares_thymus_NH1Th Homo sapiens cDNA clone IMAGE:2513276 3'
12249	26184	31555	2.39	3.0E-04	AA228301.1	EST_HUMAN	aj24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1391288 3' similar to gb:M36072 60S
12848	25987	31769	2.54	3.0E-04	AB018292.1	EST_HUMAN	RIBOSOMAL PROTEIN L7A (HUMAN);
13114	25727		4.81	3.0E-04	AL134483.1	EST_HUMAN	nc38e04.r1 NCJ_CGAP_P2 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1
180	13403	28432	1.33	2.0E-04	AF217796.1	NT	repetitive element;
491	13685	26719	2.67	2.0E-04	AI146707.1	EST_HUMAN	Homo sapiens mRNA for KIAA0749 protein, partial cds
830	14105	27168	5.02	2.0E-04	M86524.1	NT	DKFZp47L185_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp47L185 5'
830	14105	27169	5.02	2.0E-04	M86524.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related
1208	14368		2.78	2.0E-04	AI288021.1	EST_HUMAN	protein 1 (ARFRP1) genes, complete cds
1213	14374		2.6	2.0E-04	AL163203.2	NT	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
1878	15023		1.71	2.0E-04	AF224263.1	NT	Human dystrophin gene
2257	15360		1.21	2.0E-04	AA478930.1	EST_HUMAN	Human dystrophin gene
							q188e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains
							MER3.b2 MER3 repetitive element;
							Homo sapiens chromosome 21 segment HS21C003
							Mus musculus 5' flanking region of Plx3 gene
							zu38605.g1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu
							repetitive element;
							Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P,
							TCRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1,
							TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2,>
							am56c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
							Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
							QV2-BT0636-070500-194-b07 BT0636 Homo sapiens cDNA
							EST390550 MAGI resequences, MAGP Homo sapiens cDNA
							Phasodius vulgaris nitrate reductase (PVNR2) gene, complete cds
							yu01611.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
							yu01611.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4916	18048		1.22	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5171	18293	31286	1.47	2.0E-04	AB037897.1	NT	Danio rerio hagerstrom gene, exon 1 to 6, partial cds
5216	18337	31310	0.92	2.0E-04	AF067016.1	NT	Dicotyledon discolor intercalin (abpD) gene, complete cds
5551	18855	32138	1.11	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLGDUH10.3
5674	18858	32154	1.83	2.0E-04	AF690862.1	EST_HUMAN	ig03b11.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207709.3
5868	19053	32366	0.93	2.0E-04	AA298652.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
6088	19250	32578	0.92	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6368	19538	32897	1.01	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7378	20457		2.57	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798.5
7478	20553		0.84	2.0E-04	AW860983.1	EST_HUMAN	QV0-CT0387-180300-187-e10 CT0387 Homo sapiens cDNA
7798	20854		13.68	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7808	20863	34357	1.45	2.0E-04	P54298	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
8142	21224	34743	1.02	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8142	21224	34744	1.02	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8479	21560	35094	1.24	2.0E-04	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8479	21560	35095	1.24	2.0E-04	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8763	21842	35383	2.14	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
8841	22020	35581	0.67	2.0E-04	X57331.1	NT	Human Immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
8535	22600	36173	0.68	2.0E-04	AA725700.1	EST_HUMAN	ad2at12.s1 Scores_testis_NHT Homo sapiens cDNA clone 1343518.3
8619	22874	36244	0.47	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLGPF26.1
10180	23217	36808	1.16	2.0E-04	BE145303.1	EST_HUMAN	RC3-H10254-151089-011-505 HT0254 Homo sapiens cDNA
10223	23259	36847	2.06	2.0E-04	AA405777.1	EST_HUMAN	z166c11.1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:742864.5
11088	24162	37798	3.88	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAA01.5
11586	24638	38318	2.68	2.0E-04	AI440282.1	EST_HUMAN	ig01f11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269.3 similar to contains Alu repetitive element
11710	24750	38443	2.39	2.0E-04	AW136740.1	EST_HUMAN	U1-H-B1-actm-c-04-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190.3
11859	24847		2.71	2.0E-04	BE065781.1	EST_HUMAN	RC2-BT0317-150200-011-104 BT0317 Homo sapiens cDNA
12106	25086	38780	32.04	2.0E-04	P21733	SWISSPROT	HYPOPHYSICAL 2B.1 KD PROTEIN IN CRYB1 SREGION (ORF2)
12121	25101	38806	2.05	2.0E-04	L19248.1	NT	Caenorhabditis elegans homeodomain protein (lin-39) mRNA, complete cds
13191	26179		1.28	2.0E-04	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds



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788	13987	27018	0.96	1.0E-04	H99646.1	EST_HUMAN	yx26c09.s1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.11 L1 repetitive element;
1100	14285	27322	2.86	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE];
1138	14303	27358	3.78	1.0E-04	AW013847.1	EST_HUMAN	UJH-B10-aab-e-09-QJ1s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1138	14303	27359	3.79	1.0E-04	AW013847.1	EST_HUMAN	UJH-B10-aab-e-09-QJ1s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1383	14517		2.65	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (D1A1) gene, complete cds
1657	14810	27894	4.23	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphatidylinositol 3-kinase, and LAMP (LAMP) genes, complete cds
1657	14810	27895	4.23	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphatidylinositol 3-kinase, and LAMP (LAMP) genes, complete cds
1909	15052	28164	2.02	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY36
2752	15859	28978	1.06	1.0E-04	BE218833.1	EST_HUMAN	hV45c08.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176368 3'
2752	15859	28978	1.06	1.0E-04	BE218833.1	EST_HUMAN	hV45c08.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176368 3'
3358	16528	29543	1.18	1.0E-04	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 82 (SAP 82) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A68)
3829	18889	29992	0.88	1.0E-04	AI440282.1	EST_HUMAN	h01111.x1 NCI CGAP_Gae4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
4171	17321	30314	1.72	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4192	17342	30335	1.12	1.0E-04	AV047727.1	EST_HUMAN	AV047727 GLC Homo sapiens cDNA clone G1C8B004 3'
5207	18328	31298	1.24	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5207	18328	31299	1.24	1.0E-04	7662015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
5680	19168	32485	1.35	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6569	19731	33109	0.95	1.0E-04	AA177111.1	EST_HUMAN	nc02e12.s1 NCI CGAP_P3 Homo sapiens cDNA clone IMAGE:262
6877	20205	33633	0.69	1.0E-04	AA564561.1	EST_HUMAN	h125c04.s1 NCI CGAP_AA1 Homo sapiens cDNA clone IMAGE:983486 3' similar to gb:M87252
7336	20417	33879	12.52	1.0E-04	AI251880.1	EST_HUMAN	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
7744	20417	33879	13.49	1.0E-04	AI251880.1	EST_HUMAN	q57d10.x1 NCI CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
8184	21266	34788	1.02	1.0E-04	AA630453.1	EST_HUMAN	q57d10.x1 NCI CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985683 3'
9338	22603	36175	2.75	1.0E-04	AI806220.1	EST_HUMAN	ab94q08.s1 Stralagene lung (#937210) Homo sapiens cDNA clone IMAGE:854664 3'
9548	22613	36182	1.54	1.0E-04	O88969	SWISSPROT	w26e08.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9825	22680		0.76	1.0E-04	T77153.1	EST_HUMAN	GYS1/TATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
9848	22880	36466	1.06	1.0E-04	10863878	NT	y472c08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 5'
							Homo sapiens phospholipid scramblase 1 (FLSCR1), mRNA

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10382	23417		3.59	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10420	23455	37060	1.12	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10775	23808	37431	0.46	1.0E-04	P51786	SWISSPROT	ZINC FINGER PROTEIN 157
11622	24873		2.3	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11950	24938	38637	1.81	1.0E-04	AB032968.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
11991	24978	38680	1.84	1.0E-04	AW269081.1	EST_HUMAN	xx49g12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
12024	25008	38709	1.57	1.0E-04	Q03696	SWISSPROT	NEURONAL GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
12024	26008	38710	1.87	1.0E-04	Q03698	SWISSPROT	NEURONAL GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
716	13898	26936	2.44	9.0E-05	AA718933.1	EST_HUMAN	af45c11.t1 Soares_testis_NHT Homo sapiens cDNA clone 1292468 3'
4198	17346	30338	1.13	9.0E-05	AI762209.1	EST_HUMAN	wf54c11.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2394068 3' similar to contains MER6.11 MER6 repetitive element;
6084	18266	32595	1.37	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7751	20811	34301	2.44	9.0E-05	AW204988.1	EST_HUMAN	UIH-B11-aer-d-05-Q-UI.t1 NCI_CGAP_Sut3 Homo sapiens cDNA clone IMAGE:2720289 3'
7751	20811	34302	2.44	9.0E-05	AW204988.1	EST_HUMAN	UIH-B11-aer-d-05-Q-UI.s1 NCI_CGAP_Sut3 Homo sapiens cDNA clone IMAGE:2720289 3'
9877	22839		3.03	9.0E-05	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
9879	22841	38211	3.3	9.0E-05	AF120982.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11402	24463	38127	2.31	9.0E-05	AW073078.1	EST_HUMAN	xx34g05.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1 repetitive element;
11518	24574	38251	1.61	9.0E-05	AI287878.1	EST_HUMAN	gy23f08.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element repetitive element;
11918	19268	32595	3.41	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
12469	28016		3.37	9.0E-05	AF129758.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G8b, G6c, G6b, G6d, G6e, G6f, BAT6, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
844	14022	27080	1.22	8.0E-05	AJ251648.1	NT	Plum salivum mRNA for beta-1,3 glucanase3 (gns2 gene)
887	14063		3.11	8.0E-05	AJ251648.1	NT	Plum salivum mRNA for beta-1,3 glucanase3 (gns2 gene)
3015	18161		1.01	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4804	17741	30719	0.78	8.0E-05	AW044605.1	EST_HUMAN	wy78a04.x1 Soares_NSIF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
6948	22027	35568	0.51	8.0E-05	Y11868.1	NT	Mus musculus gene for hexokinase II, exon 1 (and joined GDS)
11419	24480	38146	2.59	8.0E-05	M69187.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
13169	28001		1.78	8.0E-05	AA279333.1	EST_HUMAN	zs88h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
357	13568	26596	3.16	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220899-011-E04 CT0208 Homo sapiens cDNA
357	13568	26597	3.16	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220899-011-E04 CT0208 Homo sapiens cDNA

### Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
581	13773	26793	1.14	7.0E-05	L48075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HF0072014
581	13773	26794	1.14	7.0E-05	L48075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HF0072014
1080	14246	27303	1.07	7.0E-05	Q2949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2783	15399	28008	5.16	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3227	16401	29413	3.9	7.0E-05	AB009080.1	NT	Dicysteleium discoidaeum gene for TrFA, complete cds
4188	17318		0.95	7.0E-05	AF111187.2	NT	Homo sapiens [un dimerization protein gene], partial cds; cfos gene, complete cds; and unknown gene
4492	17632	30814	1.98	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
6041	18169	31144	0.88	7.0E-05	8845300	NT	Rat cytomegaloovirus Measstricht, complete genome
8420	21501	35033	1.24	7.0E-05	AA505882.1	EST_HUMAN	rh93g01.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:866086 3'
9753	22891	36261	3.67	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Striatogene (cat#936206) Homo sapiens cDNA clone HFBEDE80
11430	24481		5.8	7.0E-05	10835046	NT	Homo sapiens sarcoglycan, epsilon (SGCE), mRNA
2083	16223	28344	1.59	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2083	16223	26345	1.59	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2655	15778	28892	1.66	6.0E-05	AI655241.1	EST_HUMAN	wh54h06.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb.J03250 DNA TOP_OISOMERASE 1 (HUMAN);
2875	13860	26912	2.54	8.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
6034	19217	32638	3.26	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6034	19217	32638	3.26	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6533	16697	33070	1.5	6.0E-05	N72829.1	EST_HUMAN	y50g11.1.r Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246212 5'
7073	20126	33542	0.74	6.0E-05	AA957680.1	EST_HUMAN	q1803.a.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1504586 3'
8276	21358	34876	1.03	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
8276	21358	34877	1.03	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
8638	21718	35255	0.62	6.0E-05	AA160482.1	EST_HUMAN	z108c08.e1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:491726 3' similar to contains element MER28 repetitive element;
8843	21723	35280	2.62	6.0E-05	AW896829.1	EST_HUMAN	PMA-NN0050-310300-001-110 NN0050 Homo sapiens cDNA
8780	21859	35402	2.93	6.0E-05	Q60401	SWISSPROT	COMPLEMENT DEAC-ACCELERATING FACTOR PRECURSOR
9452	22668	36134	1.59	6.0E-05	P08907	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9452	22668	36135	1.59	6.0E-05	P08907	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9721	22786	36357	1.77	6.0E-05	T04149.1	EST_HUMAN	yc23c12.1 Striatogene_lung (#937210) Homo sapiens cDNA clone IMAGE:118082 5'
8922	22862	36550	0.69	6.0E-05	AW627895.1	EST_HUMAN	rh37a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974444 3'
10987	24066	37701	2.42	6.0E-05	AF75639.1	EST_HUMAN	y169d08.s1 Soares_placenta_Nb2HP Homo sapiens cDNA clone IMAGE:143635 3' similar to contains Alu repetitive element; contains LTR7 repetitive element;

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11807	24797	38495	2.7	8.0E-05	AA044015.1	EST_HUMAN	zks802.r1 Soares_pregnant_uterus_NbHPJ Homo sapiens cDNA clone IMAGE:487035 5'
12899	25999	31773	9.37	8.0E-05	AW890110.1	EST_HUMAN	MR0-NT0039-250400-001-09 NT0038 Homo sapiens cDNA
1435	14598	27691	20.87	5.0E-05	AW392088.1	EST_HUMAN	QV4-S10234-241199-040-H11 ST0234 Homo sapiens cDNA
1912	18066		1.07	5.0E-05	8923891	NT	Homo sapiens 220Da perodisomal membrane protein-like (LOC55895), mRNA
2924	19102	29116	0.84	5.0E-05	AJ251058.1	NT	Homo sapiens MEF1A gene, promoter region and exon 1
4088	17243	30250	3.19	5.0E-05	AJ251894.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5642	18836	31913	11.81	5.0E-05	X68855.1	NT	Human MLC1 gene for embryonic myosin alkaline light chain, 3'UTR
6115	19295	32830	3.59	5.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCMA06 3'
6297	19470	32825	0.97	5.0E-05	AF260226.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7485	20560		1.4	5.0E-05	AB037984.1	NT	Mus musculus gene for calretinin, exon 1
12468	25503		6.26	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12759	25503		6.9	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2668	13457		2.73	4.0E-05	U12821.1	NT	Human retin (REN) gene, 5' flanking region
4605	17742	30720	0.76	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4605	17742	30721	0.76	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4997	18128		0.95	4.0E-05	AF164488.1	NT	Cryptosporidium parvum isolate Zaire 15 kDa glycoprotein gp15 gene, partial cds
5131	18266	31222	0.73	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sense) gene, complete cds
9723	22788		6.75	4.0E-05	AF202835.1	NT	Homo sapiens PP1200 mRNA, complete cds
10817	23651	37260	0.54	4.0E-05	P23780	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)(ACID BETA-GALACTOSIDASE)
11007	24088	37723	4.14	4.0E-05	AW627846.1	EST_HUMAN	h36c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element ;
12343	25248	32113	3.27	4.0E-05	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C082
12428	25302		1.47	4.0E-05	AW117680.1	EST_HUMAN	x683e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605192 3'
13189	25773		1.16	4.0E-05	AA417759.1	EST_HUMAN	z01011.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746292 3'
698	13981	28914	0.8	3.0E-05	AJ248081.1	EST_HUMAN	q184c10.x1 Soares_fetal_liver_spleen_INF1S_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element ;
1084	14250	27307	1.16	3.0E-05	AW273851.1	EST_HUMAN	xv24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1550	14702	27781	3.73	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
1550	14702	27782	3.73	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
3385	16537		0.7	3.0E-05	AJ288919.1	EST_HUMAN	q91g11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:O08632 C09632 GLYCINE TYROSINE-RICH HAIR PROTEIN. ;
4501	17641	30825	7.91	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4501	17641	30828	7.91	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4588	17725	30707	1.11	3.0E-05	AA386678.1	EST_HUMAN	EST79996 Placenta I Homo sapiens cDNA similar to similar to p53-associated protein

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4588	17725	30708	1.11	3.0E-05	AA368879.1	EST_HUMAN	EST78896 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein
4741	17876	30859	0.93	3.0E-05	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4869	13881	28014	0.7	3.0E-05	AJ248061.1	EST_HUMAN	qf84c10.x1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element contains element KER repetitive element ;
5675	18669	32155	1.72	3.0E-06	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Mylc2pl), mRNA
6897	20047	33456	1.21	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
6897	20047	33457	1.21	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
8082	21184	34681	2.26	3.0E-05	BE793157.1	EST_HUMAN	601587451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5'
8547	21628	35166	1.55	3.0E-05	AA234049.1	EST_HUMAN	zs90b05.s1 Stratiagene echizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
8094	22173	35718	1.58	3.0E-05	AW770982.1	EST_HUMAN	H94608.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008638 3'
8098	22177	35721	1.63	3.0E-05	6812431	NT	Homo sapiens Interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
9102	22181	35726	0.59	3.0E-05	P43391	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
9331	22407		0.51	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9521	22586	36154	1.4	3.0E-05	AA372562.1	EST_HUMAN	EST84476 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
9863	22903		3.62	3.0E-05	AJ768331.1	EST_HUMAN	wg35f09.x1 Soares NSF_F8_gw_OT_PALP_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10755	23788	37403	0.92	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEININELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
10786	23788	37404	0.92	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEININELL2 PRECURSOR (NEL-LIKE PROTEIN 2)
12553	25255		1.61	3.0E-05	L77570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
12551	25374		1.37	3.0E-05	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12913	26168		1.29	3.0E-05	AW518886.1	EST_HUMAN	xs89d06.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2778811 3'
2400	15531	28658	1.49	2.0E-05	AJ286021.1	EST_HUMAN	qf88e1.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element ;
2650	15773	28886	14.63	2.0E-05	M13782.1	NT	Human adenosine deaminase (ADA) gene, complete cds
2777	15893		6.89	2.0E-05	AA160562.1	EST_HUMAN	zc43a12.r1 Stratiagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:932734 5' similar to contains Alu repetitive element; contains element L1 repetitive element ;
3207	16382	28393	1.29	2.0E-05	BE066036.1	EST_HUMAN	RC3-BT0319-120200-014-h08 BT0319 Homo sapiens cDNA
3428	16597	28613	1.04	2.0E-05	AF184814.1	NT	Homo sapiens P47-phox (NCF1) gene, complete cds
3455	16622	29643	1.12	2.0E-05	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
3583	18748		0.87	2.0E-05	X98463.1	NT	S cerevisiae 12.8 kbp fragment of the left arm of chromosome XV
3909	17668		0.81	2.0E-05	AL039107.1	EST_HUMAN	DKFZp5681064_r1 506 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp5681064 5'
5003	18132	31106	0.8	2.0E-05	AJ131016.1	NT	Homo sapiens SCL gene locus
5878	18068	32376	1.84	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6039	19222		0.87	2.0E-05	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6092	19273	32601	0.91	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6092	19273	32602	0.91	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6286	19459	32811	0.79	2.0E-05	A1149272.1	EST_HUMAN	q72a02.x1 Soares_placenta_8tc9weeks_2NbpHP8tc9W Homo sapiens cDNA clone IMAGE:1715114.3'
6760	19916	33311	2.11	2.0E-05	AA714330.1	EST_HUMAN	similar to contains L1.13 L1.1 repetitive element;
7042	20096	33511	1.89	2.0E-05	Y08926.1	NT	hw05d12.s1 NCI_CGAP_SST Homo sapiens cDNA clone IMAGE:1238519.3'
7054	20107	33523	1	2.0E-05	A1492880.1	EST_HUMAN	P.falciparum mRNA for AARP1 protein, partial
7082	20115		7.24	2.0E-05	A1991025.1	EST_HUMAN	qz47b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030003.3' similar to TR:Q02711
7303	20385	33844	2	2.0E-05	AF224282.1	NT	Q02711 PRO-POLY-OUTPASE POLYPROTEIN ; wu35h07.x1 Soares_Dieckgraele_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077.3'
7303	20385	33845	2	2.0E-05	AF224282.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7524	20597		0.77	2.0E-05	AF128847.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
8069	21181	34871	1.58	2.0E-05	A1381040.1	EST_HUMAN	Homo sapiens Indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
8467	22624	36087	0.59	2.0E-05	P49457	SWISSPROT	qz20h05.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2109369.3'
8467	22524	36088	0.55	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10127	23185	36704	0.9	2.0E-05	AL163207.2	NT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
10339	23374	36984	0.94	2.0E-05	BF055939.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
10817	23850	37472	3.53	2.0E-05	N41751.1	EST_HUMAN	7175g09.y1 NCI_CGAP_Bm20 Homo sapiens cDNA clone IMAGE:3340576.5'
10817	23850	37473	3.53	2.0E-05	N41751.1	EST_HUMAN	yw81a08.r1 Soares_placenta_8tc9weeks_2NbpHP8tc9W Homo sapiens cDNA clone IMAGE:259570.5'
10881	20113		2.66	2.0E-05	A1691026.1	EST_HUMAN	yw81a08.r1 Soares_placenta_8tc9weeks_2NbpHP8tc9W Homo sapiens cDNA clone IMAGE:259570.5'
11738	23924	37549	1.95	2.0E-05	BE175801.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgraele_colon_NHCD Homo sapiens cDNA clone IMAGE:2622077.3'
11881	24968	38668	5.74	2.0E-05	A1912713.1	EST_HUMAN	RC8-H70582-280300-012-E12 H70582 Homo sapiens cDNA
12477	25921		3.7	2.0E-05	BE348229.1	EST_HUMAN	wc12h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340921.3'
12592	26104		8.13	2.0E-05	AW074604.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532.3' similar to TR:Q12832
							Q12832 GLYCOPHORIN HEP2 ;
							xx89a03.x1 NCI_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:2573932.3' similar to contains L1.b3 L1 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12650	25905		3.24	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12825	25551	32014	2.01	2.0E-05	AU131613.1	EST_HUMAN	AU131613 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
13205	25757		1.84	2.0E-05	AI200970.1	EST_HUMAN	qf68g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755236 3'
2765	16071	28983	1.86	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3740	16901	28905	1.71	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lamto 120 Suppressor of Hairless (Su(H)) gene, partial cds
3915	17074		0.97	1.0E-05	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4074	17230	30236	11.86	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4288	17433	30420	1.45	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4392	17635	30514	2.14	1.0E-05	AA431119.1	EST_HUMAN	zr68g04.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4975	18104	31080	2.24	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
5079	18207	31178	0.89	1.0E-05	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
5084	18212	31185	0.84	1.0E-05	Z18943.1	NT	H. sapiens repeat region
6891	20043	33451	1.13	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
7230	20135	33553	4.24	1.0E-05	AA841848.1	EST_HUMAN	ns19g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.1f L1
7232	20316	33769	5.19	1.0E-05	4505844	NT	L1 repetitive element
7837	20882	34394	0.73	1.0E-05	BF222648.1	EST_HUMAN	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
7956	21006		2.03	1.0E-05	P19474	SWISSPROT	MER10 repetitive element
8116	22156		2.39	1.0E-05	AL163227.2	NT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
9280	22337	35887	2.59	1.0E-05	AA452878.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
9487	22544	36107	12.29	1.0E-05	AA236110.1	EST_HUMAN	z235h12.s1 Soares_testis_N52HF8_9w Homo sapiens cDNA clone IMAGE:786519 3' similar to gb:U02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
9566	22708	36275	0.81	1.0E-05	AV732180.1	EST_HUMAN	z305e11.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element
10043	23081	36682	0.79	1.0E-05	AW510902.1	EST_HUMAN	AV732180 HTF Homo sapiens cDNA clone HTFBH01 5'
10043	23081	36683	0.79	1.0E-05	AW510902.1	EST_HUMAN	rd41b02.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.t1 OFR repetitive element
10120	23156	36756	1.18	1.0E-05	AW291521.1	EST_HUMAN	rd41b02.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.t1 OFR repetitive element
10120	23156	36757	1.18	1.0E-05	AW291521.1	EST_HUMAN	UHT-B12-egk-a-08-O-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10387	23422		2.04	1.0E-05	AW466955.1	EST_HUMAN	UHT-B12-egk-a-08-O-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11169	24230	37860	2.22	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11169	24230	37861	2.22	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
13023	26036	31683	1.4	1.0E-05	AL163303.2	NT	Human sapiens chromosome 21 segment HS21C103
2737	15834	28988	5.83	9.0E-08	AI583811.1	EST_HUMAN	h73a08.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246388 3'
3165	16340	28348	6.11	9.0E-08	AI218983.1	EST_HUMAN	cg11b08.x1 Soares_placenta_8kb8weeks_2NbpHP8b9W_Homo sapiens cDNA clone IMAGE:1759181 3'
3698	16859		2.56	9.0E-08	M61765.1	NT	Human alanine:glyoxylate aminotransferase (AGT) gene, exons 1 and 2
6025	19208	32528	2.48	9.0E-08	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
7003	20139	33557	0.82	9.0E-08	BE065042.1	EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
7598	20668	34144	2.82	9.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7953	21003	34515	12.35	9.0E-08	AI034370.1	EST_HUMAN	ox20g01.x1 Soares_fetal_liver_spleen_1NF1.S_1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element.
8659	21739	35280	1.17	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9183	22261	35803	3.3	9.0E-06	Q63789	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9183	22261	35804	3.3	9.0E-06	Q63789	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9423	22497	36083	4.43	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
11180	24248	37883	3.61	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2598	16065	28839	2.01	8.0E-06	AW382639.1	EST_HUMAN	RC3-CT0283-201199-011-h11 CT0283 Homo sapiens cDNA
6728	19884	33276	2.75	8.0E-06	AA284847.1	EST_HUMAN	z22d05.s1 Soares ovary tumor NhpOT Homo sapiens cDNA clone IMAGE:713885 3' similar to contains MER9.11 MER8 repetitive element
10761	23784	37397	0.93	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10751	23784	37398	0.93	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
1002	14173		1.73	7.0E-06	AA669729.1	EST_HUMAN	ab90f10.s1 Strategene lung (H937210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.11 MER20 repetitive element
1470	14624	27708	3.12	7.0E-06		NT	Homo sapiens KIA0555 gene product (KIA0555), mRNA
2936	18113		10.59	7.0E-06	AI368252.1	EST_HUMAN	qw18g09.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:1991286 3' similar to contains Alu repetitive element
3654	18817		0.85	7.0E-06	AA365542.1	EST_HUMAN	EST89205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5813	19003		5.49	7.0E-08	AW883141.1	EST_HUMAN	QV2-OT0062-250400-173-h01 OT0062 Homo sapiens cDNA
5925	18112	32424	0.93	7.0E-08	N98845.1	EST_HUMAN	y95c07.t1 Soares_mullepla_sclerosis_2N6HMSP Homo sapiens cDNA clone IMAGE:278412 5'
8889	22068	35508	0.83	7.0E-08	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF89S1E), mRNA
10104	23142		0.52	7.0E-08	Q81147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
12202	26131	31547	1.68	7.0E-08	BF215972.1	EST_HUMAN	601881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083972 5'
2884	19160	29177	1.17	8.0E-08	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
3784	18945	29952	1.02	8.0E-08	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-411 BT0379 Homo sapiens cDNA
4878	19163	29206	2.13	8.0E-08	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
							co08e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER8.12 MER8 repetitive element;
4883	18013	30897	2.19	8.0E-08	A1040098.1	EST_HUMAN	Mus musculus E-cadherin binding protein E7, mRNA, complete cds
5465	18665	31644	2.20	8.0E-08	AF167441.1	NT	PROTEIN XE7
5925	18722	31738	1.16	8.0E-08	Q02040	SWISSPROT	IL5-UM0070-110400-083-g02 UM0070 Homo sapiens cDNA
10060	23098		1.98	6.0E-08	AW801912.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
13142	25742	31948	2.39	8.0E-08	11418157	NT	Homo sapiens chromosome 21 segment HS21C046
6186	19362	32710	3.74	5.0E-06	AL163246.2	NT	
6487	19834	32895	1.94	5.0E-08	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7382	20460	33923	1.18	6.0E-08	AB007648.1	NT	Homo sapiens gene for LECT2, complete cds
8654	21734	35274	0.58	5.0E-08	AW556972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
8654	21734	35275	0.58	5.0E-08	AW556972.1	EST_HUMAN	RC1-CT0302-120200-013-h02 CT0302 Homo sapiens cDNA
10307	23342	36847	6.98	5.0E-08	AA313620.1	EST_HUMAN	EST185486 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' and
10731	23764	37372	0.51	5.0E-08	P06881	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
13011	25868	31957	5.49	5.0E-08	A1085045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
							y448c03.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 6' similar to contains Alu repetitive element; contains L1 repetitive element;
694	13850	28877	5.47	4.0E-08	R16287.1	EST_HUMAN	repetitive element; contains L1 repetitive element
869	14045	27110	4.73	4.0E-08	AW103354.1	EST_HUMAN	xx65g12.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER2.1 repetitive element;
1365	14519	27693	3.18	4.0E-08	A1334928.1	EST_HUMAN	tb33a09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1365	14519	27694	3.18	4.0E-08	A1334928.1	EST_HUMAN	tb33a09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1503	14858	27738	1.45	4.0E-08	BF385612.1	EST_HUMAN	QV2-NT0048-200600-250-h07 NT0048 Homo sapiens cDNA
2339	15470	28605	1.56	4.0E-08	AW015401.1	EST_HUMAN	UIH-B10-aat-405-Q.U.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710426 3'
3131	18307	29321	0.89	4.0E-08	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4000	17157	30163	0.89	4.0E-08	AW848285.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4929	18059	31041	1.89	4.0E-08	AI886938.1	EST_HUMAN	wl94c10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432592 3' similar to contains element
8898	21776	35308	0.68	4.0E-06	O15393	SWISSPROT	MER22 repetitive element;
9000	22079	35620	4.49	4.0E-08	AF009680.1	NT	TRANSMEMBRANE PROTEASE, SERINE 2
9909	22949	35535	1.28	4.0E-06	AJ272265.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
11735	23821	37546	3.99	4.0E-08	AB007955.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
13149	26162		1.33	4.0E-06	AW298734.1	EST_HUMAN	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
2232	15366	28494	1.31	3.0E-06	AA700562.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:2773388 3'
2232	15366	28495	1.31	3.0E-06	AA700562.1	EST_HUMAN	234508.s1 Soares_fetal_liver_spleen_1NF1.S_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.11 repetitive element;
2340	15471		1.48	3.0E-06	AF202835.1	NT	234508.s1 Soares_fetal_liver_spleen_1NF1.S_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.11 repetitive element;
2988	16164	29180	0.84	3.0E-06	AA688218.1	EST_HUMAN	Homo sapiens PPI200 mRNA, complete cds
3339	16512		2.67	3.0E-06	AI857779.1	EST_HUMAN	ek48g11.s1 Soares_testis_NIT Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.13
3883	17042	30040	1.47	3.0E-06	BE047084.1	EST_HUMAN	LTR1 repetitive element;
3883	17042	30041	1.47	3.0E-06	BE047084.1	EST_HUMAN	wl22a05.x1 NCI_CGAP_U1 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734
4597	17734	30714	0.8	3.0E-06	T50266.1	EST_HUMAN	LINE-1 LIKE PROTEIN; contains L1.12 L1 repetitive element;
4884	17819	30807	5.52	3.0E-06	X54816.1	NT	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
6289	19462	32814	0.82	3.0E-06	AU159412.1	EST_HUMAN	hg64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
7377	20458		2.14	3.0E-06	P08548	SWISSPROT	jp78b10.r1 Stragene ovary (#937217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1
8274	21358	34874	0.81	3.0E-06	BE562854.1	EST_HUMAN	repetitive element
8883	21962	35496	0.76	3.0E-06	P07743	SWISSPROT	Homo sapiens gene for alpha-1-microglobulin-bikunlin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus)
12656	26435		12.07	3.0E-06	AW386282.1	SWISSPROT	AU159412 THYRO1 Homo sapiens cDNA clone THYRO1001602 3'
207	13430		2.22	2.0E-06	P54366	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1599	14762		6.39	2.0E-06	P21414	SWISSPROT	601336213F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690314 5'
2451	15579	28707	2.58	2.0E-06	AI672138.1	EST_HUMAN	PAROTID SECRETORY PROTEIN PRECURSOR (PSP)
2537	15662	28785	1.69	2.0E-06	P04929	SWISSPROT	RQ3-LT0001-261199-011-A03 L1T0001 Homo sapiens cDNA
2632	15755	28870	1.81	2.0E-06	P08719	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
3607	16771	29786	0.8	2.0E-06	AV657555.1	EST_HUMAN	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
							wat4803.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1
							MER30 repetitive element;
							HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
							KNDB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
							AV857555 GLC Homo sapiens cDNA clone GLCFDB06 3'

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3853	17018	30017	1.54	2.0E-06	AA173518.1	EST_HUMAN	zp02e05.r1 Stratigene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5'
3868	17027	30028	0.88	2.0E-06	AW450215.1	EST_HUMAN	U1H-B13-aky-g-05-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2738178 3'
3878	17035	30033	1.7	2.0E-06	AB030898.1	NT	Mus musculus gene for odorant receptor A16, complete cds
6214	19389		0.92	2.0E-06	AA974932.1	EST_HUMAN	on34h01.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558609 3' similar to contains Alu repetitive element;
6248	19420	32766	0.82	2.0E-06	AI539448.1	EST_HUMAN	te51T05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080241 3' similar to TR:Q13537
6571	19733	33112	5.84	2.0E-06	AI819424.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
7635	20704	34183	0.63	2.0E-06	AA688423.1	EST_HUMAN	W90B04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
8102	21184		1.02	2.0E-06	AW889223.1	EST_HUMAN	nv59c06.s1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1234090 3' similar to contains L1 L3 L1
8281	21363	34832	0.76	2.0E-06	T12238.1	EST_HUMAN	repetitive element ;
9036	22115		1.05	2.0E-06	AA772497.1	EST_HUMAN	MR3-SN0067-120400-002-102 SN0067 Homo sapiens cDNA
9049	22128	35872	1.59	2.0E-06	HE2051.1	EST_HUMAN	AA47R Heart Homo sapiens cDNA clone A447
9417	22491	36056	0.9	2.0E-06	AF003529.1	NT	zh27c11.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413300 3' similar to
9417	22491	36057	0.9	2.0E-06	AF003529.1	NT	TR:P70467 P70467 REVERSE TRANSCRIPTASE ;
9439	22510		0.48	2.0E-06	AI473450.1	EST_HUMAN	y437c04.r1 Soares_ovary_tumor_NbHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb-X74929
9802	22842	34527	0.89	2.0E-06	N30576.1	EST_HUMAN	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
10123	23161		0.7	2.0E-06	AV748969.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
12548	28135	31649	1.34	2.0E-06	P23249	SWISSPROT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
12711	28473		5.94	2.0E-06	BE328232.1	EST_HUMAN	U18g10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141730 3'
34	13272	28276	1.16	1.0E-06	O76082	SWISSPROT	yw68a03.s1 Soares_placenta_8to9weeks_2NbHP8c9W Homo sapiens cDNA clone IMAGE:257212 3'
874	13860	28891	1.8	1.0E-06	AF084364.1	NT	AV748969 NPC Homo sapiens cDNA clone NPCAXD05 5'
1482	14635	27719	1.8	1.0E-06	P09125	SWISSPROT	PROTEIN MOV-10
1553	14708	27788	1	1.0E-06	AI163278.2	NT	h59202.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144699 3' similar to contains L1 L2 L1
1603	14758	27837	1.19	1.0E-06	AA034141.1	EST_HUMAN	repetitive element ;
1603	14758	27838	1.19	1.0E-06	AA034141.1	EST_HUMAN	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
							Mus musculus D6M5E protein (D6M5E)mRNA, complete cds
							MEROZOITE SURFACE PROTEIN CMZ-6;
							Homo sapiens chromosome 21 segment HS21C078
							z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428982 3' similar to contains Alu repetitive element;
							z106a12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428982 3' similar to contains Alu repetitive element;

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1615	14768		0.99	1.0E-08	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2050	16191	28303	4.49	1.0E-08	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2060	16191	28304	4.49	1.0E-08	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4489	17623	30610	15.97	1.0E-08	U07681.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Mat protein (M8604 Mat) gene, complete cds
5215	18335	31308	1.18	1.0E-08	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5215	18335	31308	1.18	1.0E-08	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5342	18455	31422	0.72	1.0E-08	N65946.1	EST_HUMAN	zaz27a08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:263750 3'
5405	18507	31579	5.14	1.0E-08	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
5430	18630	31607	0.94	1.0E-08	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5430	18630	31607	0.94	1.0E-08	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-e04 FN0004 Homo sapiens cDNA
5592	18787	31834	1.04	1.0E-08	O60613	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
5915	19103		0.72	1.0E-08	BE05327.1	EST_HUMAN	CM0-BT0281-031189-087-h04 BT0281 Homo sapiens cDNA
7012	20148	33569	7.53	1.0E-08	P02871	SWISSPROT	FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR
7923	26223		0.73	1.0E-08	BE185330.1	EST_HUMAN	IL6-HT0730-020500-074-g01 HT0730 Homo sapiens cDNA
8190	21272		0.89	1.0E-08	AA912823.1	EST_HUMAN	d28c08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524878 3'
8468	21549	35079	1.12	1.0E-08	A347010.1	EST_HUMAN	qp54e02.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1926842 3'
8685	21765	35297					qv23f06.x1 NCI_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1882435 3' similar to contains element
8685	21765	35297	1.31	1.0E-08	A1287878.1	EST_HUMAN	MIR repetitive element :
9504	22770	36341	0.81	1.0E-08	N74635.1	EST_HUMAN	z855e01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:286472 3'
9578	22721	36291	0.81	1.0E-08	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9884	22924	36507	3.47	1.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9884	22924	36508	3.47	1.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
9929	22869	36558	5.22	1.0E-08	AA132611.1	EST_HUMAN	z017e08.r1 Stratiogene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 6'
9991	23030		3.55	1.0E-08	AA449267.1	EST_HUMAN	z04d11.s1 Soares fetal_liver_Nb2HF8_Hv Homo sapiens cDNA clone IMAGE:785493 3' similar to
10705	23738		2.19	1.0E-08	AL163203.2	NT	g5:D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
11849	24935		3.1	1.0E-08	AW890841.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12369	25366	32041	8.24	1.0E-08	L78810.1	NT	RC4-NT0054-120500-012-b03 NT0054 Homo sapiens cDNA
371	13680	26613	1.95	9.0E-07	AF003529.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
371	13580	26614	1.95	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8602	21683		0.69	9.0E-07	AL163280.2	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
11525	24581	38267	1.83	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C080
4893	18023	31008	4.23	8.0E-07	AI288608.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
							ql82g07.x1 Soares_NHMFu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF-SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4893	18023	31009	4.23	8.0E-07	A1288588.1	EST_HUMAN	q182g07.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:187887/8 3'
6007	19182		8.17	8.0E-07	P21414	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8101	21273		8.44	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11821	24907		5.84	8.0E-07	T07770.1	EST_HUMAN	EST05660 Fetal brain, Strelagene (cat#838206) Homo sapiens cDNA clone HFBEN89
12183	25143		6.1	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1814	15057	28167	0.97	7.0E-07	AF187341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL-1RAP) gene, exons 10 and 11
5636	18830	31808	0.88	7.0E-07	G055700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5636	18830	31807	0.88	7.0E-07	G055700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
1862	15105	28205	3.47	6.0E-07	AW855558.1	EST_HUMAN	CN3-CT0277-221089-024-e11 CT0277 Homo sapiens cDNA
							Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds: cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helixase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes;>
2561	15686	28812	2.43	6.0E-07	AF018413.1	NT	HYPOHETICAL 24.1 RD PROTEIN IN LEF4-P33 INTERGENIC REGION
4080	17236		1.74	6.0E-07	P41479	SWISSPROT	7g94f07.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920 4F5L.1
9342	22418	36972	1.31	8.0E-07	BF001867.1	EST_HUMAN	CN3-BT0281-031188-087-a03 BT0281 Homo sapiens cDNA
12115	25095	38800	1.45	8.0E-07	BE063508.1	EST_HUMAN	CN4-NN1028-250300-121-112 NN1028 Homo sapiens cDNA
12444	26087		1.72	6.0E-07	AW803222.1	EST_HUMAN	hu11h06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168328 3' similar to contains L1.52 L1 L1
13229	25992		1.32	6.0E-07	BE223980.1	EST_HUMAN	repetitive element;
336	13549		1.04	5.0E-07	A1831893.1	EST_HUMAN	wh84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1082	14248		2.39	6.0E-07	AA390630.1	EST_HUMAN	EST06815 Supt cells Homo sapiens cDNA 5' and
3086	16272		0.73	5.0E-07	A1831893.1	EST_HUMAN	wh84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
4769	17804	30886	0.97	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
6247	18421	32767	1.33	5.0E-07	U85087.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
							Ig06505.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu
7210	20076	33487	1.71	5.0E-07	A1393981.1	EST_HUMAN	repetitive element contains element A3R repetitive element;
							Ig06505.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu
7210	20075	33488	1.71	5.0E-07	A1393981.1	EST_HUMAN	repetitive element contains element A3R repetitive element;
							xa31e02.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2588362 3' similar to gb-X15341
7503	20578	34050	18.93	5.0E-07	AW070885.1	EST_HUMAN	CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8470	21551	35081	1.02	5.0E-07	Q9WUQ1	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN
8887	21767		0.89	5.0E-07	P09593	SWISSPROT	MOTIFS 1) (ADAM-TS1) (ADAM-TS1)

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10577	23612	37217	5.47	5.0E-07	A1908587.1	EST_HUMAN	GM-BT178-220499-014 BT178 Homo sapiens cDNA
11805	24766	39493	5.69	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11880	24868		2.08	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12256	25988		1.2	5.0E-07	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
12918	26966		3.08	5.0E-07	AW662537.1	EST_HUMAN	QV0-CT0383-210400-204-612 CT0383 Homo sapiens cDNA
4106	17290	30261	1.88	4.0E-07	AW009602.1	EST_HUMAN	ws84h05.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2804697 3'
7328	20410		0.8	4.0E-07	AJ272285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7417	20465	33963	0.97	4.0E-07	Q92ZV6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7417	20495	33964	0.97	4.0E-07	Q92ZV6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
8107	21189	34709	0.51	4.0E-07	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
9251	22328	35875	4.9	4.0E-07	AW419734.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
10332	23367	36976	0.63	4.0E-07	BE001975.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956651 5'
10332	23367	36977	0.53	4.0E-07	BE001976.1	EST_HUMAN	601676748F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956651 5'
10531	23566	37174	0.56	4.0E-07	AL163216.2	NT	Homo sapiens chromosome 21 segment HS21C018
11179	24248	37881	3.88	4.0E-07	AJ765528.1	EST_HUMAN	wi81b08.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2398703 3'
11179	24248	37882	3.88	4.0E-07	AJ765528.1	EST_HUMAN	wi81b08.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2398703 3'
11495	24553		1.69	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-012 BN0083 Homo sapiens cDNA
11819	24905		1.32	4.0E-07	BE967557.1	EST_HUMAN	601649083F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932924 5'
13207	25788		1.71	4.0E-07	11437071	NT	Homo sapiens deleted in lymphocytic leukemia, 1 (DLEU1), mRNA
454	13650	26896	5.39	3.0E-07	U19719.1	NT	Human microfilin-associated glycoprotein (MIFAP2) gene, putative promoter region and alternatively spliced
598	13786	26806	3.59	3.0E-07	AJ271735.1	NT	untitrated exons
1405	14559	27633	1.43	3.0E-07	M99149.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1659	14808		3.62	3.0E-07	M64857.1	NT	Human polymorphic microsatellite DNA
2104	15243		2.32	3.0E-07	AA526763.1	EST_HUMAN	Human Igk subgroup I germline gene, exons 1 and 2, V-region 018 allele
2361	15492	28621	1.14	3.0E-07	M89149.1	NT	Human Igk subgroup I germline gene, exons 1 and 2, V-region 018 allele
2540	15665	28789	4.99	3.0E-07	BE005077.1	EST_HUMAN	element contains L1.13 L1 repetitive element
2540	15665	28790	4.69	3.0E-07	BE005077.1	EST_HUMAN	Human polymorphic microsatellite DNA
3099	16275	29289	0.97	3.0E-07	T84704.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3228	16402	29414	1.78	3.0E-07	P38739	SWISSPROT	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
4802	17937		0.64	3.0E-07	P20740	EST_HUMAN	Y450F12.f1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:111695 5'
4849	17992	30970	8.04	3.0E-07	AV650201.1	EST_HUMAN	HYPOPHYSAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4885	18015	30999	0.7	3.0E-07	AJ787236.1	EST_HUMAN	OVOSTATIN PRECURSOR (OVOMACROGLOBULIN)
							AV650201 GLC Homo sapiens cDNA clone GLOCCD01 3'
							w86b612.x1 Soares_NFL_T_GEC_S1 Homo sapiens cDNA clone IMAGE:2347987 3'

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6175	18297	31259	1.43	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb-M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
6175	18297	31260	1.43	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb-M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
6783	18975	32281	12.38	3.0E-07	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6895	18276	32805	0.7	3.0E-07	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
6842	19995		6.09	3.0E-07	AA815175.1	EST_HUMAN	cc04c10.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339890 3'
7678	20743	34224	3.53	3.0E-07	AW707168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UN0038 Homo sapiens cDNA
7841	20898		1.3	3.0E-07	AI591065.1	EST_HUMAN	tw28h11.x1 NCL CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element; contains element MSR1 MSR1 repetitive element ;
9330	22406	35959	0.48	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
9330	22406	35960	0.48	3.0E-07	P33240	SWISSPROT	CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT (CSTF 64 KD SUBUNIT) (CF-1 64 KD SUBUNIT)
13184	25777		4.26	3.0E-07	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
29	13267	26270	7.32	2.0E-07	AF262988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
158	13383	26413	6.06	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
158	13383	26414	6.06	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
186	13408	26437	35.88	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic (vascular) actin gene, complete cds
767	13948	26995	1.48	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
767	13948	26996	1.48	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
779	13959		1.36	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POL. POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ; ENDONUCLEASE]
968	14139	27200	2.32	2.0E-07	AA223260.1	EST_HUMAN	zr08b07.s1 Stralagene NT2 neuronal precursor 837230 Homo sapiens cDNA clone IMAGE:850869 3' similar to gb:L31860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element
967	14140	27201	2.02	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element ;
1189	14351	27409	1.55	2.0E-07	O26768	SWISSPROT	IIG AUTOANTIGEN
1630	14782	27868	2.06	2.0E-07	Q09701	SWISSPROT	HYPOPHYSICAL 72.5 KD PROTEIN C27.10 IN CHROMOSOME 1
3708	16868		0.63	2.0E-07	BF131397.1	EST_HUMAN	601818916F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3779	16940	28946	21.71	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5238	18360		0.6	2.0E-07	AW902219.1	EST_HUMAN	QV3-NN1023-280400-168-h11 NN1023 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5460	18680	31638	1.52	2.0E-07	AW89066.1	EST_HUMAN	RC3-NN0066-260400-021-g11 NN0066 Homo sapiens cDNA
6881	26826	33229	0.73	2.0E-07	AW448968.1	EST_HUMAN	U1H-B13-aka-b-01-QUI.s1 NCL_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2734008 3'
6802	18957	33357	3.39	2.0E-07	AI208715.1	EST_HUMAN	q05d05.X1 Soares_fetalis_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
8864	21744		3.87	2.0E-07	AV729390.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone H1CAEG02 5'
8893	21672	35508	1.11	2.0E-07	AA035198.1	EST_HUMAN	2427g09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471808 3'
8863	23002		1.44	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10474	23509	37122	6.34	2.0E-07	AW882507.1	EST_HUMAN	CM4-NN0003-280300-124-408 NN0003 Homo sapiens cDNA
10708	23739	37342	1.01	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
10706	23739	37343	1.01	2.0E-07	P00751	SWISSPROT	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
12138	26855		2.06	2.0E-07	BE15317.1	EST_HUMAN	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B)
12226	25967		2.38	2.0E-07	AI732492.1	EST_HUMAN	(GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
1128	14291		0.76	1.0E-07	AL163282.2	NT	PM0-HT0339-260100-006-H07 HT0339 Homo sapiens cDNA
2888	14704	27784	2.08	1.0E-07	P09256	SWISSPROT	z18sh11.x5 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:365029 3' similar to contains THR.b2 THR repetitive element
3838	14291		1.24	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4408	17560	30534	2.81	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLGCFNF04 5'
4408	17550	30535	2.81	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLGCFNF04 5'
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), cellitactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and U>
6832	19761	33180	0.8	1.0E-07	U82671.2	NT	
7006	20142	33560	4.69	1.0E-07	BE047871.1	EST_HUMAN	tz43d08.y1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2281339 5'
7006	20142	33561	4.69	1.0E-07	BE047871.1	EST_HUMAN	tz43d08.y1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2281339 5'
7662	20729	34205	7.6	1.0E-07	N55081.1	EST_HUMAN	y43c07.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:245484 3'
7828	20881	34382	0.69	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7828	20881	34383	0.69	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7854	20809	34413	1.24	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
8410	21491	35020	2.76	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8410	21491	35021	2.78	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
9155	22233	35776	2.7	1.0E-07	AA693576.1	EST_HUMAN	z18t10.s1 Soares_fetal_liver_spleen_TNFSL_S1 Homo sapiens cDNA clone IMAGE:434346 3'
							ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAM-TS8) (ADAM-TS9) (MEITH-2)
9470	22527	36090	1.05	1.0E-07	P57110	SWISSPROT	



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9816	22856	36438	0.6	1.0E-07	BE327843.1	EST_HUMAN	hu28h06.x1 NCI_CGAP_Mel16 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
10140	23178	36778	2.35	1.0E-07	BF874524.1	EST_HUMAN	MER18 repetitive element;
10149	23187	36784	1.23	1.0E-07	AA386311.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
10582	23716		1.22	1.0E-07	AL163282.2	NT	EST185054 Brain IV Homo sapiens cDNA
12085	25065	36771	2.35	1.0E-07	AI341136.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
12505	25539	31761	3.37	1.0E-07	BE048770.1	EST_HUMAN	q88603.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2009682 3'
12558	25438		1.45	1.0E-07	X64467.1	NT	h33ct11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:085722 O85722
12852	25563		2.1	1.0E-07	X51755.1	NT	DJ1163J1.1;
7433	20510	33682	0.75	9.0E-08	AI539382.1	EST_HUMAN	H. sapiens ALAD gene for porphobilinogen synthase
10091	23129	36732	2.04	8.0E-08	AV734919.1	EST_HUMAN	Human lambda3a-immunoglobulin constant region complex (germline)
11457	24517	38185	1.92	9.0E-08	AI891032.1	EST_HUMAN	hs51b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2080195 3'
11665	24850	36656	2.38	9.0E-08	AL163301.2	NT	AV734819 cda Homo sapiens cDNA clone cdABF806 5'
12458	26320		2.51	9.0E-08	AJ251973.1	NT	h330a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446832 3' similar to contains OFR.12
622	16017		2.09	8.0E-08	AI911352.1	EST_HUMAN	OFR repetitive element;
1075	14241		1.01	8.0E-08	BE795469.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
3334	16788		1.57	8.0E-08	BE795469.1	EST_HUMAN	Homo sapiens partial steerin-1 gene
8937	22018	36657	6.35	8.0E-08	AI752367.1	EST_HUMAN	wd16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
8937	22018	35558	5.35	8.0E-08	AI752387.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943978 5'
8927	22867	36449	3.03	8.0E-08	AW970693.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943978 5'
10788	23821	37445	0.48	8.0E-08	AF111167.2	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
11523	24678		1.73	8.0E-08	AF253417.1	NT	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
82	13317	26345	3.91	7.0E-08	Q02357	SWISSPROT	EST1382778 IMAGE resequences, MAGK Homo sapiens cDNA
1392	14346	27822	19.51	7.0E-08	X04809.1	NT	Homo sapiens Jun dimerization protein gene; partial cds; cfos gene, complete cds; and unknown gene
3666	16828	29839	0.86	7.0E-08	P15305	SWISSPROT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
3666	16828	29840	0.88	7.0E-08	P15305	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
5332	18445	31413	0.62	7.0E-08	T65691.1	EST_HUMAN	Rat mRNA for ribosomal protein L31
11052	24129		1.73	7.0E-08	AI635743.1	EST_HUMAN	DYNEIN HEAVY CHAIN (DYHC)
11970	24955	36658	4.1	7.0E-08	U24070.1	NT	DYNEIN HEAVY CHAIN (DYHC)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12978	16823	26839	1.84	7.0E-08	P16305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
12978	16823	26840	1.84	7.0E-08	P16305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
840	14018	27073	3.3	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
840	14018	27074	3.3	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2436	15594	28693	1.77	6.0E-08	BE144398.1	EST_HUMAN	MRD-HT0168-191189-004-q09 HT0168 Homo sapiens cDNA
3129	16305	29319	0.88	6.0E-08	7662473	NT	Homo sapiens KIAA1074 protein (KIAA1074), mRNA
4383	17506	30487	1.15	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8137	21219		0.59	6.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8529	22594		0.55	6.0E-08	AA827075.1	EST_HUMAN	ob56c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1335388 3' similar to contains MER12.b3 MER12 repetitive element ;
11701	24088	38390	2.16	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
11823	24812		1.43	6.0E-08	AL163209.2	NT	ENDONUCLEASE
87	13322	26350	2.17	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C009
2309	16441	28578	3.93	5.0E-08	AA493851.1	EST_HUMAN	rh03b09.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element;
12185	25144		4.55	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12392	26271	32077	1.77	5.0E-08	AW851878.1	EST_HUMAN	QV0-CT0225-131089-034-a12 CT0225 Homo sapiens cDNA
1789	14948	28040	1.03	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLL-0ID PROTEIN PRECURSOR
1799	14948	28041	1.03	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLL-0ID PROTEIN PRECURSOR
2860	16127		1.06	4.0E-08	AL079581.1	EST_HUMAN	DKFZp434J0426.J1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434J0426 5'
3132	18308		1.01	4.0E-08	AI078417.1	EST_HUMAN	cd05e02.x1 Soares_fetal_liver_spleen_1NF15_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to contains Alu repetitive element;
4024	17180	30189	0.85	4.0E-08	U82688.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6535	18698	33071	1.07	4.0E-08	P62824	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
6998	22077	35617	0.9	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9340	22416	36869	1.13	4.0E-08	L42571.1	NT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
8845	22865		1.65	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10336	23571		0.85	4.0E-08	AI016342.1	EST_HUMAN	cd78d12.s1 Soares_fetal_tumor_Nb2HF8_9v Homo sapiens cDNA clone IMAGE:1622903 3'
10597	23632	37241	4.75	4.0E-08	AI050027.1	EST_HUMAN	ar22d10.x1 Gessler_Wilms tumor Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element; contains element MER22 (repetitive element) ;
11328	24391	38037	5.16	4.0E-08	AA393827.1	EST_HUMAN	z7f6b08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579 G505579 NA/JCA-K-EXCHANGER ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11328	24391	38098	5.16	4.0E-08	AA393627.1	EST_HUMAN	z76508.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728247 5' similar to TR:G505579
11349	24411	38064	11.86	4.0E-08	BF692493.1	EST_HUMAN	G505579 NAICA.K-EXCHANGER. ;
11349	24411	38065	11.86	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
12190	26108		1.83	4.0E-08	W76159.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
12804	26598		2.01	4.0E-08	A1343353.1	EST_HUMAN	z485g03.r1 Soares_fetal_heart_NbHH19W/Homo sapiens cDNA clone IMAGE:345555 5' similar to contains L1.11 L1 repetitive element ;
5728	18921	32216	2.27	3.0E-08	BE018348.1	EST_HUMAN	1b95a11.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2062078 3' similar to contains MER18.B3
7115	18541	31488	8.01	3.0E-08	A1792737.1	EST_HUMAN	MER18 MER18 repetitive element ;
7111	20776	34282	1.43	3.0E-08	AL163246.2	NT	bb78a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z168 Q9Z168
7928	20978		3.32	3.0E-08	AK436352.1	EST_HUMAN	SYNTAXIN 17. ;
10102	23140		0.63	3.0E-08	AF050566.1	NT	gs78f11.y5 NCI_CGAP_PT28 Homo sapiens cDNA clone IMAGE:1944045 5'
11278	24343	37893	1.64	3.0E-08	A1218001.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
11957	24942	38646	1.32	3.0E-08	AF111167.2	NT	th93h09.x1 Soares_NSIF_F8_gW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126273 3' similar to TR:Q13537 Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
12156	28125		33.85	3.0E-08	R18420.1	EST_HUMAN	Homo sapiens MHC class 1 region
211	13434		4.16	2.0E-08	AW302996.1	EST_HUMAN	qh21a04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846294 3'
236	13458		5.76	2.0E-08	AA425598.1	EST_HUMAN	Homo sapiens Jun dimerization protein gene, partial cds; cfc3 gene, complete cds; and unknown gene
509	13703	28732	4.46	2.0E-08	AF189349.1	NT	y00204.r1 Soares_infant_brain_1N1B Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element ;
677	13863	28893	9.7	2.0E-08	AW888438.1	EST_HUMAN	xr87f05.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767139 3'
677	13863	28894	9.7	2.0E-08	AW888438.1	EST_HUMAN	zr448f07.r1 Soares_testis_Nb2HFB_9y/Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element ; contains element MER16 repetitive element ;
1014	14188		7.75	2.0E-08	BE280477.1	EST_HUMAN	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
1373	14528	27602	1.46	2.0E-08	AL163247.2	NT	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1774	14923	28017	0.98	2.0E-08	AW841890.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1760	14929		2.08	2.0E-08	BE734671.1	EST_HUMAN	MRO-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1902	15045		6.7	2.0E-08	AW270271.1	EST_HUMAN	601165321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
2608	15732		1.86	2.0E-08	K00216.1	NT	Homo sapiens chromosome 21 segment HS21C047
3279	18453	29474	5.61	2.0E-08	O42280	SWISSPROT	IL5-CN0024-030300-026-C01 CN0024 Homo sapiens cDNA
							601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845189 5'
							xp43f11.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
							Sheep Hic-IRNA-GUG
							WNT-14 PROTEIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3279	16453	29475	5.61	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3682	17120		1.63	2.0E-08	AW813820.1	EST_HUMAN	RC3-ST0197-1G1099-012-b03 ST0197 Homo sapiens cDNA
4189	17339	30332	0.62	2.0E-08	UB2668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4525	17664		1.49	2.0E-08	AA459040.1	EST_HUMAN	aa26c07.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element ;
5072	18200		3.5	2.0E-08	AW572881.1	EST_HUMAN	he17f08.x2 NCL_CGAP_GML1 Homo sapiens cDNA clone IMAGE:2919327 3' similar to contains Alu repetitive element
5763	18945	32247	0.85	2.0E-08	AA813204.1	EST_HUMAN	al80h1.1 sf Soares testis NHT Homo sapiens cDNA clone 1377189 3'
5965	19141	32457	1	2.0E-08	AW088924.1	EST_HUMAN	xd32c04.x1 NCL_CGAP_OV29 Homo sapiens cDNA clone IMAGE:2595482 3' similar to contains MER18.b3 MER18 MER18 repetitive element ;
6193	21275	34798	1.11	2.0E-08	P10272	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8301	21363	34604	1.5	2.0E-08	AA490121.1	EST_HUMAN	ab02g06.e1 Striatogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'
9286	22362		0.89	2.0E-08	AA439978.1	EST_HUMAN	AU138978 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'
10738	23771	37381	0.89	2.0E-08	N78097.1	EST_HUMAN	yw72f02.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element ;
10738	23771	37382	0.83	2.0E-08	N78097.1	EST_HUMAN	yw72f02.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1.b3 LTR1 repetitive element ;
12476	26329		1.77	2.0E-08	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
13065	26159		1.8	2.0E-08	11431676	NT	Homo sapiens hypothetical protein FLJ11342 (FLJ11342), mRNA
1539	16041	27770	1.05	1.0E-08	P31792	SWISSPROT	POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
1672	14824	27807	1.33	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)
1672	14824	27808	1.33	1.0E-08	P13002	SWISSPROT	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1)
1816	14865	28058	1.66	1.0E-08	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
2110	15248		2.97	1.0E-08	BE141959.1	EST_HUMAN	PM2-H10130-150999-001-112 HT0130 Homo sapiens cDNA
3261	18435	29453	0.66	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP5232
3261	18435	29454	0.95	1.0E-08	BE246844.1	EST_HUMAN	TCBAP1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP5232
5716	19809	32204	4.51	1.0E-08	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
7846	20890	34507	0.94	1.0E-08	P10474	SWISSPROT	52 KD RO PROTEIN (SIOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8224	21306	34826	0.62	1.0E-08	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8320	21402	34927	0.54	1.0E-08	AF224680.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8320	21402	34928	0.54	1.0E-08	AF224680.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8744	21823	35358	2.27	1.0E-08	AI016304.1	EST_HUMAN	alpha3503.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1618736 3'
9405	22479		0.56	1.0E-08	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
9406	22480	36043	0.85	1.0E-08	BE072572.1	EST_HUMAN	PM2-BT0546-210100-004-d02 BT0546 Homo sapiens cDNA
10171	23208	36801	0.84	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP)
10778	23811	37434	0.87	1.0E-08	P88083	SWISSPROT	(TRICARBOXYLATE CARRIER PROTEIN)
11595	24048	36332	3.55	1.0E-08	AF044083.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12581	25391		3.06	1.0E-08	X51755.1	NT	Homo sapiens major histocompatibility locus class III region
13137	25825		1.26	1.0E-08	BF375398.1	EST_HUMAN	Human lambda-immunoglobulin constant region complex (germline)
4357	17500	30481	4.17	9.0E-09	AL163279.2	NT	MR4-ST0240-240700-013-g04 ST0240 Homo sapiens cDNA
4357	17500	30482	4.17	9.0E-09	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
10287	23302		0.63	9.0E-09	T97950.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
7414	20492	33960	8.1	8.0E-09	AI183500.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS1 Homo sapiens cDNA clone IMAGE:121918 3'
8189	21271	34798	2.54	8.0E-09	AW800159.1	EST_HUMAN	qd42e07.x1 Soares fetal heart NbhH19W/Homo sapiens cDNA clone IMAGE:1732184 3' similar to contains MSR1.t1 MSR1 repetitive element ;
9189	22267		2.53	8.0E-09	AA838892.1	EST_HUMAN	CM0-NN1004-100300-273-e08 NN1004 Homo sapiens cDNA
							qp74d08.s1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'
3695	16856		1.98	7.0E-09	D86842.1	NT	Homo sapiens DNA for 3-ketoadyl-CoA thiolase beta-subunit of mitochondrial trifunctional protein, exon 2, 3
4115	17269		0.98	7.0E-09	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
8088	21168		0.59	7.0E-09	BF108755.1	EST_HUMAN	7145e10.x1 Soares NSF F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element ;
8237	21319		0.99	7.0E-09	AA256200.1	EST_HUMAN	zr80cd5.r1 Soares NHHMPu_S1 Homo sapiens cDNA clone IMAGE:881992 5' similar to contains L1.12 L1 repetitive element ;
9460	22517	36080	2.86	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10386	23421	37028	1.95	7.0E-09	BE254850.1	EST_HUMAN	60111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
10564	23589		0.76	7.0E-09	AA058826.1	EST_HUMAN	zr59e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.12 L1 repetitive element ;
10910	23993		2.01	7.0E-09	T97950.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS1 Homo sapiens cDNA clone IMAGE:121918 3'
2221	15355		0.95	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0514 5'
5095	18223	31195	6.2	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-h05 HT0527 Homo sapiens cDNA

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## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6498	18696	31711	9.33	6.0E-09	AW195784.1	EST_HUMAN	xn85h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8775	21854	35398	1.11	8.0E-09	BE181653.1	EST_HUMAN	MR3-HT0448-260300-201-h12 HT0448 Homo sapiens cDNA
9377	22452	36014	2.18	8.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10483	23518		3.4	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds contains MER29.b2 MER29 repetitive element;
10989	24049	37882	1.86	6.0E-09	BF108755.1	EST_HUMAN	745a10.x1 Soares_NSF_F8_9W_OT_PA_IP_S1 Homo sapiens cDNA
12089	25069	38776	1.37	6.0E-09	C01803.1	EST_HUMAN	HUMGS0003762 Human adult (K Okubo) Homo sapiens cDNA
1447	14800	27677	3.47	5.0E-09	BE149284.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
1800	15043	28154	7.4	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6640	19703	33075	2.22	5.0E-09	AA359464.1	EST_HUMAN	EST68748 Fetal lung II Homo sapiens cDNA 5' end
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
6988	18507	31523	0.56	5.0E-09	U68059.1	NT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
8785	21864	35407	0.83	5.0E-09	P37071	SWISSPROT	PM2-JM0059-240300-005-c09 JM0053 Homo sapiens cDNA
10300	23395	36940	3.25	5.0E-09	AW798667.1	EST_HUMAN	zx60e09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795880 3'
11944	24830	38632	1.87	5.0E-09	AA460142.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
534	13727		1.64	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C085
987	14159		2.75	4.0E-09	AL163285.2	NT	Homo sapiens hypothetical protein (AF038159), mRNA
1497	14860	27732	1.86	4.0E-09	9558718	NT	EST15385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
2500	15627	28747	5.32	4.0E-09	AA350878.1	EST_HUMAN	zx04c06.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:768298 5'
8030	21113	34631	0.53	4.0E-09	AA495747.1	EST_HUMAN	yd11a07.s1 Soares_fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:86804 3'
8719	21769	35334	1.02	4.0E-09	T84942.1	EST_HUMAN	wn94f10.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443627 3'
11330	24393	38041	9.51	4.0E-09	A1886401.1	EST_HUMAN	zx34a12.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:865278 5' similar to gb:L07807
11379	24440		1.44	4.0E-09	AA195142.1	EST_HUMAN	DYNAMIN-1 (HUMAN);
							hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2427	18555	28682	4.51	3.0E-09	BE222239.1	EST_HUMAN	MER18 repetitive element;
2819	15742	28856	1.06	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
2716	15834	28944	0.69	3.0E-09	P23249	SWISSPROT	MER18 repetitive element;
							PROTEIN MOV-10
3408	16576	29593	0.9	3.0E-09	BE222239.1	EST_HUMAN	hu09e09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13
							MER18 repetitive element;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3484	16631		0.7	3.0E-09	AA442272.1	EST_HUMAN	z64a04.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4212	17361		0.82	3.0E-09	X16874.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
4546	17694	30666	3.47	3.0E-09	AF175325.1	NT	Homo sapiens oukaryotic initiation factor 4A1 (EIF4A1) gene, partial cde
4634	17770	30751	1.19	3.0E-09	Q9Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0893)
8084	21166	34682	1.1	3.0E-09	BE465780.1	EST_HUMAN	h280a02.x1 NCI_CGAP_Kid117 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O55091
10453	23488	37096	1.87	3.0E-09	AL163247.2	NT	O55091 IMPACT PROTEIN.;
10782	23826	37448	0.46	3.0E-09	Q10940	SWISSPROT	Homo sapiens chromosome 21 segment HS21C047
11272	24340	37878	3.15	3.0E-08	BF109843.1	EST_HUMAN	HYPOTHETICAL 13.1 KD PROTEIN B0310.4 IN CHROMOSOME X
11272	24340	37978	3.15	3.0E-08	BF109843.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
835	14013		0.98	2.0E-08	X16874.1	NT	7172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
1287	14443	27511	4.7	2.0E-09	AL163284.2	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1691	14843		10.71	2.0E-09	AL118573.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
2403	15534	28661	2.24	2.0E-09	Q9Y3R5	SWISSPROT	DKF26761B1710_r1 761 (synonym: harny2) Homo sapiens cDNA clone DKF2p761B1710 5'
4048	17204	30214	3.01	2.0E-09	O60241	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0893)
4119	17273	30272	0.9	2.0E-09	AI263478.1	EST_HUMAN	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
5264	18363	31348	0.82	2.0E-09	M23161.1	NT	q107d09.x1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1855793 3'
5837	19027	32333	0.87	2.0E-09	AI004082.1	EST_HUMAN	Human transposon-like element mRNA
6278	19452		0.75	2.0E-09	AL163249.2	NT	q147609.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619897 3'
6919	20234		0.88	2.0E-09	AA357407.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C049
7609	20679	34155	8.81	2.0E-09	AA461430.1	EST_HUMAN	EST66142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7692	20757	34242	0.66	2.0E-09	W28834.1	EST_HUMAN	z63h06.r1 Soares_testis_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786187 5' similar to contains
7871	21021	34534	0.59	2.0E-09	AI243732.1	EST_HUMAN	Alu repetitive element;
8909	21888	35528	1.2	2.0E-09	AJ271735.1	NT	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
10824	23857	37480	0.85	2.0E-09	AV988642.1	EST_HUMAN	gh88g10.x1 Soares_NFL_T_CGEC_S1 Homo sapiens cDNA clone IMAGE:1864114 3'
12745	14013		20.08	2.0E-09	X16874.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12830	20168		1.89	2.0E-09	AA226070.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
1019	14190		1.19	1.0E-09	W78152.1	EST_HUMAN	AV688642 GKG Homo sapiens cDNA clone GKACACAT1 5'
1133	14268	27353	1.43	1.0E-09	5031624	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1133	14268	27354	1.43	1.0E-09	5031624	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1133	14268	27354	1.43	1.0E-09	5031624	NT	nc11c02.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;
1133	14268	27354	1.43	1.0E-09	5031624	NT	zdf79d03.s1 Soares_fetal_heart_NbH119W Homo sapiens cDNA clone IMAGE:346863 3' similar to
1133	14268	27354	1.43	1.0E-09	5031624	NT	gbLQ2992 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1133	14268	27354	1.43	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1133	14268	27354	1.43	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2571	16396		1.15	1.0E-09	A1356088.1	EST_HUMAN	qy4e11.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2016812.3' similar to contains MER12.12 MER12 repetitive element;
2854	16131	29148	2.02	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (snm) genes, complete cds
2892	16168	29184	6.17	1.0E-09	M29699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
2892	16168	29185	6.17	1.0E-09	M29699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3103	16279	29283	0.99	1.0E-09	BE535440.1	EST_HUMAN	601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3446177.5'
4820	18050		8.15	1.0E-09	AA719287.1	EST_HUMAN	zh35b03.s1 Soares_pined_gland_NGHPG Homo sapiens cDNA clone IMAGE:414029.3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
5341	18454		0.6	1.0E-09	AA921958.1	EST_HUMAN	cm44g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1543942.3'
5620	18814	31882	0.85	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6652	19138	32454	1.29	1.0E-09	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
6272	19446	32704	3.34	1.0E-09	P26694	SWISSPROT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
8584	21665	35206	0.92	1.0E-09	A1688474.1	EST_HUMAN	w039605.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481.3' similar to contains MER25.11 MER25 repetitive element;
10520	23555		2.72	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12642	28120	31688	1.71	1.0E-09	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
12767	26510		1.42	1.0E-09	T57366.1	EST_HUMAN	y651g12.s1 Strategene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:74758.3'
13132	26020		1.66	1.0E-09	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
1337	14484	27564	1.52	9.0E-10	AW867740.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
2895	16074	28092	3.74	9.0E-10	A1870071.1	EST_HUMAN	w078h03.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2347253.3' similar to SW-RL29_HUMAN P-7614.60S RIBOSOMAL PROTEIN L29; contains element PTR5 repetitive element;
6973	20201	33627	4.88	9.0E-10	A1452982.1	EST_HUMAN	y46609.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144637.3' similar to TR:O00372 O00372 PUTATIVE P150.;
151	13376	26408	9.26	8.0E-10	U63630.2	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
3423	16592	29607	0.66	8.0E-10	BE080748.1	EST_HUMAN	QV71-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
4318	17461	30446	5.43	8.0E-10	AA376832.1	EST_HUMAN	EST89584 Small Intestine 1 Homo sapiens cDNA 5' end
10170	23207		2.51	8.0E-10	U36308.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
719	13901	26941	21.38	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC61686), mRNA
719	13901	26942	21.38	7.0E-10	7706225	NT	Homo sapiens TPA inducible protein (LOC61686), mRNA
1651	14904	27890	2.58	7.0E-10	Q13942	SWISSPROT	LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
2626	15749		20.25	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3167	16332	29341	2.25	7.0E-10	X00855.1	NT	H.sapiens DHFR gene, exon 3



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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6314	19486	32841	4.06	7.0E-10	AA345220.1	EST_HUMAN	EST61247 Gall bladder II Homo sapiens cDNA 5' end
7574	20846	34124	1.37	7.0E-10	BF362883.1	EST_HUMAN	IL3-HT0619-110700-209-D12 HT0619 Homo sapiens cDNA
7834	20899		1.85	7.0E-10	P35084	SWISSPROT	CNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8163	21245	34764	1.54	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
8163	21246	34765	1.54	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
836	14111	27171	8.44	6.0E-10	AJ400877.1	NT	Homo sapiens ASOL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2742	15859	28971	1.83	6.0E-10	A1424405.1	EST_HUMAN	h02007.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2095021 3'
4815	17752	30733	1.88	6.0E-10	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
4861	17894		3.15	6.0E-10	AW853719.1	EST_HUMAN	RC3-CT0254-031095-012-g12 CT0254 Homo sapiens cDNA
6983	22062	35602	0.96	6.0E-10	P33730	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
6983	22062	35603	0.96	6.0E-10	P33730	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
9834	22874	36458	0.48	6.0E-10	P86073	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
12223	25172		1.95	6.0E-10	AW971923.1	EST_HUMAN	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
780	13960		5.29	5.0E-10	AL048804.1	EST_HUMAN	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
3564	18729	28745	1.14	5.0E-10	Q01033	SWISSPROT	EST364012 IMAGE resequences, MAGI Homo sapiens cDNA
5103	18233	31202	1.4	5.0E-10	AF181897.1	NT	DKFZp434N219.1 434 (synonym: h16c3) Homo sapiens cDNA clone DKFZp434N219 5'
7478	20560		1.85	5.0E-10	BF105159.1	EST_HUMAN	HYPOTHETICAL GENE 48 PROTEIN
9736	22801	36374	2.24	5.0E-10	P34678	SWISSPROT	Homo sapiens WRN (WRN) gene, complete cds
9736	22801	36375	2.24	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
							HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
12040	26021	38725	1.31	5.0E-10	AF091415.1	NT	Macaca tonkeana isolate 669tonkeana NADH dehydrogenase subunit 4L gene, complete cds; and NADH dehydrogenase subunit 4 gene, mitochondrial genes encoding mitochondrial proteins, partial cds
114	13345		1.09	4.0E-10	A1221083.1	EST_HUMAN	qg09f08.x1 Soares_placenta_8b9weeks_2YbHP8b9W Homo sapiens cDNA clone IMAGE:1759049 3' similar to contains LTR8.b2 LTR8 repetitive element
2062	15163	28308	1.4	4.0E-10	AW594709.1	EST_HUMAN	hg55g03.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element
2640	15763	28877	6.79	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7327	20409	33871	17.76	4.0E-10	AF224869.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
10398	23433	37039	0.71	4.0E-10	AW293243.1	EST_HUMAN	U1-H-B12-eh-a-07-D-J1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727081 3'
10962	23696	37305	1.12	4.0E-10	A1287342.1	EST_HUMAN	ec63h11.x1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035853

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10794	23827	37450	0.54	4.0E-10	BE169208.1	EST_HUMAN	PM1-HT0521-120200-001-f08 HT0521 Homo sapiens cDNA
10794	23827	37451	0.54	4.0E-10	BE169208.1	EST_HUMAN	PM1-HT0521-120200-001-f08 HT0521 Homo sapiens cDNA
839	14112	27173	2.24	3.0E-10	N98113.1	EST_HUMAN	y42f08.s1 Soares melanocyte 2NHIM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.1 L1 repetitive element;
1382	14537		5.3	3.0E-10	AY005160.1	NT	Homo sapiens extracellular glycoprotein lactoferrin precursor, gene, complete cds
4657	17753	30777	0.94	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4657	17753	30778	0.94	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
6360	18463	31428	0.89	3.0E-10	L34078.1	NT	Human XRCC1 DNA repair gene, genomic
5571	18787	31808	0.78	3.0E-10	N50109.1	EST_HUMAN	Human XRCC1 DNA repair gene, genomic
6332	18503	32861	2.06	3.0E-10	P20350	SWISSPROT	RHOMBOD PROTEIN (VEINLET PROTEIN)
6481	18648	33010	3.82	3.0E-10	BE302870.1	EST_HUMAN	bat6d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2908319 5'
7637	20987	34495	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
7637	20987	34488	1.42	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
8928	22007	35548	1.57	3.0E-10	H87208.1	EST_HUMAN	y574b12.s1 Soares retina Nzb4HR Homo sapiens cDNA clone IMAGE:220611 3' similar to contains MER29 repetitive element;
9249	22326	35872	1.52	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9249	22326	35873	1.52	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B06 CT0219 Homo sapiens cDNA
9541	22606		0.78	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10679	23713		1.95	3.0E-10	T65891.1	EST_HUMAN	yc11612.r1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:80398 5'
10820	23853		0.96	3.0E-10	AA769284.1	EST_HUMAN	nc38g03.s1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:1289908 3'
12641	25619	31877	1.87	3.0E-10	BE178517.1	EST_HUMAN	IL3-HT0618-110500-138-E07 HT0618 Homo sapiens cDNA
38	13274	26278	2.08	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN 3 (CENTROMERE PROTEIN B) (CENP-B)
36	13274	26278	2.08	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN 3 (CENTROMERE PROTEIN B) (CENP-B)
1946	15086		1.66	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
3051	16227		0.84	2.0E-10	BF875047.1	EST_HUMAN	602136640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5924	19111		2.3	2.0E-10	Q28640	SWISSPROT	(HPRG)
6380	19549	32905	1.66	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450
7537	20610	34084	6.41	2.0E-10	BE791082.1	EST_HUMAN	polypeptide 5 (CYP3A5) gene, partial cds
8203	21285	34807	0.58	2.0E-10	P28909	SWISSPROT	601588208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'
8203	21285	34808	0.58	2.0E-10	P28909	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
8203	21285	34808	0.58	2.0E-10	P28909	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9502	22558		1.06	2.0E-10	BF434565.1	EST_HUMAN	7078d08.x1 NCL_CGAP_K1a11 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.13 L1 repetitive element:
11609	24632		1.33	2.0E-10	AI862153.1	EST_HUMAN	1a10f12.x1 Soares fetal_tetus_Nb2HFB_9y Homo sapiens cDNA clone IMAGE:2043695 3'
1538	14691		3.09	1.0E-10	AW867767.1	EST_HUMAN	MR0-SN0038-280300-001-001 SN0038 Homo sapiens cDNA
1637	14789	27874	3.37	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCCXA11 3'
2649	15772		2.16	1.0E-10	AW852001.1	EST_HUMAN	QV0-C10225-191199-058-e08 C10225 Homo sapiens cDNA
3689	16763	29768	0.9	1.0E-10	AW852912.1	EST_HUMAN	QV2-TT0003-181199-013-g10 TT0003 Homo sapiens cDNA
3829	16793		0.87	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
3947	16793		0.78	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N1317 5'
4123	17277		7.33	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4245	17391	30378	18.24	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy/protein >
4245	17391	30379	18.24	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy/protein >
4253	17399	30388	1.76	1.0E-10	AB031069.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, last exon
4285	17430		2.28	1.0E-10	M30829.1	NT	Human sapiens PCCX1 mRNA for protein containing CXC domain 1, complete cds
5277	18398		1.01	1.0E-10	A1707745.1	EST_HUMAN	W83204.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains MER31.1 MER31 repetitive element:
7044	20713		0.59	1.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7850	20914	34419	0.69	1.0E-10	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'
8434	21616	36048	1.14	1.0E-10	AW408990.1	EST_HUMAN	7B_6A4 Fetal brain library Homo sapiens cDNA
8855	21834		1.62	1.0E-10	AI298340.1	EST_HUMAN	qm04610.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1880874 3' similar to contains L1.11 L1 repetitive element:
10406	23441		6.24	1.0E-10	AA081888.1	EST_HUMAN	2n23g06.r1 Stragelene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548314 5'
11164	24223	37834	3.3	1.0E-10	AI038280.1	EST_HUMAN	cy65h03.x1 Soares_fetal_liver_spleen_1NF1.S_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
12165	18503		1.8	1.0E-10	X87344.1	NT	H.sapiens DNA, DMB, HLA-Z1, JPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
272	13480	26521	0.87	8.0E-11	BE145600.1	EST_HUMAN	IL2-HT0203-291089-016-c08 HT0203 Homo sapiens cDNA
2171	15306	28433	6.02	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
2171	15306	28434	6.02	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3470	16637	29657	2.98	9.0E-11	AL134396.1	EST_HUMAN	DKFZp547D225.t1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5'
3470	16637	29658	2.98	9.0E-11	AL134396.1	EST_HUMAN	DKFZp547D225.t1 547 (synonym: hfr1) Homo sapiens cDNA clone DKFZp547D225 5'
4622	17759	30741	0.8	9.0E-11	AA775989.1	EST_HUMAN	ae78f01.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:970297 3'
5892	18868		3.05	9.0E-11	BE079780.1	EST_HUMAN	RC6-BT0827-140200-011-E06 BT0827 Homo sapiens cDNA
10357	23392	37002	1.17	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10357	23392	37003	1.17	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
12556	25378	32072	2.45	9.0E-11	C16635.1	EST_HUMAN	C16635 Clontech human aorta p4ya+ mRNA (#9572) Homo sapiens cDNA clone GEN-508508 5'
3185	16360		10.53	8.0E-11	H19971.1	EST_HUMAN	yn53f11.s1 Soares adult brain N25h5HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element;
4154	17306	30300	5.37	8.0E-11	N23712.1	EST_HUMAN	yn46e06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255298 3'
5913	19101	32415	0.66	8.0E-11	AW674318.1	EST_HUMAN	ba60g04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800982 3'
6811	19965		0.82	8.0E-11	AW166159.1	EST_HUMAN	x44h11.x1 NCI_CGAP_Brm50 Homo sapiens cDNA clone IMAGE:2621081 3' similar to contains MER10.t1 MER10 repetitive element;
1479	14832	27717	2.09	7.0E-11	AA330642.1	EST_HUMAN	EST34392 Embryo, 6 week I Homo sapiens cDNA 5' end
8695	21775	35307	2.61	7.0E-11	AF163884.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10434	23459		1.37	7.0E-11	P11399	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
425	13620	26681	6.19	8.0E-11	M55270.1	NT	Human matrix Gla protein (MGSP) gene, complete cds
425	13620	26682	6.19	8.0E-11	M55270.1	NT	Human matrix Gla protein (MGSP) gene, complete cds
6862	20014	33424	0.91	8.0E-11	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
7870	20824	34431	3.5	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8559	21640	35179	0.89	8.0E-11	AV727659.1	EST_HUMAN	AV727659 HTC Homo sapiens cDNA clone HTCASC06 5'
9514	22579	36145	0.5	6.0E-11	BE063509.1	EST_HUMAN	CMO-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
12	13250	26250	1	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3450	13250	26250	1.24	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6846	19804	33181	1.92	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7699	20764	34248	11.57	5.0E-11	11416798	NT	Homo sapiens prolactin beta 3 (PCHB3), mRNA
1433	14586		1.39	4.0E-11	AA436042.1	EST_HUMAN	z01b12.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:730559 5'
2851	15965	29074	9.84	4.0E-11	BE885900.1	EST_HUMAN	601507631F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3809295 5'
3034	16210	29233	1.26	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4740	17875	30858	0.81	4.0E-11	D44666.1	EST_HUMAN	HUMSUPY089 Human brain cDNA Homo sapiens cDNA clone 069
6905	19765	33194	3.29	4.0E-11	P20085	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2

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Table 4

## Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7141	20276	33718	0.82	4.0E-11	AA442630.1	EST_HUMAN	z/59110.1 Soares_testis_NHT: Homo sapiens cDNA clone IMAGE:757863 5' similar to TR:G1055250
7532	20605						G1055260 PHEROMONE RECEPTOR VN4:
9595	22650						Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
							(UBE2D3) genes, complete cds
8882	22802	36487	0.79	4.0E-11	AI608753.1	EST_HUMAN	RC1-HT0255-210100-013-008 HT0258 Homo sapiens cDNA
10859	23892	37513	0.94	4.0E-11	BF367283.1	EST_HUMAN	tr2g12.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WP:ZK353.1
12794	25500	32008	1.71	4.0E-11	11545732	NT	CE00385:
1521	14874	27766	4	3.0E-11	6679077	NT	MR0-GN0024-180900-008-H09 GN0024 Homo sapiens cDNA
4391	17534		1.35	3.0E-11	AA309248.1	EST_HUMAN	Homo sapiens SH3-domain binding protein1 (SH3BP1), mRNA
882	14165	27215	1.43	2.0E-11	AI160502.1	EST_HUMAN	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
1212	14373	27434	20.98	2.0E-11	R24807.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
1212	14373	27435	20.98	2.0E-11	R24807.1	EST_HUMAN	qf36c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
1844	14798	27880	4.44	2.0E-11	L17432.1	NT	MER10 repetitive element:
1844	14798	27881	4.44	2.0E-11	L17432.1	NT	Yg43e12.1 Soares infant brain: INIB Homo sapiens cDNA clone IMAGE:35144 5'
2823	15937	29047	1.09	2.0E-11	AF087913.1	NT	Yg43e12.1 Soares infant brain: INIB Homo sapiens cDNA clone IMAGE:35144 5'
3266	18440	28461	5.96	2.0E-11	P10263	SWISSPROT	Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
3403	18573	28588	0.82	2.0E-11	AI478617.1	EST_HUMAN	COR3 beta (COR3 beta) genes, complete cds
							Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
3448	16618	29634	0.67	2.0E-11	Q10473	SWISSPROT	COR3 beta (COR3 beta) genes, complete cds
							Human endogenous retrovirus HERV-P-T47D
							RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
							tr54c09.x1 NCL_CGAP_K611 Homo sapiens cDNA clone IMAGE:2101938 3'
							POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP
							ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC-POLYPEPTIDE, N-
							ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
3566	16750		1.01	2.0E-11	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3797	18958	29962	0.64	2.0E-11	P70213	SWISSPROT	FRIEND VIRUS SUSCEPTIBILITY PROTEIN 1
4566	17704		1.07	2.0E-11	BE065637.1	EST_HUMAN	RC3-BT0318-170200-014-e05 BT0316 Homo sapiens cDNA
4728	17863		0.8	2.0E-11	AI163227.2	NT	Homo sapiens chromosome 21 segment H521C027
5051	18179		1.85	2.0E-11	BE062568.1	EST_HUMAN	QV2-BT0258-261099-014-e01 BT0258 Homo sapiens cDNA
							EST178228 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to alpha-2-
6142	18265	31234	0.82	2.0E-11	AA307331.1	EST_HUMAN	macroglobulin
6263	19437	32784	1.23	2.0E-11	AW877808.1	EST_HUMAN	QV2-PT0073-280300-109-H09 PT0073 Homo sapiens cDNA

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6440	19607	32970	2	2.0E-11	AA581028.1	EST_HUMAN	nc83h05.r1 NCI_CGAP_G01 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW.PR10_YEAST
7345	20425	33888	0.85	2.0E-11	BF592945.1	EST_HUMAN	P15838 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16.1
8086	21148		0.59	2.0E-11	P37072	SWISSPROT	7f97c03.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:3442565 3'
							OLFATORY RECEPTOR-LIKE PROTEIN COR6
9424	22498		1.39	2.0E-11	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
10491	23526	37135	5.13	2.0E-11	Q13608	SWISSPROT	OLFATORY RECEPTOR 5H1 (OLFATORY RECEPTOR-LIKE PROTEIN OLF1)
10734	23767	37376	1.09	2.0E-11	AW865874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10734	23767	37377	1.09	2.0E-11	AW865874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
11375	24436	38094	1.84	2.0E-11	AA035369.1	EST_HUMAN	2k27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11375	24436	38095	1.84	2.0E-11	AA035369.1	EST_HUMAN	2k27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794 3'
11408	24468	38133	1.4	2.0E-11	AA281850.1	EST_HUMAN	2k18b04.r1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:685519 5'
12122	25102	38807	12.19	2.0E-11	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
12297	26105		1.85	2.0E-11	AA704195.1	EST_HUMAN	7f97e03.s1 Soares_fetal_liver_spleen_INFUS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
12328	26237		1.44	2.0E-11	AW842143.1	EST_HUMAN	RC2-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
12354	26256	32115	2.15	2.0E-11	BF377859.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12641	26431		1.43	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12813	25542		3.62	2.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
13180	26767		2.5	2.0E-11	11417968	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
693	13876	26909	1.57	1.0E-11	AJ131016.1	NT	Homo sapiens SCL gene locus
808	13968	27038	1.72	1.0E-11	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1244	14403	27484	2.91	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1628	14681		1.82	1.0E-11	AF119814.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2095	15235	28356	0.94	1.0E-11	P16258	SWISSPROT	OXYSTEROL-BINDING PROTEIN
2195	15330	28455	3.69	1.0E-11	AF000573.1	NT	Homo sapiens homogenate 1,2-dioxygenase gene, complete cds
2229	15363	28492	1.1	1.0E-11	AA309318.1	EST_HUMAN	EST180188 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end similar to EST containing Alu repeat
3588	18752	28787	0.95	1.0E-11	BE004315.1	EST_HUMAN	CM2-BN0705-170300-292-d12 BN0705 Homo sapiens cDNA
5447	18847	31625	14.68	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
							7e57d01.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3648945 3' similar to contains MER10.b3
5953	19139	32455	0.78	1.0E-11	BF222846.1	EST_HUMAN	MER10 repetitive element;
8398	21477	35004	2.65	1.0E-11	4885546	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
8781	21860	35403	4.61	1.0E-11	R13174.1	EST_HUMAN	y73d08.r1 Soares_infant_brain_1N1B Homo sapiens cDNA clone IMAGE:28168 5'
9248	22325	35870	1.49	1.0E-11	BF365119.1	EST_HUMAN	QV4-NN1149-250900-423-g03 NN1149 Homo sapiens cDNA

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8248	22325	35871	1.49	1.0E-11	BF365118.1	EST_HUMAN	QV4-NN1149-250900-423-603 NN1149 Homo sapiens cDNA
10626	23660		0.54	1.0E-11	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
11566	24621	38302	2.02	1.0E-11	BF680078.1	EST_HUMAN	602154807FT NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285977 5'
12903	26879		1.37	1.0E-11	Z20377.1	EST_HUMAN	HSAAACADH P, Human fetal Brain Whole tissue Homo sapiens cDNA
3017	16193	28216	0.75	9.0E-12	P20742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
10002	23040	36632	1.17	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
10002	23040	36633	1.17	9.0E-12	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9539	22604		0.88	8.0E-12	BE074720.1	EST_HUMAN	IL5-BT0578-130300-038-G12 BT0578 Homo sapiens cDNA
12408	25267		4.88	8.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4783	17918	30905	1.57	7.0E-12	Q08904	SWISSPROT	34 KD SPICULE MATRIX PROTEIN PRECURSOR (LSM34)
11631	24711	38402	6.8	7.0E-12	AA704735.1	EST_HUMAN	z23g01.s1 Soares_fetal_liver_spleen_influs_s1 Homo sapiens cDNA clone IMAGE:451152 3'
13225	25903		1.18	7.0E-12	D16473.1	NT	Human mRNA, Xq terminal portion
3637	16801		0.86	8.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF06 5'
4468	17608	30586	9.23	8.0E-12	AA732516.1	EST_HUMAN	rz8811.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element
5336	18449	31418	5.12	8.0E-12	AI459161.1	EST_HUMAN	i95g12.x1 Soares_NSF_F8_gw_OT_PA_F_S1 Homo sapiens cDNA clone IMAGE:2148438 3' similar to contains MER10.12 MER10 MER10 repetitive element:
9196	22274	35811	1.09	6.0E-12	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9876	22637		1.81	6.0E-12	AB47898.1	EST_HUMAN	cd10g11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1387888 similar to contains MER29.12 MER29 repetitive element:
13205	25766		1.25	6.0E-12	AW885846.1	EST_HUMAN	RC4-O10072-060400-012-111 O10072 Homo sapiens cDNA
1066	14234	27283	2.37	5.0E-12	T06573.1	EST_HUMAN	EST04462 Fetal brain, Striatum (cat#938266) Homo sapiens cDNA clone HFB0V33
3477	16844	29683	1.28	6.0E-12	BE047779.1	EST_HUMAN	t42d05.y1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291217 5'
3821	16881	28984	7.44	6.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6145	19323	32866	6.13	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6145	19323	32667	6.13	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6620	19760	33168	9.99	5.0E-12	AW974760.1	EST_HUMAN	EST386850 IMAGE reassessment, MAGN Homo sapiens cDNA
7176	20052	33462	1.06	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B1615 3'
7187	20052	33462	0.93	5.0E-12	AL040739.1	EST_HUMAN	DKFZp434B1615_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B1615 3'
8424	21606	35038	1.28	6.0E-12	AA033745.1	EST_HUMAN	z01g12.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1 L3 L1 repetitive element:
8867	21946		0.56	5.0E-12	AW887037.1	EST_HUMAN	RC1-O10086-220300-011-607 O10086 Homo sapiens cDNA
9195	22273		0.77	6.0E-12	AL079581.1	EST_HUMAN	DKFZp434J0426_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434J0426 5'
8808	22384	35636	2.92	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9823	22878	36247	1.22	5.0E-12	P34982	SWISSPROT	OLFATORY RECEPTOR 1D2 (OLFATORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFATORY RECEPTOR 17-4) (OR17-4)
10482	23517		4.8	5.0E-12	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10573	23608	37213	0.69	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10793	23823	37449	0.6	5.0E-12	6978754	NT	Rattus norvegicus Deleted in colorectal cancer (rat homolog) (Dcc), mRNA
254	13474	28503	3.29	4.0E-12	AA700326.1	EST_HUMAN	Z74g11.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
255	13474	28505	3.42	4.0E-12	AA700326.1	EST_HUMAN	Z74g11.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4742	17877	30860	0.88	4.0E-12	AI899984.1	EST_HUMAN	b28h05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE.;
7797	20853		0.71	4.0E-12	BF445140.1	EST_HUMAN	na21b03.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3368077 3' similar to contains MER7.b2 MER7 repetitive element.;
8437	21518		4.81	4.0E-12	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
11338	24401	38050	4.33	4.0E-12	AJ228043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
12884	25455		2.11	4.0E-12	U78027.1	NT	Homo sapiens Bruton's tyrosine Kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
631	13816	26839	2.58	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP.;
631	13816	26840	2.58	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517 O14517 SMRP.;
5276	18365	31363	0.78	3.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5568	18765	31806	1.44	3.0E-12	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
5870	21651	35183	0.5	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSPIN
10891	23975	37606	2.32	3.0E-12	U37872.1	NT	Human prostate specific antigen gene, 5' flanking region
10891	23975	37607	2.32	3.0E-12	U37872.1	NT	Human prostate specific antigen gene, 5' flanking region
1685	14837	27821	1.24	2.0E-12	AW802131.1	EST_HUMAN	IL5-JM0071-120400-085-a05 UM0071 Homo sapiens cDNA
3556	16721	29736	0.83	2.0E-12	6754495	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4230	17377	30365	1.28	2.0E-12	J01894.1	NT	Rat U3A small nuclear RNA
4230	17377	30366	1.28	2.0E-12	J01894.1	NT	Rat U3A small nuclear RNA
4541	17879		2.03	2.0E-12	BE063809.1	EST_HUMAN	CM6-BT0281-031198-087-a03 BT0281 Homo sapiens cDNA
5018	18147	31123	0.71	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
5018	18147	31124	0.71	2.0E-12	O70306	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
6008	18766		2.08	2.0E-12	AW971857.1	EST_HUMAN	EST363946 IMAGE resseques, MAGI, Homo sapiens cDNA
7328	20408	33870	3.85	2.0E-12	T08189.1	EST_HUMAN	ES T08090 Infant Brain, Bonto Soares Homo sapiens cDNA clone HIBBA13 5' end



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7499	20574	34047	1.33	2.0E-12	BE173035.1	EST_HUMAN	MFO-HT0559-200400-015-608 HT0559 Homo sapiens cDNA
7838	20893	34395	2.19	2.0E-12	11422229	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
9508	22774		1.88	2.0E-12	AF196894.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
10191	23228		8.32	2.0E-12	BE165980.1	EST_HUMAN	M/R3-HT0487-160200-113-g01 HT0487 Homo sapiens cDNA
10733	23766	37375	0.78	2.0E-12	AI334130.1	EST_HUMAN	qq0702.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1831835 3' similar to TR:Q13538
12120	25109	38813	1.53	2.0E-12	AW242834.1	EST_HUMAN	Q13538 ORF2: FUNCTION UNKNOWN ;
12313	25228		1.34	2.0E-12	AL183283.2	NT	Homo sapiens chromosome 21 segment HS21C083
12516	25352		1.46	2.0E-12	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
125	13354	26385	1.64	1.0E-12	AW827674.1	EST_HUMAN	hm90a08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2870040 3' similar to contains MER18.11
2044	15185		1.78	1.0E-12	AI871728.1	EST_HUMAN	MER18 repetitive element ;
3138	16314	28326	1.04	1.0E-12	AF000991.1	NT	wm5107.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1
3138	16314	28327	1.04	1.0E-12	AF000991.1	NT	repetitive element ;
3978	17135	30138	40.43	1.0E-12	AU132248.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
3978	17135	30139	40.43	1.0E-12	AU132248.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 2 (TTY2) mRNA, partial cds
6088	18289		1.6	1.0E-12	U82828.1	NT	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' -
6165	18342		1.82	1.0E-12	Q87207	SWISSPROT	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5' -
6282	18455	32804	0.59	1.0E-12	BF642800.1	EST_HUMAN	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
6282	19455	32805	0.59	1.0E-12	BF642800.1	EST_HUMAN	HYPOPHYSICAL ZINC FINGER PROTEIN KIAA0981
6662	18821	33208	0.83	1.0E-12	AF229843.1	NT	EST00008 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
7265	20348	33800	2.53	1.0E-12	AF186884.1	NT	EST00008 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1847869 5'
7300	20382	33840	10.78	1.0E-12	AI248533.1	EST_HUMAN	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane
7300	20382	33841	10.78	1.0E-12	AI248533.1	EST_HUMAN	conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
							Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
							q66a04.x1 Soares_fetal_liver_spleen_1NF1.S_S1 Homo sapiens cDNA clone IMAGE:1849514 3' similar to
							gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10
							repetitive element ;
							q66a04.x1 Soares_fetal_liver_spleen_1NF1.S_S1 Homo sapiens cDNA clone IMAGE:1849514 3' similar to
							gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.11 MER10
							repetitive element ;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
8686	21768	35298	0.59	1.0E-12	U66059.1	NT	ec2a005.s1 Stralagene ovary (#937217) Homo sapiens cDNA clone IMAGE:857577 3'
8902	21081	35521	1.25	1.0E-12	AA782323.1	EST_HUMAN	EST374237 MAGE sequences, MAGG Homo sapiens cDNA
12215	26168	38835	2.92	1.0E-12	AW062164.1	EST_HUMAN	w33h09.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2392095 3'
12437	26310		1.54	1.0E-12	AI738592.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C088
12800	26088		1.93	1.0E-12	AL163288.2	NT	PROBABLE TONB-DEPENDENT RECEPTOR H10712 PRECURSOR
12788	26168		1.19	1.0E-12	P44836	SWISSPROT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12951	25681		2.82	1.0E-12	AF224693.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
4050	17212	30223	1.21	9.0E-13	AB029900.1	NT	za28b06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:293651 3'
9801	22841		2.81	9.0E-13	N89653.1	EST_HUMAN	Homo sapiens prion protein (PrP) gene, complete cds
735	13917	26957	5.03	8.0E-13	U29188.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
735	13917	26958	5.03	8.0E-13	U29185.1	NT	Homo sapiens basic transcription factor 2 p14 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nail) and survival motor neuron protein (smn) genes, complete cds
1885	15029	28138	2.73	8.0E-13	U80017.1	NT	wm31h09.x1 NCI_CGAP_U44 Homo sapiens cDNA clone IMAGE:2437601 3'
8303	21385	34908	0.63	8.0E-13	A1894398.1	EST_HUMAN	wm31h09.x1 NCI_CGAP_U44 Homo sapiens cDNA clone IMAGE:2437601 3'
8303	21385	34907	0.63	8.0E-13	A1884398.1	EST_HUMAN	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
10360	23385		2.82	8.0E-13	U78027.1	NT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
9429	21510		0.77	7.0E-13	Q05155	SWISSPROT	601463285F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866613 5'
12713	25474		32	7.0E-13	BE778223.1	EST_HUMAN	POLYPEPTIDE N-ACETYLGLALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACETYLGLALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGLALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
12976	25635		1.53	7.0E-13	Q10473	SWISSPROT	Homo sapiens chromosome 21 segment HS21C007
2168	16303	28430	5.85	6.0E-13	AL163207.2	NT	qo44a09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1811352 3'
6239	16391	31329	0.93	8.0E-13	AI267928.1	EST_HUMAN	y82h04.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5'
3399	16569		1.15	5.0E-13	R78338.1	EST_HUMAN	z177a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu repetitive element/contains dement MER22 (repetitive element); GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
3484	16652		1.56	5.0E-13	AA435773.1	EST_HUMAN	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
7018	20162	33572	0.99	5.0E-13	P08983	SWISSPROT	PM2-HT0224-221098-001-e11 HT0224 Homo sapiens cDNA
11100	24173	37808	2.84	5.0E-13	P07313	SWISSPROT	
1918	15059		4.88	4.0E-13	AW378614.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2531	15656		1.91	4.0E-13	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
4869	18002		1.08	4.0E-13	AA454054.1	EST_HUMAN	zfx8d07.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795469 5'
6704	18897	32189	4.47	4.0E-13	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
7355	20434	33998	1.09	4.0E-13	AB037760.1	NT	Homo sapiens mRNA for KIAA1329 protein, partial cds
7788	20844	34337	1.08	4.0E-13	AA431529.1	EST_HUMAN	zw76g12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763
							G452763 COR1 MRNA ;
7898	20850		2.82	4.0E-13	N444291.1	EST_HUMAN	y93g05.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32995
9042	22121	35683	1.38	4.0E-13	AL043810.1	EST_HUMAN	322985 t complex sterility protein - mouse ;
9702	22731	36321	0.47	4.0E-13	AA076907.1	EST_HUMAN	DKFP494AA0128_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFP494AA0128 5'
10228	23262	36850	4.44	4.0E-13	A1269831.1	EST_HUMAN	7B04H11 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B04H11
11439	24500	38167	1.54	4.0E-13	AA435819.1	EST_HUMAN	gn32d05.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1898945 3' similar to contains Aliu
11439	24500	38168	1.54	4.0E-13	AA435819.1	EST_HUMAN	repetitive element ;
							z178g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
							z178g10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
184	13408		4.35	3.0E-13	AF003528.1	NT	
888	14084		1.81	3.0E-13	AA430310.1	EST_HUMAN	zxv8g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781408 5'
1502	14855	27737	0.88	3.0E-13	A1804151.1	EST_HUMAN	GM-BT043-090299-075 BT043 Homo sapiens cDNA
2443	15571	28700	1.93	3.0E-13	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2548	15673		2.28	3.0E-13	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2729	15847	28957	3.69	3.0E-13	BF372862.1	EST_HUMAN	GM3-PT0100-140700-242-H08 FT0100 Homo sapiens cDNA
3256	16430		2.44	3.0E-13	AA745844.1	EST_HUMAN	cb18d02.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1324035 3'
3592	16756	28771	9.73	3.0E-13	P18816	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
3592	16766	28772	9.73	3.0E-13	P18816	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
							zn18h10.r1 Stratagene lung carcinoma 9372718 Homo sapiens cDNA clone IMAGE:565315 5' similar to
							contains THR.12 THR repetitive element ;
5657	18851	32193	0.68	3.0E-13	AA134017.1	EST_HUMAN	zn18h10.r1 Stratagene lung carcinoma 9372718 Homo sapiens cDNA clone IMAGE:565315 5' similar to
5657	18851	32194	0.88	3.0E-13	AA134017.1	EST_HUMAN	contains THR.12 THR repetitive element ;
6114	19294	32829	0.73	3.0E-13	AA005639.1	EST_HUMAN	w269c02.x1 NCI_CGAP_Bin26 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:O75139
							O75139 KIAA0644 PROTEIN. ;
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 8 (DUSP8), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
8067	21149	34880	7.1	3.0E-13	U52111.2	NT	

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8268	21350	34865	0.6	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra-reactive factor
8268	21350	34866	0.6	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' end similar to similar to serine protease P100, Ra-reactive factor
10401	23436	37043	0.58	3.0E-13	AW935487.1	EST_HUMAN	RC2-DT0007-110100-014-g10 DT0007 Homo sapiens cDNA
10915	23938		3.1	3.0E-13	AI054768.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Homo sapiens cDNA
11301	24367	38008	3.41	3.0E-13	BE063506.1	EST_HUMAN	CN0-BT0281-031189-087-a03 BT0281 Homo sapiens cDNA
11898	24886	38585	1.62	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
154	13379	26411	3.52	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
249	13470	26502	2.06	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor, 4 mRNA, complete cds
1269	14455	27621	8.93	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3070	16246	29266	0.61	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3070	16246	29267	0.61	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3595	16780	29778	1.88	2.0E-13	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
4224	17372		2.07	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6250	18424	32770	4.34	2.0E-13	Q08852	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
6335	19506		0.58	2.0E-13	X79417.1	NT	S.scrofa tp812 mRNA for ribosomal protein S12
6954	20267	33704	5.73	2.0E-13	X16912.1	NT	Human PFKL gene for liver-type 6-phosphofructokinase (EC 2.7.1.11) exon 2
7169	20064	33474	0.6	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NM/T1), mRNA
7189	20064	33475	0.6	2.0E-13	10835072	NT	Homo sapiens N-myristoyltransferase 1 (NM/T1), mRNA
10675	23709	37317	2.41	2.0E-13	5031898	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
12389	25274		22.49	2.0E-13	AW892155.1	EST_HUMAN	CN0-NN0001-100300-274-s11 NN0001 Homo sapiens cDNA
302	13518	26561	1.34	1.0E-13	S74129.1	NT	FGF-1 fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
911	14086	27151	5.53	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1367	14521	27596	1.4	1.0E-13	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2079	15219	28339	2.61	1.0E-13	AA720574.1	EST_HUMAN	hw21g02.s1 NCI_CGAP GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.3 THR repetitive element.
4715	17850	30833	1.32	1.0E-13	BF340987.1	EST_HUMAN	602036006F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4185868 5'

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8094	21178	34891	0.97	1.0E-13	AA577812.1	EST_HUMAN	nm24401.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
8094	21178	34892	0.97	1.0E-13	AA577812.1	EST_HUMAN	nm24401.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu repetitive element; contains element MER24 repetitive element;
10256	23330		1.04	1.0E-13	O15481	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN B4 (IMAGE-B4 ANTIGEN)
10508	23643	37154	0.6	1.0E-13	AF300701.1	NT	Mus musculus osteoblastic protein tyrosine phosphatase mRNA, complete cds
11681	24740	38431	9.74	1.0E-13	BF108755.1	EST_HUMAN	745610.x1 Soares NSF_F8_QW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
12206	25160		1.38	1.0E-13	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
12920	25605		3.48	1.0E-13	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
13077	25706		1.85	1.0E-13	X87578.1	NT	H. sapiens CD4 gene
343	13554	26583	3.78	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element;
344	13555	26584	1.84	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element;
2569	15994		4.13	9.0E-14	AW861577.1	EST_HUMAN	RC4-CT0322-080100-073-d09 CT0322 Homo sapiens cDNA
2811	15925	28038	7.9	9.0E-14	AB038182.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
3180	16355	28360	7.5	9.0E-14	AW513286.1	EST_HUMAN	xe54hp05.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2707833 3'
3310	13554	26583	1	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.t1 MER19 repetitive element;
3896	17057	30057	7.37	9.0E-14	D14547.1	NT	Human DNA, SINE repetitive element
4879	18010	30894	2.23	8.0E-14	AJ002153.1	NT	Saginus oedipus gene for seminal vesicle secreted protein semenogelin 1
3587	18751		1.17	8.0E-14	BE468263.1	EST_HUMAN	hiz71609.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
4068	17222		3.84	8.0E-14	R76269.1	EST_HUMAN	y72603.t1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144786 3'
9847	21090	34806	38.93	8.0E-14	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
9760	22898	36268	3.22	8.0E-14	AA219316.1	EST_HUMAN	zq17c10.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:628970 3'
11717	24757		1.79	8.0E-14	BE082693.1	EST_HUMAN	QV2-BT0258-261099-074-a01 BT0258 Homo sapiens cDNA
12811	25410	32048	2.43	8.0E-14	AI688118.1	EST_HUMAN	wc32h08.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2328143 3'
1658	16044		4.76	7.0E-14	AW151673.1	EST_HUMAN	x167a10.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
9120	22188		0.73	7.0E-14	AL163285.2	NT	MER10 repetitive element;
378	13588	26620	12.43	6.0E-14	AF020503.1	NT	Homo sapiens chromosome 21 segment HS21C085
							Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10027	23066	36562	2.19	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
10027	23066	36863	2.19	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
633	13818	26842	4.17	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5166	18288	31254	1.32	5.0E-14	AW073791.1	EST_HUMAN	xb03505.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1:12 L1 repetitive element:
5650	18944	32125	5.28	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1147	16030	P04928	1.61	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1926	15069	28174	10.15	4.0E-14	AJ007873.1	NT	Homo sapiens LGMD2B gene
3847	17007		0.73	4.0E-14	A4046502.1	EST_HUMAN	z667a08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
4407	17549	30533	1.04	4.0E-14	N46328.1	EST_HUMAN	y73c12.x1 Soares_multiple_sclerosis_2NBHMP Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1:13 L1 repetitive element:
8145	21227		0.71	4.0E-14	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, LMP7, TAP1, LMP7, TAP2, DOB, DOB2 and RING9, 9, 13 and 14 genes
12043	25024	38729	5.5	4.0E-14	BE242486.1	EST_HUMAN	TCAAP1D1470 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1470
12966	28203		5.59	4.0E-14	A1886224.1	EST_HUMAN	wm08c03.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element:
972	14145	27204	1.56	3.0E-14	X95469.1	NT	R.norvegicus mRNA for CPG2 protein
6873	20025	33434	0.93	3.0E-14	A1420786.1	EST_HUMAN	1891c12.x1 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE :
6873	20025	33435	0.93	3.0E-14	A1420786.1	EST_HUMAN	1891c12.x1 NCL_CGAP_P728 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE :
7173	20306	33749	0.6	3.0E-14	AA388311.1	EST_HUMAN	EST185054 Brain IV Homo sapiens cDNA
8887	22066	35606	0.86	3.0E-14	N42165.1	EST_HUMAN	y97b10.r1 Soares_melanocyte_2NBHM Homo sapiens cDNA clone IMAGE:270523 5'
11512	18496	31533	5.87	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCL_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element:contains element MER9 repetitive element:
12894	26041		1.98	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
13212	25894	31853	1.51	3.0E-14	BE891550.1	EST_HUMAN	601435233F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920189 5'
401	13598	26634	2.33	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
401	13598	26635	2.33	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
708	16019	26925	11.38	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2461	15588		1.04	2.0E-14	AW372868.1	EST_HUMAN	RC5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA
2535	15660		0.89	2.0E-14	7657529	NT	Homo sapiens rhadoid tumor deletion region protein 1 (RTDR1), mRNA
2593	15718	28835	1.63	2.0E-14	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5641	18835	31812	0.87	2.0E-14	BF380661.1	EST_HUMAN	IL2-JT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5738	18931	32229	1.03	2.0E-14	A1312351.1	EST_HUMAN	ta78h01.x2 NCL_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.3 L1 repetitive element;
5838	19028	32334	3	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
7023	20169		1.04	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-e08 BN0072 Homo sapiens cDNA
7437	20514	33987	1.06	2.0E-14	P68163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7676	20741	34221	24.48	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
7676	20741	34222	24.48	2.0E-14	BE158761.1	EST_HUMAN	IL2-HT0397-071289-024-D04 HT0397 Homo sapiens cDNA
10121	23159	36769	0.59	2.0E-14	A1978795.1	EST_HUMAN	wf59g10.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element;
10630	23684	37273	0.51	2.0E-14	AV741648.1	EST_HUMAN	U741648 CB Homo sapiens cDNA clone CBFBFBF04 5'
11018	24098	37736	3.62	2.0E-14	AW139800.1	EST_HUMAN	UJH-BI1-adv-a-10-Q-U1.s1 NCL_CGAP_Sub53 Homo sapiens cDNA clone IMAGE:2718234 3'
12890	26045		2.5	2.0E-14	AF008191.1	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
13163	15660		1.26	2.0E-14	7657529	NT	Homo sapiens rhadoid tumor deletion region protein 1 (RTDR1), mRNA
1092	14257	27313	2.32	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
1438	14591	27664	7.01	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1438	14591	27665	7.01	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2057	16198	28312	8.9	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
2258	15391	28517	6.33	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2480	15607	28731	8.44	1.0E-14	AF001689.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
3010	16186	29210	1.41	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3236	16410	29424	3.14	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3236	16410	29425	3.14	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3992	17149	30166	1.69	1.0E-14	AA682894.1	EST_HUMAN	ae86c12.s1 Stratiotes schizobrain S11 Homo sapiens cDNA clone IMAGE:971350 3'
4596	17793	30713	2.01	1.0E-14	AW276862.1	EST_HUMAN	xa39h10.x1 NCL_CGAP_Luz28 Homo sapiens cDNA clone IMAGE:2753059 3'
5830	19116	32429	1.96	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6813	25834	33371	10.9	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
6813	25834	33372	10.9	1.0E-14	11437150	NT	Homo sapiens prominin (mouse)-like 1 (PROML1), mRNA
1607	14760	27839	1.81	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR1), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2242	15375		1.38	9.0E-15	AF198779.1	NT	Homo sapiens transcription factor IGFBP3 enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel.
7665	20732	34207	4.24	9.0E-15	P21418	SWISSPROT	GAG POLYPROTEIN [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
8208	21288	34810	1.24	9.0E-15	BE93359.1	EST_HUMAN	60167750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960150 5'
13089	25716		2.87	9.0E-15	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2872	13687		1.53	8.0E-15	BE261482.1	EST_HUMAN	60114863F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
7331	20412	33874	1.13	7.0E-15	BF033327.1	EST_HUMAN	60145853F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3892086 5'
10650	23684		2.34	7.0E-15	AW241958.1	EST_HUMAN	Xn77d02.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element;
12270	25203		1.44	7.0E-15	AA284465.1	EST_HUMAN	Zs57d08.11 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701983 5' similar to gp.L21934 STEROL O-ACYLTRANSFERASE (HUMAN); contains L1 L1 L1 repetitive element;
1018	14180	27250	7.51	6.0E-15	AJ271793.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5283	18382		0.98	6.0E-15	AW601258.1	EST_HUMAN	CM4-NN1011-100300-110-310 NN1011 Homo sapiens cDNA
6041	19224	32546	1.02	6.0E-15	X73462.1	NT	O. aries mRNA for hair keratin cysteine-rich protein
6041	19224	32547	1.02	6.0E-15	X73462.1	NT	O. aries mRNA for hair keratin cysteine-rich protein
11583	26231		1.54	6.0E-15	AW836843.1	EST_HUMAN	QV1-LT0036-150200-070-c10 LT0036 Homo sapiens cDNA
423	13818	26858	3.57	5.0E-15	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
2819	15933	29044	1.76	5.0E-15	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5233	18355		0.91	5.0E-15	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
440	13240	26240	2.33	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6804	19959	33359	0.8	4.0E-15	AB007870.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
11318	21065	34577	2.11	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
11318	21065	34578	2.11	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4333	17476		7.57	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
5141	18264	31232	0.57	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5141	18264	31233	0.57	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6953	20266		1.11	3.0E-15	Q64625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7430	20507	33978	3.13	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7430	20507	33979	3.13	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds



Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10129	23167		2.38	3.0E-15	AA807128.1	EST_HUMAN	cc36a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11 MER19 repetitive element:
11033	24112	37748	8.11	3.0E-15	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12820	20081		65.8	3.0E-15	AJ271755.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
260	13478	26511	3.71	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
378	13587	26821	3.28	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
379	13587	26822	3.28	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1559	14712		0.99	2.0E-15	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
3599	16763	29778	0.72	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3599	16763	29779	0.72	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4745	17880		2.76	2.0E-15	AI806335.1	EST_HUMAN	wf07f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348923 3' similar to TR:Q81043 Q81043 NINEIN.
6311	19483	32838	1.11	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877268 5'
6311	19483	32839	1.11	2.0E-15	BE562352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3877268 5'
7283	20348		1.58	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7421	20498	33969	2.73	2.0E-15	AA704195.1	EST_HUMAN	z177603.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460824 3'
7554	20628	34102	5.05	2.0E-15	W05084.1	EST_HUMAN	z178d10.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:288575 5' similar to WPIF44F4.8 CE02227 TRANSPOSASE
9107	22188	35730	2.86	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
9273	22349	35898	0.91	2.0E-15	AA397758.1	EST_HUMAN	z177g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9273	22349	35900	0.91	2.0E-15	AA397758.1	EST_HUMAN	z177g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9604	22659	36231	1.18	2.0E-15	AW378465.1	EST_HUMAN	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
9604	22659	36232	1.18	2.0E-15	AW378465.1	EST_HUMAN	CM0-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
11077	24152		3.68	2.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
13016	16763	29778	3.89	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13016	16763	28779	3.99	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2834	15848		3.09	1.0E-15	AI689984.1	EST_HUMAN	t26h05.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE.
3077	16253	29275	1.42	1.0E-15	BE043584.1	EST_HUMAN	tk40e02.y1 NCL_CGAP_Ov34 Homo sapiens cDNA clone IMAGE:2989162 5'
3211	16385	29398	1.18	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4479	17819	30601	0.61	1.0E-15	BE182698.1	EST_HUMAN	RC3-HT0849-100500-022-b05 HT0849 Homo sapiens cDNA
6502	19868	33032	1.72	1.0E-15	T95763.1	EST_HUMAN	ye40e10.a1 Scars fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains
7149	20294		1.98	1.0E-15	BE074217.1	EST_HUMAN	MER6 repetitive element;
7184	20049	33480	0.78	1.0E-15	P36057	SWISSPROT	QV3-BT0569-270100-074-g05 BT0568 Homo sapiens cDNA
8427	21508	35040	0.99	1.0E-15	AL163280.2	NT	DYNEIN BETA CHAIN, CILIARY
8616	21696	35232	4.94	1.0E-15	AI200976.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
8615	21695	35233	4.94	1.0E-15	AI200976.1	EST_HUMAN	q68h06.x1 Scars testis NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9239	22316	35858	0.78	1.0E-15	AL163207.2	NT	q68h06.x1 Scars testis NHT Homo sapiens cDNA clone IMAGE:1755227 3'
9242	22319	35862	0.96	1.0E-15	4507208	NT	Homo sapiens chromosome 21 segment HS21C007
9448	22594	36127	0.99	1.0E-15	Q39575	SWISSPROT	Homo sapiens spermidine synthase (SRM) mRNA
9832	22872	36455	0.94	1.0E-15	AA864653.1	EST_HUMAN	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
11057	24194	37770	3.04	1.0E-15	AF044083.1	NT	ch37c03.e1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459972 3' similar to contains L1.13 L1 repetitive element;
13104	25892	31858	13.05	1.0E-15	AI783944.1	EST_HUMAN	Homo sapiens major histocompatibility locus class III region
4826	17762	30744	0.93	9.0E-16	4603188	NT	tg31c03.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219912 3' similar to contains Alu repetitive element;
11241	24310	37947	1.41	9.0E-16	F08888.1	EST_HUMAN	Homo sapiens cut (Drosophila)-like 1 (CCAA1 displacement protein) (CUTL1) mRNA
11895	24880	38885	1.48	9.0E-16	AI244341.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
11896	24880	38886	1.48	9.0E-16	AI244341.1	EST_HUMAN	q78a02.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3
5819	19009	32315	0.85	7.0E-16	4885120	NT	MER10 repetitive element;
7496	20571	34043	1.3	7.0E-16	O88807	SWISSPROT	q78a02.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3
7496	20571	34044	1.3	7.0E-16	O88807	SWISSPROT	MER10 repetitive element;
13043	25895		38.08	7.0E-16	T94149.1	EST_HUMAN	q78a02.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.t3
							Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
							PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
							(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
							PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
							(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
							ye28e12.r1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:118082 5'

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2208	15342		9.12	8.0E-16	AW972611.1	EST_HUMAN	EST384702 IMAGE resequences, MAGI Homo sapiens cDNA
1522	14875	27757	0.96	5.0E-16	AJ251154.1	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene cd90c04.s1 Scores total Tctus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:1623078 3' similar to contains element L1 repetitive element;
2745	15862	28973	2.21	5.0E-16	AA992176.1	EST_HUMAN	
11809	24709	39498	2.88	6.0E-16	BF217388.1	EST_HUMAN	601885734F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4104129 5'
13162	25749		14.16	5.0E-16	11418127	NT	Homo sapiens GTP binding protein 1 (GTRBP1), mRNA
2312	15444		1.01	4.0E-16	AB001523.1	NT	Homo sapiens gene for TMEM1 and PWP2, complete end partial cds
2453	15581	28708	2.87	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
2453	15581	28708	2.87	4.0E-16	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
3546	16711	29722	5.29	4.0E-16	Q16653	SWISSPROT	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4260	17405	30391	8.88	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
4260	17405	30392	8.69	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
5257	18377	31343	0.91	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7890	20942	34448	42.68	4.0E-16	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9495	22552	36114	0.72	4.0E-16	11423181	NT	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA
12293	25218		1.95	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12381	25270		8.66	4.0E-16	C05947.1	EST_HUMAN	C05947 Human pancreatic islet Homo sapiens cDNA clone hbc5355
12392	25277	32078	3.23	4.0E-16	C05947.1	EST_HUMAN	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12682	25454		1.33	4.0E-16	R18591.1	EST_HUMAN	Y88b11.1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:30489 5'
135	13361	26395	1.09	3.0E-16	AW022862.1	EST_HUMAN	df45c01.yt Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
136	13361	26396	1.09	3.0E-16	AW022862.1	EST_HUMAN	df45c01.yt Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
478	13873		1.56	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434P037 5'
488	13682		2.33	3.0E-16	AF135448.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1483	14536	27720	2.73	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
							ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3041	16217	29237	4.71	3.0E-16	P03200	SWISSPROT	au76508.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782163 5' similar to SW-KID1_MOUSE O61751 RENAL TRANSCRIPTION FACTOR KID-1;
4711	17848	30830	0.59	3.0E-16	AW160828.1	EST_HUMAN	AV661393 GLC Homo sapiens cDNA clone GLCGSA01 3'
5057	18185	31160	1.32	3.0E-16	AV661393.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5392	18594		0.99	3.0E-16	AA07725.1	EST_HUMAN	Homo sapiens glycan 3 (GPC3) gene, partial cds and flanking regions
6734	18927	32223	1.67	3.0E-16	AF003529.1	NT	am98h05.g1 Stragatena echino brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element;
8558	21937	35473	4.25	3.0E-16	AI002836.1	EST_HUMAN	

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
10094	23132		1.09	3.0E-16	EST_HUMAN	60224658F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
10324	23359	36969	2.59	3.0E-16	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
13187	26171	31557	3.62	3.0E-16	EST_HUMAN	DKFZp434L1623_r1 434 (synonym: hsa3) Homo sapiens cDNA clone DKFZp434L1623 5'
984	14168		1.03	2.0E-16	NT	Homo sapiens chromosome 21 segment HS21C079
2459	15596		0.96	2.0E-16	EST_HUMAN	af0804.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2753	15870		1.14	2.0E-16	NT	Human SNAV-related endogenous retroviral LTR-like element
4294	17437	30424	1.62	2.0E-16	NT	H. sapiens DNA for endogenous retroviral like element
4603	17740	30718	1.27	2.0E-16	EST_HUMAN	q95603.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839197 3' similar to contains MER28.13
5299	18418	31385	0.84	2.0E-16	EST_HUMAN	MER29 repetitive element;
6880	20032	33442	0.68	2.0E-16	SWISSPROT	RC3-BT0046-131199-003-H12 BT0048 Homo sapiens cDNA HISTIDINE-RICH PROTEIN KE4
7893	20945	34451	0.89	2.0E-16	EST_HUMAN	g18a11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element MER33 repetitive element;
8154	21236	34757	1.67	2.0E-16	EST_HUMAN	nz47103.x5 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1280947 similar to TR:054849 OS4849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:008905; contains MER7.11 MER7 repetitive element;
8352	21433	34957	0.81	2.0E-16	EST_HUMAN	782h09.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
8352	21433	34958	0.81	2.0E-16	EST_HUMAN	782h09.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3303521 3'
8724	21804	35340	0.78	2.0E-16	EST_HUMAN	CM4-PT0034-180200-506-a01 P T0034 Homo sapiens cDNA
8724	21804	35341	0.78	2.0E-16	EST_HUMAN	CM4-PT0034-180200-506-a01 P T0034 Homo sapiens cDNA
189	13411	26438	2.28	1.0E-16	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
393	13650		22.93	1.0E-16	EST_HUMAN	af39g11.s1 Soares_testis_Nb2-IF8_gw Homo sapiens cDNA clone IMAGE:1034084 3' similar to contains OFR.12 OFR repetitive element;
2026	15189	28276	3.42	1.0E-16	EST_HUMAN	QV0-BN0148-070700-293-a10 BN0148 Homo sapiens cDNA
5839	19029	32335	0.6	1.0E-16	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6565	19727		18	1.0E-16	NT	Homo sapiens COR8 chemokine receptor (CMKBR8) gene, complete cds
6704	18892	33252	2.96	1.0E-16	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7726	19727		6.39	1.0E-16	NT	Homo sapiens CCR8 chemokins receptor (CMKBR8) gene, complete cds
9483	22340	36103	0.81	1.0E-16	EST_HUMAN	QV2-PT0012-040400-124-a05 PT0012 Homo sapiens cDNA
3832	16992	29984	2.08	9.0E-17	EST_HUMAN	CM1-NN1003-200300-153-a01 NN1003 Homo sapiens cDNA
6884	20016		2.15	9.0E-17	EST_HUMAN	ig22c11.x1 NCL_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:2108924 3' similar to contains MER28.12

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8289	21381		3.66	9.0E-17	AW150267.1	EST_HUMAN	xg49g12.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630950 3' similar to contains OFR.12 OFR repetitive element:
10429	23464		2.35	8.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PITG) gene, complete cds
1043	14209		2.43	8.0E-17	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-001 OT0032 Homo sapiens cDNA
3988	17156		0.78	8.0E-17	AL163280.2	NT	Homo sapiens chromosome 21 segment H321C080
5701	25809	32187	4.09	8.0E-17	BE172081.1	EST_HUMAN	MR0-HT0559-060300-003-004 HT0559 Homo sapiens cDNA
7425	20502		1.78	8.0E-17	AV730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 6'
1487	14840		2.58	7.0E-17	6753097	NT	Mus musculus apolipoprotein B editing complex 2 (ApoBec2), mRNA
5438	18638		3.11	7.0E-17	AF218650.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6828	19979	33387	7.91	7.0E-17	AF228843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
208	13431	26493	5.62	6.0E-17	AW1983980.1	EST_HUMAN	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA
6443	19810	32973	2.09	8.0E-17	AW662772.1	EST_HUMAN	H1d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878695 3' similar to contains L1.12 L1 repetitive element:
10499	23534	37144	0.54	6.0E-17	P20138	SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)
434	13234	26234	2.97	5.0E-17	T64110.1	EST_HUMAN	yc05h08.r1 Stratiogene lung (#8937210) Homo sapiens cDNA clone IMAGE:78839 5'
7759	20818	34308	1.81	6.0E-17	T81043.1	EST_HUMAN	yc26b04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109327 5'
8582	22704	36270	1.32	4.0E-17	AW128165.1	EST_HUMAN	yc20e04.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2818622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element;
11783	24773	39469	2.51	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12308	25226		1.82	4.0E-17	AI073548.1	EST_HUMAN	ov45e04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640286 3' similar to TR.Q16530 Q16530 PMS3 MRNA; contains MER10.12 MER10 repetitive element:
2165	15300	28428	1.85	3.0E-17	AW119123.1	EST_HUMAN	xd89c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3283	19437		1.17	3.0E-17	P35410	SWISSPROT	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3732	18893	28897	1.91	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181899 3'
3732	18893	28898	1.91	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181899 3'
8463	21644	35074	1.12	3.0E-17	N68451.1	EST_HUMAN	zai14b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:282491 3' similar to contains PTR5.13 PTR5 repetitive element:
8903	22943	36528	5.19	3.0E-17	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10591	23826	37234	0.72	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
10591	23826	37236	0.72	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
12268	23201		4.2	3.0E-17	11417898	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA

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Table 4

## Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
13155	25751		1.23	3.0E-17	AV720204.1	AV720204 GLC Homo sapiens cDNA clone GLC1F08 5'
363	13574	26605	2.85	2.0E-17	AI270080.1	qf63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959822 3' similar to contains Alu repetitive element
364	13574	26605	2.78	2.0E-17	AI270080.1	qf63a06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1959822 3' similar to contains Alu repetitive element
1012	14184		1.43	2.0E-17	AA728932.1	zq81d04.x1 Scores fetal heart N6HH19W Homo sapiens cDNA clone IMAGE:390751 3'
2518	15644	28765	2.59	2.0E-17	Q28983	ZONADHESIN PRECURSOR
2618	16644	28768	2.59	2.0E-17	Q28983	ZONADHESIN PRECURSOR
2696	16172	29191	6.98	2.0E-17	P12036	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5482	16681	31686	1.75	2.0E-17	M27685.1	Mus musculus ultra high sulfur keratin gene, complete cds
5482	16681	31687	1.75	2.0E-17	M27685.1	Mus musculus ultra high sulfur keratin gene, complete cds
6394	19563		1.92	2.0E-17	AF050066.1	Homo sapiens MHC class 1 region
6619	19779		1.39	2.0E-17	AL134881.1	DKFZp762J0610 J1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762J0610 5'
8008	21056	34568	0.89	2.0E-17	AB037839.1	Homo sapiens mRNA for KIAA1418 protein, partial cds
8276	21357	34876	1.24	2.0E-17	Q95156	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
8651	21731	35270	1.05	2.0E-17	AA300640.1	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to glycogenin
10073	23111	39715	2.71	2.0E-17	BE289888.1	600944690F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860815 6'
10108	23146	38744	3.53	2.0E-17	AL163247.2	Homo sapiens chromosome 21 segment HS21C047
10108	23146	38745	3.53	2.0E-17	AL163247.2	Homo sapiens chromosome 21 segment HS21C047
10468	23601	37114	6.02	2.0E-17	D19391.1	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10590	23625	37232	0.87	2.0E-17	P98063	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10590	23625	37233	0.97	2.0E-17	P98063	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10618	23652	37261	0.93	2.0E-17	A1788902.1	we94b04.x1 Scores_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10618	23652	37262	0.93	2.0E-17	A1788902.1	we94b04.x1 Scores_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
769	13950	26868	2.79	1.0E-17	P08163	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1745	14894		2.01	1.0E-17	AJ271736.1	Homo sapiens Xq pseudautosomal region; segment 2/2
1807	14966	26350	4.83	1.0E-17	AL163207.2	Homo sapiens chromosome 21 segment HS21C007
2184	15319	26445	2.05	1.0E-17	P02461	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2412	15642	26659	3.16	1.0E-17	U78410.1	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3657	16820		1.03	1.0E-17	AF224689.1	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
4258	17401		9.42	1.0E-17	R03942.1	(UBE2D) genes, complete cds
					EST_HUMAN	y30a07.r1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:128388 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8791	19946	33344	1.82	1.0E-17	AI185642.1	EST_HUMAN	q65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
8791	19946	33348	1.82	1.0E-17	AI185642.1	EST_HUMAN	q65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7238	20322	33768	1.33	1.0E-17	Q18831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8792	21871	35410	1.26	1.0E-17	BE062744.1	EST_HUMAN	QV0-BT0263-101299-072-07 BT0263 Homo sapiens cDNA
10210	23246	36836	1.04	1.0E-17	AW996538.1	EST_HUMAN	QV3-BN0046-220300-129-c10 BN0046 Homo sapiens cDNA
11703	24700	38383	1.52	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MCK) [CONTAINS: TELOKIN]
9698	22747		3.05	9.0E-18	AI472197.1	EST_HUMAN	g83d03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
3886	17045	30044	2.14	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
359	13570	26589	16.47	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
359	13570	26600	16.47	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
7601	20871	34146	1.09	7.0E-18	AW897642.1	EST_HUMAN	RC3-OT0091-170300-011-403 OT0091 Homo sapiens cDNA
12826	13570	26599	10.85	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCL_CGAP_Part1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20888 60S
12826	13570	26600	10.85	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCL_CGAP_Part1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20888 60S
3387	19539	29552	1.23	8.0E-18	X71791.2	NT	Rattus norvegicus partial Gdn(Pn-1) gene for glia-derived natriuretic peptide enhancer region
4888	18001		3.99	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYL TRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8444	21525		3.47	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA
8543	21624	35161	0.78	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
9291	22367	35916	0.48	6.0E-18	AI808256.1	EST_HUMAN	RC-BT168-020499-014 BT168 Homo sapiens cDNA
9291	22367	35917	0.48	6.0E-18	AI808256.1	EST_HUMAN	RC-BT168-020499-014 BT168 Homo sapiens cDNA
11399	24490	38124	3.63	6.0E-18	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11612	24684	38351	1.89	6.0E-18	X87344.1	NT	H. sapiens DNA, DM1B, HLA-Z1, IPP2, LMP7, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
12534	25364	32058	3.91	6.0E-18	U87929.1	NT	Human acetylcholinesterase (AChE) gene, exon 4
1171	14334	27390	12.48	5.0E-18	AI280214.1	EST_HUMAN	gm85g11.x1 Soares_placenta_8to9weeks_2NBHP809W Homo sapiens cDNA clone IMAGE:1803688 3'
4433	17573	30555	0.59	5.0E-18	10846685	NT	similar to contig Alu repetitive element;
5387	18589	31561	1.29	5.0E-18	AF087913.1	NT	Mus musculus gelsolin (Gsdm), mRNA
8917	21896	35535	3.47	5.0E-18	BE143312.1	EST_HUMAN	Human endogenous retrovirus HERV-P-T47D
							MR0-HT0161-221069-002-c06 HT0161 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11223	24282	37832	3.43	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
11223	24282	37833	3.43	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12675	25450		6.29	5.0E-18	AW807182.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
13063	25696		28.95	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLC Homo sapiens cDNA clone GLCGGA02 3'
127	13355	26388	0.91	4.0E-18	BE044076.1	EST_HUMAN	h36h04.x1 NCL_CGAP_UT1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
127	13355	26387	0.91	4.0E-18	BE044076.1	EST_HUMAN	h36h04.x1 NCL_CGAP_UT1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
1754	14903	27968	52.82	4.0E-18	AA821814.1	EST_HUMAN	h24111.a1 NCL_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:114845 3' similar to gb:M26326 KERA TIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1838	15031		1.05	4.0E-18	AI736592.1	EST_HUMAN	w33h08.x1 NCL_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:2392095 3'
2274	16407	28536	1.26	4.0E-18	Q09430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYL TRANSFERASE (N- ACETYLGLUCOSAMINYL TRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
2274	16407	28537	1.26	4.0E-18	Q09430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYL TRANSFERASE (N- ACETYLGLUCOSAMINYL TRANSFERASE) (I-BRANCHING ENZYME) (IGNT)
3892	17051	30050	0.61	4.0E-18	AI581586.1	EST_HUMAN	ar93b06.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173139 3' similar to contains Alu repetitive element;
5479	18878	31681	2.47	4.0E-18	AI017565.1	EST_HUMAN	cu23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1827138 3'
5479	18878	31692	2.47	4.0E-18	AI017565.1	EST_HUMAN	cu23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1827138 3'
8029	21112		0.82	4.0E-18	AA746811.1	EST_HUMAN	h36h408.s1 NCL_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1268098 similar to contains L1.12 L1 repetitive element;
11254	24323	37854	7.59	4.0E-18	AA371807.1	EST_HUMAN	EST T83683 Pituitary gland, subcloned (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
872	14048	27114	3.81	3.0E-18	AA814186.1	EST_HUMAN	cd23h11.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW:RS5_HUMAN
853	14126	27187	2.25	3.0E-18	BE088634.1	EST_HUMAN	P46782 40S RIBOSOMAL PROTEIN S6.
4060	17216	30225	1.08	3.0E-18	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
8688	20196	33622	4.72	3.0E-18	BE001671.1	EST_HUMAN	PMO-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
11167	24238	37859	1.95	3.0E-18	BF218650.1	EST_HUMAN	601984856F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103662 5'
12632	26664		4.55	3.0E-18	AW022015.1	EST_HUMAN	af31h12.y1 Marton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485128 5'
261	13460	26512	4.2	2.0E-18	AW836820.1	EST_HUMAN	QV1-T0036-150200-070-e07 L T0036 Homo sapiens cDNA
1176	14339		74.12	2.0E-18	BE256097.1	EST_HUMAN	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
3163	16368	28374	0.94	2.0E-18	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM



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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5527	18724		4.2	2.0E-18	AA868810.1	EST_HUMAN	alC3a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409652 3' similar to TR:O14577
5623	18817	31886	3.51	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A06 FROM TQ31, COMPLETE SEQUENCE. ;
5623	18817	31887	3.51	2.0E-18	D14547.1	NT	Human DNA, SINE repetitive element
5899	19184		1.84	2.0E-18	BF347229.1	EST_HUMAN	Human DNA, SINE repetitive element
6294	19487	32820	0.81	2.0E-18	X60459.1	NT	G02021164F1 NCI_CGAP_Brt07 Homo sapiens cDNA clone IMAGE:4156870 5'
6294	19487	32821	0.81	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6408	19577	32938	0.9	2.0E-18	BF352840.1	EST_HUMAN	Human IFNAR gene for interferon alpha/beta receptor
6448	19815	32979	2.63	2.0E-18	AW665853.1	EST_HUMAN	IL3-HT0619-220700-222-C12 HT0619 Homo sapiens cDNA
7594	20685	34141	0.59	2.0E-18	AA457619.1	EST_HUMAN	h184901.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2879984 3' similar to contains
8341	21422	34847	0.6	2.0E-18	BE436524.1	EST_HUMAN	MER19.12 MER19 repetitive element ;
10253	23288	36884	0.95	2.0E-18	AW151873.1	EST_HUMAN	aa93d11.1r1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838495 5' similar to
10253	23288	36885	0.95	2.0E-18	AW151873.1	EST_HUMAN	TR:G61834 G61834 POLYPEPTIDE PR7 ;
11217	24286	37625	2.81	2.0E-18	AW470761.1	EST_HUMAN	HTM1-160F1 HTM1 Homo sapiens cDNA
12031	25014	38716	4.46	2.0E-18	AW151289.1	EST_HUMAN	X67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623148 3' similar to contains MER10.12
12465	14339		12.67	2.0E-18	BE260087.1	EST_HUMAN	MER10 repetitive element ;
4937	17675		0.75	1.0E-18	T85408.1	EST_HUMAN	X67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623148 3' similar to contains MER10.12
5471	18871	31651	2.64	1.0E-18	AV653405.1	EST_HUMAN	MER10 repetitive element ;
5688	18882	32174	3.08	1.0E-18	D00099.1	NT	h633d08.x1 NCI_CGAP_KH12 Homo sapiens cDNA clone IMAGE:2875498 3' similar to contains THR.b3
5888	18882	32175	3.08	1.0E-18	D00099.1	NT	THR repetitive element ;
6584	19746	33128	1.31	1.0E-18	AL163280.2	NT	Xg47e09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8.b2
8637	21717	35254	1.05	1.0E-18	AI149288.1	EST_HUMAN	MER8 repetitive element ;
10103	23141	38740	4.63	1.0E-18	U91328.1	NT	Y643g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120536 5' similar to contains
12418	25284	32084	4.65	1.0E-18	AF003529.1	NT	L1 repetitive element ;
							AV653405 GLC Homo sapiens cDNA clone GLCDKE11 3'
							Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
							Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
							Homo sapiens chromosome 21 segment HS21C080
							oz69d08.x1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680593 3' similar to
							contains L1.L1 repetitive element ;
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
							Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
559	13752	26780	5.1	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element:
560	13762	26780	3.91	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element:
8032	21115		3.69	9.0E-19	F08683.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
8886	21885	35501	2.57	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8886	21865	35502	2.57	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11392	24453	38116	3.15	9.0E-19	AB032669.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
12171	13752	26780	19.34	9.0E-19	AA281961.1	EST_HUMAN	z11d06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12 MER19 repetitive element:
1073	14239		1.58	8.0E-19	AW674902.1	EST_HUMAN	EST387007 MAGE resequences, MAGN Homo sapiens cDNA
8342	21423	34948	1.12	8.0E-19	BE158936.1	EST_HUMAN	MFO-HT0404-210200-001-g06 HT0404 Homo sapiens cDNA
2319	15461	28583	1.74	7.0E-19	4758139	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp) box polypeptide 6 (RNA helicase, 54kD) [DDX6] mRNA
6585	19747	33129	2.11	7.0E-19	AF092030.1	NT	Rattus norvegicus cp151 mRNA, partial cds
7452	20529	34002	0.94	7.0E-19	P28444	SWISSPROT	BETA CRYSTALLIN A2
10216	23252	36841	0.54	7.0E-19	A1344951.1	EST_HUMAN	1b07G08.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052302 3'
12316	26183		1.72	7.0E-19	AA705694.1	EST_HUMAN	z60b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'
3879	17038		1.16	6.0E-19	AW652830.1	EST_HUMAN	PMO-GT0248-131099-001-g01 CT0248 Homo sapiens cDNA
4585	17722	30705	1.56	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4585	17722	30706	1.58	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4921	18051		1.2	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
5978	19163	32483	6.17	6.0E-19	Q00183	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
6346	18516	32873	0.59	5.0E-19	AW663302.1	EST_HUMAN	ht77b08.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5'
10639	23673	37283	1.18	5.0E-19	AJ297689.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11828	24818	36509	8.14	5.0E-19	AW183725.1	EST_HUMAN	x87b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2664171 3' similar to contains element MSR1 repetitive element:
13063	25895		1.34	5.0E-19	U66060.1	NT	Human germline T-cell receptor beta chain TORBV13S1, TORBV6S8A2T, TORBV5S6A3N2T, TORBV13S6A2T, TORBV6S5P, TORBV5S3A2T, TORBV13S8P, TORBV6S3A1N1T, TORBV5S2, TORBV6S8A2T, TORBV5S7P, TORBV13S4, TORBV6S2A1N1T, TORBV5S4A2T, TORBV6S4A1, TORBV2S1A2T, TORBV12-
588	13760	28784	0.96	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2747	15864	28975	1.15	4.0E-19	BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5512	18710	31725	1.2	4.0E-19	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3955	17113	30114	1.02	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3955	17113	30115	1.02	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4400	17643	30526	0.85	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4400	17543	30527	0.85	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4588	17707	30868	1.42	3.0E-19	AV708136.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11 5'
5394	18596		0.69	3.0E-19	AF223467.1	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
7543	20615		1.88	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC68222), mRNA
9658	21101	34614	1.09	3.0E-19	X89686.1	NT	M. musculus mRNA for TFCR33 protein
12583	25385		16.36	3.0E-19	AF165520.1	NT	Homo sapiens phorbol 1 protein (PB1) mRNA, complete cds
2627	19750	28868	20.06	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4588	17706		1.34	2.0E-19	AI311783.1	EST_HUMAN	q91602.X1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:191568 3' similar to TR:Q68388 Q68388 POL/ENV GENE:
6179	19356	32703	0.81	2.0E-19	AV731382.1	EST_HUMAN	AV731382 HTF Homo sapiens cDNA clone HTFAZC06 5'
7493	20568	34040	0.63	2.0E-19	7657286	NT	Mus musculus keratin-associated protein 9-1 (Krtap9-1), mRNA
8526	21606	35146	10.24	2.0E-19	AA012854.1	EST_HUMAN	za34c09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880 5'
10113	23151	36753	0.84	2.0E-19	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
494	13639		1.88	1.0E-19	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
2233	15357	28498	1.64	1.0E-19	H30795.1	EST_HUMAN	y07907.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains MER10 repetitive element;
2782	15888		2.4	1.0E-19	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
2909	16087		6.72	1.0E-19	4758377	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3488	16655	29869	1.18	1.0E-19	AA834987.1	EST_HUMAN	a49b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12 MER37 repetitive element;
5462	18652	31631	0.73	1.0E-19	AI890866.1	EST_HUMAN	wm91b08.x1 NCI_CGAP_U02 Homo sapiens cDNA clone IMAGE:2443287 3' similar to TR:Q16630 Q16630 PMS3 MRNA;
6199	18374	32725	2.9	1.0E-19	U12186.1	NT	Oryzobagus cuticulus sodium/dicarboxylate cotransporter mRNA, partial cds
6337	26213		*0.63	1.0E-19	AA595527.1	EST_HUMAN	nt22d03.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:963093 similar to contains L1.1 L1 repetitive element;
7806	20882	34355	1.05	1.0E-19	U08813.1	NT	Oryzobagus cuticulus Na+/glucose cotransporter-related protein mRNA, complete cds
7806	20882	34356	1.05	1.0E-19	U08813.1	NT	Oryzobagus cuticulus Na+/glucose cotransporter-related protein mRNA, complete cds
7977	25856		0.75	1.0E-19	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8644	21724	35281	1.94	1.0E-19	M84857.1	NT	Rabbit phosphatase kinase beta subunit mRNA, complete cds
8939	22018		2.72	1.0E-19	T98920.1	EST_HUMAN	ye72b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains ORF repetitive element;
8950	22989		0.89	1.0E-19	U00822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
10390	23425	37032	26.12	1.0E-19	AW812259.1	EST_HUMAN	RCO-ST0174-191089-031-508 ST0174 Homo sapiens cDNA
10400	23435	37042	1.59	1.0E-19	N44631.1	EST_HUMAN	W81e09.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:272872 5'
11184	24253	37888	1.87	1.0E-19	BE16028.1	EST_HUMAN	601278882F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611493 5'
6784	19939	33336	2.4	8.0E-20	7857286	NT	Mus musculus keratin-associated protein 9;1 (Krtap9-1), mRNA
6784	19939	33337	2.4	8.0E-20	7857286	NT	Mus musculus keratin-associated protein 9;1 (Krtap9-1), mRNA
7687	20752	34234	1.48	8.0E-20	A121371.1	EST_HUMAN	q956f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
7687	20752	34235	1.46	8.0E-20	A121371.1	EST_HUMAN	q956f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3349	18521	29537	0.71	7.0E-20	BF328455.1	EST_HUMAN	PM4-AN00086-050800-003-004 AN00086 Homo sapiens cDNA
7134	18560	31474	5.66	7.0E-20	AL139120.1	EST_HUMAN	DKFZp647D092.r1 547 (synonym: h10r1) Homo sapiens cDNA clone DKFZp647D092 5'
8693	21773	35305	8.83	7.0E-20	AA557657.1	EST_HUMAN	n46c04.s1 NCI_CGAP_P44 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element;
8693	21773	35306	8.83	7.0E-20	AA557657.1	EST_HUMAN	n46c04.s1 NCI_CGAP_P44 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2 MER29 repetitive element;
12014	24998		2.89	7.0E-20	6912833	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
3645	16808	29822	3.64	6.0E-20	P39188	SWISSPROT	ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
4387	17530	30511	4.58	6.0E-20	BE822434.1	EST_HUMAN	601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'
4718	17853		1.8	5.0E-20	AV725123.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTCBTA01 5'
7264	20347	33799	1.42	5.0E-20	AF076301.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0280
8131	21213	34733	6.96	5.0E-20	W80525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element;
8131	21213	34734	6.96	5.0E-20	W80525.1	EST_HUMAN	zh78d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.11 MER30 repetitive element;
8295	21377	34868	0.79	5.0E-20	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-901 HT0487 Homo sapiens cDNA
9035	22114	35557	1.28	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9035	22114	35558	1.28	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9644	21087		1.13	5.0E-20	O60809	SWISSPROT	HYPOTHETICAL PROTEIN DUB45024.1
1649	14802	27859	0.94	4.0E-20	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21G047
6765	18957		1.13	4.0E-20	Q99880	SWISSPROT	HISTONE H2B C (H2B/C)
8110	21192		5.61	4.0E-20	A1874352.1	EST_HUMAN	z64g03.x1 NCI_CGAP_OV65 Homo sapiens cDNA clone IMAGE:2283396 3'
10717	23750	37357	1.13	4.0E-20	AW697469.1	EST_HUMAN	QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2207	15341	28468	1.22	3.0E-20	U03888.1	NT	Human BXP21 gene
4325	17468	30455	1.29	3.0E-20	P23273	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN 114
4747	17882	30864	1.08	3.0E-20	AA037616.1	EST_HUMAN	ZK33612.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element;
9135	22214		2.65	3.0E-20	D14647.1	NT	Human DNA, SINE repetitive element
10527	23562	37168	0.47	3.0E-20	BF185264.1	EST_HUMAN	601849561.F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064343 5'
10900	23984		1.59	3.0E-20	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
12331	25239	32109	6.08	3.0E-20	BE889422.1	EST_HUMAN	ENDONUCLEASE
853	14030		5.65	2.0E-20	AW303868.1	EST_HUMAN	601514180.F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
1135	14300	27355	2.49	2.0E-20	AA516335.1	EST_HUMAN	x24610.x1 NCI_CGAP_U44 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
1135	14300	27356	2.49	2.0E-20	AA516335.1	EST_HUMAN	P67461 40S RIBOSOMAL PROTEIN S5 ;
2878	14030		5.32	2.0E-20	AW303868.1	EST_HUMAN	ng98h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940087 similar to TR:G1224068
5061	18189	31163	5.16	2.0E-20	Q28983	SWISSPROT	G1224066 ORF2: FUNCTION UNKNOWN ;
5061	18189	31164	5.15	2.0E-20	Q28983	SWISSPROT	ng98h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940087 similar to TR:G1224068
5256	18376		0.9	2.0E-20	G174538	NT	G1224066 ORF2: FUNCTION UNKNOWN ;
8309	21391	34915	0.97	2.0E-20	AA309457.1	EST_HUMAN	x24610.x1 NCI_CGAP_U44 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
8391	22466	36030	2.65	2.0E-20	D10083.1	NT	P67461 40S RIBOSOMAL PROTEIN S5 ;
8391	22466	36031	2.65	2.0E-20	D10083.1	NT	ZONADHESIN PRECURSOR
12743	26878	31862	2.17	2.0E-20	H55371.1	EST_HUMAN	ZONADHESIN PRECURSOR
2070	15995	28327	6.61	1.0E-20	AA281961.1	EST_HUMAN	Homo sapiens male dehydrogenase 1, NAD (soluble) (MDH1) mRNA
4560	17698	30679	1.02	1.0E-20	BF115153.1	EST_HUMAN	EST180326 Liver III Homo sapiens cDNA 5' end
7034	20170	33592	0.74	1.0E-20	AF049567.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
9364	22439	35998	2.08	1.0E-20	11418491	NT	Homo sapiens RGH1 gene, retrovirus-like element
11847	24836	38530	2.03	1.0E-20	AF223361.1	NT	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391 5'
12461	26323		2.91	1.0E-20	AA420453.1	EST_HUMAN	z11406.t1 NCI_CGAP_GC31 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
							MER19 repetitive element ;
							h64606.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1
							repetitive element ;
							AF049567 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
							Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							nc60g08.t1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745684 similar to contains L1.13 L1
							repetitive element ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2979	16155		1.18	9.0E-21	AJ003514.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIp12-8J21
12174	25135		3.98	9.0E-21	AW698189.1	EST_HUMAN	RC3-NN0069-090500-021-b03 NN0068 Homo sapiens cDNA
9011	22090		0.98	8.0E-21	AW674891.1	EST_HUMAN	B530a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2884714 5' similar to SW:NIAM_HUMAN
11630	24819	38610	3.81	8.0E-21	AA809411.1	EST_HUMAN	OS5169 NADH-JBIQUINONE OXIDOREDUCTASE ASHI SUBUNIT PRECURSOR ;
12345	25250		3.8	8.0E-21	OZ1330	SWISSPROT	ab7166.s1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
2130	15268	28385	3.85	7.0E-21	P18800	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 6)
2130	15268	28386	3.85	7.0E-21	P18800	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
3792	18963	28968	1.36	7.0E-21	AL163300.2	NT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
4369	17512		6.29	7.0E-21	AA046502.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
6584	18728	33104	0.94	7.0E-21	AL163218.2	NT	2k67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
8582	21653	35203	1.46	7.0E-21	AJ277557.1	NT	Homo sapiens chromosome 21 segment HS21C018
8875	21954	35490	4.94	7.0E-21	D14718.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidase (dNT-2 gene), exon 1-6
10319	23354	36963	1.07	7.0E-21	AW656922.1	EST_HUMAN	Human chromosomal protein HMGT related gene
10934	24016	37648	1.94	7.0E-21	AAT23404.1	EST_HUMAN	RC0-C10301-271189-031-F03 CT0301 Homo sapiens cDNA
4220	17369	30358	0.75	6.0E-21	BE408811.1	EST_HUMAN	2q73d03.s1 Soares_fetal_heart_NbHH16W Homo sapiens cDNA clone IMAGE:386981 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); contains THR.13 OFR repetitive element ;
6335	22412		1.39	6.0E-21	BE162737.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
947	14120	27181	1.34	5.0E-21	5602031	NT	PM1-HT0454-080100-002-109 HT0454 Homo sapiens cDNA
2354	15485	28617	1.23	5.0E-21	AA928194.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4483	17623	30604	3.21	5.0E-21	BE968839.1	EST_HUMAN	om23g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541808 3' similar to TR:O02711
4809	14120	27181	1.16	5.0E-21	5602031	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
4923	18053	31039	8.33	5.0E-21	4885474	NT	601049871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
6902	20217		0.77	5.0E-21	AW440864.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
7157	20291	33734	1	5.0E-21	BE858505.1	EST_HUMAN	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
10801	23834	37457	0.54	5.0E-21	O91680	SWISSPROT	7f93d11.x1 NCJ_CGAP_P128 Homo sapiens cDNA clone IMAGE:2918154 3'
10801	23834	37458	0.54	5.0E-21	O91680	SWISSPROT	OFR repetitive element ;
12259	25195		1.28	5.0E-21	AA333574.1	EST_HUMAN	ZINC FINGER PROTEIN GLI1 (GLI-1)
1772	14921	28015	1.88	4.0E-21	AA970713.1	EST_HUMAN	ZINC FINGER PROTEIN GLI1 (GLI-1)
							2f72cd04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5'
							cc86e08.s1 NCJ_CGAP_K185 Homo sapiens cDNA clone IMAGE:1573084 3' similar to TR:Q16630 Q16630
							PMS3 MRNA ; contains OFR.11 OFR repetitive element ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7011	20147	33568	2.61	4.0E-21	AB016576.1	NT	Rattus norvegicus mRNA for rTIM, complete cds
6983	23022	36814	0.82	4.0E-21	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RcrRet gene, and sodium phosphate transporter (NPTS) gene, complete cds
10010	23048	36642	0.61	4.0E-21	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
1884	15028	28135	1.1	3.0E-21	AA218891.1	EST_HUMAN	z415d06.s1 Stratiotes fetal retina 83/202 Homo sapiens cDNA clone IMAGE:629771 3'
2348	15478	28611	1.51	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3149	16324	29335	6.41	3.0E-21	AJ007873.1	NT	Homo sapiens LGMD2B gene
5616	18810	31878	0.92	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidease (dNT-2 gene), exons 1-5
5616	18810	31878	0.92	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(3')-deoxyribonucleotidease (dNT-2 gene), exons 1-5
5856	19046		0.9	3.0E-21	AV661044.1	EST_HUMAN	AV661044 GLC Homo sapiens cDNA clone GLC0A10 3'
6308	19480		2.74	3.0E-21	BF184739.1	EST_HUMAN	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064946 5'
7215	20080	33463	7.52	3.0E-21	BF361083.1	EST_HUMAN	RC1-OT0083-100800-019-908 OT0083 Homo sapiens cDNA
9894	22834	36518	0.92	3.0E-21	AW897760.1	EST_HUMAN	CM1-NN0063-280400-203-108 NN0063 Homo sapiens cDNA
12678	26089	31695	3.58	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
150	13376		24.6	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
958	14131	27189	0.61	2.0E-21	AB007657.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
958	14131	27190	0.61	2.0E-21	AB007657.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1241	14400		3.03	2.0E-21	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-108 BT0311 Homo sapiens cDNA
2703	15821	28937	2.59	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2703	15821	28938	2.59	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5601	18786	31848	1.86	2.0E-21	AI624582.1	EST_HUMAN	ts30f03.x1 NC1 CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q98854 Q98854
5694	18888	32178	0.8	2.0E-21	AA027211.1	EST_HUMAN	HYPOTHETICAL 51.1 KD PROTEIN ;
5694	18888	32179	0.8	2.0E-21	AA027211.1	EST_HUMAN	z897a12.r1 Scores_fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:3669310 5'
6167	19333	32878	0.74	2.0E-21	W44463.1	EST_HUMAN	z897a12.r1 Scores_fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:3669310 5'
8467	21546	35078	0.58	2.0E-21	AJ010770.1	NT	z228102.r1 Scores_senescent fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323687 5'
8558	21639	35178	8.13	2.0E-21	BE141785.1	EST_HUMAN	Homo sapiens hypericin gene, exons 1-50
9023	22102	35642	3.27	2.0E-21	AU136778.1	EST_HUMAN	QV0-HT0103-091199-050-g11 HT0103 Homo sapiens cDNA
11313	24377		2.04	2.0E-21	BE350127.1	EST_HUMAN	AU136778 PLAGE1 Homo sapiens cDNA clone PLAGE1005052 5'
11699	24652	36335	2.88	2.0E-21	BE973829.1	EST_HUMAN	ht09g01.x1 NC1 CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29 b3
							MER29 repetitive element ;
							601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11589	24652	38336	2.88	2.0E-21	BE973829.1	EST_HUMAN	601880636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
12572	26389		8.44	2.0E-21	AF176815.1	NT	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
1284	14440	27509	1.89	1.0E-21	AA557657.1	EST_HUMAN	n48c04.s1 NCI_CGAP_P74 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
1434	14597		4.93	1.0E-21	AI601264.1	EST_HUMAN	MER29 repetitive element;
6818	19778		2.73	1.0E-21	AL079752.1	EST_HUMAN	at88d12.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
							DKFZp4340830_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp4340830 5'
7342	20422	33885	4.7	1.0E-21	AI223104.1	EST_HUMAN	gg47e05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838338 3' similar to gb:M64241 QM
10448	23483	37092	0.47	1.0E-21	AL163203.2	NT	PROTEIN (HUMAN);
10448	23483	37093	0.47	1.0E-21	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10812	23845		1.31	1.0E-21	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
13014	26697		1.87	1.0E-21	AF048133.1	NT	Homo sapiens chromosome Xp22 410-8
4530	17898	30854	2.38	9.0E-22	AI702438.1	EST_HUMAN	524a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:Q15408 Q15408
8803	21892	35420	2.02	9.0E-22	AL163201.2	NT	NEUTRAL PROTEASE LARGE SUBUNIT;
8803	21892	35421	2.02	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
11031	24110	37748	3.1	9.0E-22	AV761874.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C001
12007	24992	38696	1.39	9.0E-22	AU140358.1	EST_HUMAN	AV761874 MDS Homo sapiens cDNA clone MDS00059 5'
971	14144		7.93	8.0E-22	BE144748.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLACE2000394 5'
8080	21192		3.39	8.0E-22	AA046502.1	EST_HUMAN	CX00-H10179-281099-076-h05 HT0179 Homo sapiens cDNA
682	13887	26898	3.78	7.0E-22	AL163246.2	NT	2k67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487658 5'
4398	17541	30522	3.27	7.0E-22	Q61838	SWISSPROT	Homo sapiens chromosome 21 segment HS21C046
5150	18272	31241	0.91	7.0E-22	AB006881.1	NT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
8888	21897		1.24	7.0E-22	AF151054.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8032	22111	35653	2.77	7.0E-22	M76590.1	EST_HUMAN	Homo sapiens HSPC220 mRNA, complete cds
8802	22842	39418	2.05	7.0E-22	AF009660.1	NT	EST00738 Fetal brain, Stragene (cat#838206) Homo sapiens cDNA clone HFBCF07
8436	21517		1.26	6.0E-22	AW029123.1	EST_HUMAN	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
6646	18905	33192	3.27	6.0E-22	AL163303.2	NT	wo05d07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542812 3'
10325	23560	37167	2.98	6.0E-22	U60822.1	NT	Homo sapiens chromosome 21 segment HS21C103
							Human dystrophin (DMD) gene, exons 7, 8, and 9, and partial cds
12833	25556		1.63	5.0E-22	BF476811.1	EST_HUMAN	naa27p06.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3255898 3' similar to contains Alu
3726	18887		0.77	4.0E-22	AI271735.1	NT	repetitive element;
8608	26224		2.81	4.0E-22	AL163202.2	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
10981	24042	37677	1.97	4.0E-22	BF218030.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
							601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085434 5'



Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13021	26672		3.85	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
981	14164		1.34	3.0E-22	AI469879.1	EST_HUMAN	hm14h10.x1 NCI CGAP_C014 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb.L19593 HIGH AFFINITY INTERLEUKIN-3 RECEPTOR B (HUMAN); contains L1.L1 L1 repetitive element;
2838	15759	28873	1.33	3.0E-22	AI859038.1	EST_HUMAN	w060504.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428839 3' similar to SW:RL21_HUMAN
3763	16824		1.65	3.0E-22	D14718.1	NT	P46778 60S RIBOSOMAL PROTEIN L21.;
4922	18052	31038	3.18	3.0E-22	AI090125.1	EST_HUMAN	Human chromosomal protein HMG1 related gene
8011	21061	34573	0.8	3.0E-22	P11369	SWISSPROT	qb28c07.x1 Soares_pregnant Uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.12 MER12 repetitive element;
8425	21506		1.11	3.0E-22	BE166813.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
8430	21511	35042	1.88	3.0E-22	BE089841.1	EST_HUMAN	QV0-HT0368-090200-099-112 HT0368 Homo sapiens cDNA
8555	21636	35172	1.14	3.0E-22	X60660.1	NT	RC5-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
8555	21636	35173	1.14	3.0E-22	X60660.1	NT	Rattus RY2G5 mRNA for a potential ligand-binding protein
2008	15148		4.04	2.0E-22	N24942.1	EST_HUMAN	Rattus RY2G5 mRNA for a potential ligand-binding protein
2590	15715	28833	1.72	2.0E-22	P24916	SWISSPROT	yk73d05.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:287369 3'
3507	16674	28684	3.98	2.0E-22	8394043	NT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
4341	17484	30466	1.41	2.0E-22	AW817794.1	EST_HUMAN	Homo sapiens protein Kinase AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
5973	26614	32476	1.47	2.0E-22	W39456.1	EST_HUMAN	PM1-ST0262-261199-001-d12 ST0262 Homo sapiens cDNA
6306	19478	32833	3.58	2.0E-22	BF092116.1	EST_HUMAN	gb.X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
9904	22944	36529	1.78	2.0E-22	A1276522.1	EST_HUMAN	RCQ-TN0079-150900-025-h12 TN0078 Homo sapiens cDNA
10001	23039	36630	0.95	2.0E-22	AA715316.1	EST_HUMAN	q78h06.x1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:1878299 3' similar to contains MER29.13 MER29 repetitive element;
10001	23039	36631	0.85	2.0E-22	AA715315.1	EST_HUMAN	nv04h11.s1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:1219289 3'
12058	25037	38745	1.52	2.0E-22	AW418660.1	EST_HUMAN	nv04h11.s1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:1219289 3'
12139	26656	31964	2.33	2.0E-22	AL163280.2	NT	ha24f04.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2874655 3'
1927	16070	28175	2.05	1.0E-22	AW865517.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2651	16774	28987	2.36	1.0E-22	U50871.1	NT	PM4-SN0020-010400-009-h02 SN0020 Homo sapiens cDNA
3497	16664	29676	1.53	1.0E-22	D14547.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
7920	20971	34478	1.09	1.0E-22	BE084667.1	EST_HUMAN	Human DNA, SINE repetitive element
10778	23809	37432	1.05	1.0E-22	AI365435.1	EST_HUMAN	MR0-BT0659-220200-002-h07 BT0659 Homo sapiens cDNA
							MR0-BT0659-220200-002-h07 BT0659 Homo sapiens cDNA
							q209b07.x1 NCI CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2020881 3' similar to contains MER29.b2
							MER29 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10776	23809	37433	1.05	1.0E-22	AI365435.1	EST_HUMAN	q20807.x1 NC1_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER29.b2
13078	26707		12.31	9.0E-23	AW802801.1	EST_HUMAN	MER29 repetitive element;
3681	19824	28833	0.74	8.0E-23	AF198348.1	NT	IL2-UM0078-070400-001-F11 UM0078 Homo sapiens cDNA
3385	16535		2.21	7.0E-23	AV647246.1	EST_HUMAN	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
11293	24359	38000	3.74	7.0E-23	5031952	NT	AV647246 GLC Homo sapiens cDNA clone GLCAW C07 3'
3520	16586		1.83	6.0E-23	AF198333.1	NT	Homo sapiens Ncl56 (D. melanogaster)-like protein (NOT56L) mRNA
4383	17526	30507	1.15	6.0E-23	AL163249.2	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
12283	25211	32097	4.93	6.0E-23	AF224659.1	NT	Homo sapiens chromosome 21 segment HS21C049
12283	25211	32098	4.93	6.0E-23	AF224659.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
12463	25335	32056	3.18	6.0E-23	AI209130.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
							(UBE2D3) genes, complete cds
5560	18757	31798	4.01	5.0E-23	U82871.2	NT	(UBE2D3) genes, complete cds
6369	25824	32898	3.69	5.0E-23	AF179818.1	NT	q25903.x1 Soares testis NIH Homo sapiens cDNA clone IMAGE:1830460 3' similar to
7695	25824	32898	2.78	5.0E-23	AF179818.1	NT	SW/MV10_MOUSE P23249 PROTEIN MOV-10;
6570	19732	33110	0.67	3.0E-23	AL163227.2	NT	(MAGEA12), melanoma antigen family A2a (MAGEA2A), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calreticlin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LIP
6370	19732	33111	0.67	3.0E-23	AL163227.2	NT	Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
							Pongo pygmaeus olfactory receptor (PPY116) gene, partial cds
8022	21105	34622	3.26	3.0E-23	AA130165.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
9450	22566	38130	3.72	3.0E-23	Z70684.1	NT	Homo sapiens chromosome 21 segment HS21C027
9450	22566	38131	3.72	3.0E-23	Z70684.1	NT	236908.r1 Soares_pregnant uterus_Nb-HPU Homo sapiens cDNA clone IMAGE:503968 5' similar to
10523	23558		1.42	3.0E-23	AW897827.1	EST_HUMAN	contains MER29.12 MER29 repetitive element;
							Human endogenous retroviral element HC2
11372	24433		1.35	3.0E-23	AF280107.1	NT	Human endogenous retroviral element HC2
683	13668	26599	3.69	2.0E-23	AI289860.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450
1166	15988		3.46	2.0E-23	M55270.1	NT	polypeptide 5 (CYP3A5) gene, partial cds
2856	15970	29079	1	2.0E-23	P22105	SWISSPROT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
2856	15970	29080	1	2.0E-23	P22105	SWISSPROT	Human matrix Gla protein (MGF) gene, complete cds
							TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
							TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3457	16824		1.11	2.0E-23	AI201458.1	EST_HUMAN	qs73f11.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537
3810	16970		3.83	2.0E-23	BE165980.1	EST_HUMAN	MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
4085	17240	30246	4.43	2.0E-23	H59931.1	EST_HUMAN	MR3-HT0487-150200-119-g01 HT0487 Homo sapiens cDNA
4085	17240	30247	4.43	2.0E-23	H59931.1	EST_HUMAN	Y16A02.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
							Y16A02.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205418 5'
8057	21140		5.28	2.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A4) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450
8044	22123	35695	0.95	2.0E-23	AL163303.2	NT	polypeptide 5 (CYP3A5) gene, partial cds.
12565	26199		8.7	2.0E-23	M32658.1	NT	Homo sapiens chromosome 21 segment HS21C103
12644	26561		3.68	2.0E-23	AF009660.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
12683	26103		2.3	2.0E-23	AU133931.1	EST_HUMAN	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
4650	17786	30769	1.57	1.0E-23	AL163252.2	NT	AU133931 OVARC1 Homo sapiens cDNA clone OVARC1000946 5'
4888	18018		5.42	1.0E-23	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C052
6861	20013		3.27	1.0E-23	BE378471.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
8551	21632	35189	4.61	1.0E-23	AA448067.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3608653 5'
10909	23992	37626	2.19	1.0E-23	BE409843.1	EST_HUMAN	zxr82c06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.12
10909	23992	37626	2.19	1.0E-23	BE409843.1	EST_HUMAN	PTR5 repetitive element ;
13082	26074	31654	1.35	1.0E-23	AW501816.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
566	13759		1.87	9.0E-24	AA663213.1	EST_HUMAN	601301762F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636254 5'
4771	17906	30888	1.12	8.0E-24	P23289	SWISSPROT	QV0-NN1020-170400-195-a11 NN1020 Homo sapiens cDNA
4771	17906	30889	1.12	8.0E-24	P23289	SWISSPROT	ab75a08.s1 Stralagene fetal retina 937203 Homo sapiens cDNA clone IMAGE:852758 3' similar to
6578	19740	33121	0.95	8.0E-24		NT	TR:19822 E19822 CA PROTEIN. ;
3976	17133		0.84	7.0E-24	AW937854.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN 13
5281	18400		16.79	7.0E-24	AL039498.1	EST_HUMAN	OLFACTORY RECEPTOR-LIKE PROTEIN 13
10878	23981		1.61	7.0E-24	AW309317.1	EST_HUMAN	Homo sapiens capping protein (actin filament) muscle Z-liver, alpha 2 (CAPZA2), mRNA
724	13906		2.21	6.0E-24	AB001421.1	NT	QV0-DT0047-170200-122-a06 DT0047 Homo sapiens cDNA
861	14038	27100	12.8	6.0E-24	AL163249.2	NT	DKFZp434A2311_1 434 (synonym: hless) Homo sapiens cDNA clone DKFZp434A2311 6'
4078	17234	30241	9.39	5.0E-24	AJ228043.1	NT	xv17f03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element ;
7635	20885	34493	1.27	5.0E-24	AF223391.1	NT	Mecosa fuscata mRNA for Testis-Specific Protein Y (TSPY), complete cds
							Homo sapiens chromosome 21 segment HS21C049
							Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4371	17514		0.9	4.0E-24	BF389469.1	EST_HUMAN	RCO-GN0090-250900-022409 GN0090 Homo sapiens cDNA nn31h05.a1 NCI CGAP Gas1 Homo sapiens cDNA clone IMAGE:1085528 3' similar to SW:POL_MLVK
8052	18234	32559	2.77	4.0E-24	AA594178.1	EST_HUMAN	P31795 POL POLYPROTEIN ;
8880	21059	35484	0.71	4.0E-24	AW813711.1	EST_HUMAN	RC3-ST0197-130100-014-06 ST0197 Homo sapiens cDNA
11454	24514	38182	2.05	4.0E-24	BE54822.1	EST_HUMAN	301078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464488 5'
12659	25448	32054	4.02	4.0E-24	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
7229	20134	33551	0.73	3.0E-24	U68081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV16S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2.>
7229	20134	33552	0.73	3.0E-24	U68081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV16S1P, TCRBV16S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2.>
8818	21698		2.94	3.0E-24	AW614871.1	EST_HUMAN	h186c08.x1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2867850 3' similar to contains MER28 b2
8873	21763		1.24	3.0E-24	AW62076.1	EST_HUMAN	MER29 repetitive element ;
8865	22627	36188	3.79	3.0E-24	AL163262.2	NT	EST374149 MAGE resequences, MAGE Homo sapiens cDNA
12756	25501	32034	1.94	3.0E-24	BF127762.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21G052
2422	19551	28678	2.55	2.0E-24	AA167839.1	EST_HUMAN	60181049F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053398 5'
3689	17058		0.82	2.0E-24	AW898189.1	EST_HUMAN	zp11409.r1 Stralagene fetal retina 037202 Homo sapiens cDNA clone IMAGE:609161 5'
7515	26219		0.63	2.0E-24	AL163209.2	NT	RC3-NN0068-090500-021-b03 NN0068 Homo sapiens cDNA
7643	20712	34191	0.9	2.0E-24	AF086824.1	NT	Homo sapiens chromosome 21 segment HS21C009
7648	20717	34194	0.98	2.0E-24	AJ003536.1	EST_HUMAN	Mus musculus rho/rae-interacting citron kinase (Crik) mRNA, complete cds.
8938	22017	35550	3.81	2.0E-24	AL119158.1	EST_HUMAN	AJ003536 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPIp12-5H13
8977	22056		0.9	2.0E-24	H69214.1	EST_HUMAN	DKFZp781L1712_r1 761 (synonym: hamv2) Homo sapiens cDNA clone DKFZp781L1712 5'
10058	23096	36698	1.08	2.0E-24	AI521759.1	EST_HUMAN	y92509.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729 5' similar to contains MER28 repetitive element ;
10058	23096	36699	1.06	2.0E-24	AI521759.1	EST_HUMAN	U77609.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
12580	26153		21.43	2.0E-24	M28877.1	NT	U77609.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008 3'
1731	14881	27972	4.81	1.0E-24	7706340	NT	Human O family dispersed repeat element
2738	15655		1.65	1.0E-24	AW820194.1	EST_HUMAN	Homo sapiens CGI-127 protein (LOC51646), mRNA
3085	16261	29278	0.72	1.0E-24	D86423.1	NT	QVO-ST0284-100400-185-c10 ST0284 Homo sapiens cDNA
4385	17528		1.93	1.0E-24	AF143313.1	NT	Mus musculus mRNA for HGT keratin, partial cds Homo sapiens PTEN (PTEN) gene, exon 2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6531	19695	33088	1.13	1.0E-24	7105336	NT	Mus musculus keratin complex-1, gene C29 (Krt1-c29), mRNA
7720	20784	34272	4.65	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7907	20959	34485	5.07	1.0E-24	BE144326.1	EST_HUMAN	MRO-HT0189-271189-005-409 HT0189 Homo sapiens cDNA
8130	21212	34732	2.29	1.0E-24	AW901164.1	EST_HUMAN	CM0-NN1010-130300-281-407 NN1010 Homo sapiens cDNA
11989	24984	38689	1.37	8.0E-25	7706707	NT	Homo sapiens putative secreted protein (SIG11), mRNA
6111	18239	31206	2.7	7.0E-25	AA483944.1	EST_HUMAN	ne92a10.s1 NCL_CGAP_Kld: Homo sapiens cDNA clone IMAGE:911764 similar to contains MER1.b2 MER1 repetitive element;
8413	21494	35025	3.7	7.0E-25	AA468846.1	EST_HUMAN	ne00a09.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element;
12003	24988	38693	3.64	7.0E-25	AA583540.1	EST_HUMAN	nt25h08.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:914843 similar to SW:R14A_YEAST P36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA. ;
7131	18557		5.04	6.0E-25	W87823.1	EST_HUMAN	zh65h07.r1 Scores fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:416989 5'
7899	20951	34458	11.72	6.0E-25	7305360	NT	Mus musculus obogelin (Olog), mRNA
1683	14835	27820	1.81	5.0E-25	AW850271.1	EST_HUMAN	IL3-CT0219-161189-031-D04 CT0219 Homo sapiens cDNA
11598	24649	38333	3.12	5.0E-25	AW079107.1	EST_HUMAN	EST391217 MAGE resequences, MAGP1-Homo sapiens cDNA
1478	14631	27716	2.66	4.0E-25	T98107.1	EST_HUMAN	ye65h04.r1 Scores fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:121783 5'
3489	16556		2.81	4.0E-25	AW887671.1	EST_HUMAN	FW3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
4436	17576		4.06	4.0E-25	BE170967.1	EST_HUMAN	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
10144	23182	38779	0.83	4.0E-25	AA383873.1	EST_HUMAN	EST187317 Thymus 1 Homo sapiens cDNA 5' end similar to EST containing O family repeat
2256	16399	28516	1.02	3.0E-25	BE068922.1	EST_HUMAN	RC3-BT0377-131299-031-F02 BT0377 Homo sapiens cDNA
3399	18566	29581	3.12	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
3396	16566	29582	3.12	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
5015	18144	31119	0.7	3.0E-25	P29822	SWISSPROT	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
6532	21613	35149	6.42	3.0E-25	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11287	24353	37693	2.7	3.0E-25	AA579013.1	EST_HUMAN	nt30h10.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.11 L1 repetitive element;
1378	14533	27607	4.9	2.0E-25	6032168	NT	Homo sapiens transducin (beta)-like 1 (TSL1) mRNA
2382	15513	28841	7.33	2.0E-25	BE888018.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
2893	18731	28848	3.71	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4307	17450	30436	1.61	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4307	17450	30437	1.61	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
8967	23006	36801	2.13	2.0E-25	AL449573.1	EST_HUMAN	AL449573 Homo sapiens Testis (Slavides GS) Homo sapiens cDNA
375	13983	28817	0.81	1.0E-25	AL040229.1	EST_HUMAN	DKFZp434H0313_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434H0313 5'
1277	14434		2.07	1.0E-25	9935487	NT	Human endogenous retrovirus, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4983	18112	31089	2.71	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002:109 HT0454 Homo sapiens cDNA
5298	18415	31383	1.16	1.0E-25	8823786	NT	Homo sapiens HSPC059 protein (HSPC059), mRNA
5298	18415	31384	1.16	1.0E-25	8923786	NT	Homo sapiens HSPC059 protein (HSPC059), mRNA
6697	18855		0.85	1.0E-25	AA189080.1	EST_HUMAN	z44506.s1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element.
6936	28838	33688	2.95	1.0E-25	AA582680.1	EST_HUMAN	nn54h11.s1 NCJ_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087749 3'
8098	21180	34698	3.56	1.0E-25	AA709079.1	EST_HUMAN	z186304.s1 Soares_fetal_Heart_NbHH181W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains PTR5.13 PTR5 repetitive element.
9746	22810	36388	1.32	1.0E-25	X60680.1	NT	Rattus RY2G5 mRNA for a potential ligand-binding protein
9746	22810	36389	1.32	1.0E-25	X60680.1	NT	Rattus RY2G5 mRNA for a potential ligand-binding protein
11212	24281	37820	3.11	1.0E-25	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12280	25209	38384	1.82	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
12280	25209	38385	1.62	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
2553	15678	28802	1.94	9.0E-26	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11252	24321		2.35	9.0E-26	AI905386.1	EST_HUMAN	QV-BT087-301288-008 BT087 Homo sapiens cDNA
12140	25901		5.33	9.0E-26	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
8811	16001		1.51	8.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
1608	14761	27840	5.61	7.0E-26	AF003328.1	NT	Homo sapiens X-linked embryonic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4089	17244	30251	1.88	7.0E-26	X80211.1	NT	H. sapiens DNA for endogenous retroviral like element
4275	17420	30407	1.92	7.0E-26	AW340163.1	EST_HUMAN	hd02et2.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2908369 3'
5755	18947	32249	0.84	7.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11968	24851		6.85	7.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Stralagene neuroepithelium NT2RAM1 697234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gbM14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
12901	26596		5.49	7.0E-26	AW954559.1	EST_HUMAN	EST366629 MAGE resequences, MAGE Homo sapiens cDNA
2300	16432	28565	3.83	6.0E-26	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
3427	16595	29811	0.69	6.0E-26	AA206131.1	EST_HUMAN	zn52h04.r1 Stralagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271 5'
10753	23786	37400	0.62	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10753	23786	37401	0.62	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11979	24984	38665	2.15	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1204	14366	27426	0.89	5.0E-26	AI708235.1	EST_HUMAN	as38h08.x1 Barstead acta HPLRB6 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP.F49C12.11 CE03371;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1204	14366	27427	0.89	5.0E-26	AI708235.1	EST_HUMAN	aa38h08.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2318519 3' similar to WP:F49C12.11 CE03371;
9912	22867		3.29	4.0E-26	7657870	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
10897	23081	37613	2.84	4.0E-26	BE266187.1	EST_HUMAN	G01191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535210 5'
11604	24657	38342	1.38	4.0E-26	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1787	14948	28038	1.25	3.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
2059	15200	28314	1.14	3.0E-26	AL049866.2	EST_HUMAN	DKFZp434I066_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434I066 5'
2088	15228		3.34	3.0E-26	AA115895.1	EST_HUMAN	zn30d08.r1 Striatagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5'
3878	17037	30035	1.41	3.0E-26	AA152464.1	EST_HUMAN	similar to gb:MI4338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3878	17037	30035	1.41	3.0E-26	AA152464.1	EST_HUMAN	zn30f10.r1 Striatagene cdon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
3878	17037	30035	1.41	3.0E-26	AA152464.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
3878	17037	30035	1.41	3.0E-26	AA152464.1	EST_HUMAN	zn30f10.r1 Striatagene cdon (#937204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374
7051	20104	33521	0.09	3.0E-26	BF245458.1	EST_HUMAN	G695374 THYROID RECEPTOR INTERACTOR ;
11887	24855	38551	1.97	3.0E-26	AW875661.1	EST_HUMAN	60186493F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:4083278 5'
11887	24855	38551	1.97	3.0E-26	AW875661.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
11902	24890	38591	7.79	3.0E-26	AA583173.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
699	13882	26916	6.84	2.0E-26	AL163282.2	NT	nn37d05.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.11
1917	13060		3.07	2.0E-26	AL038099.2	EST_HUMAN	OFR repetitive element ;
3303	18477	28499	5.22	2.0E-26	X86694.1	NT	Homo sapiens chromosome 21 segment HS21C082
10981	24070		1.93	2.0E-26	D87875.1	NT	DKFZp566L171_s1 586 (synonym: hfkid2) Homo sapiens cDNA clone DKFZp566L171 3'
11493	24551	38226	2.96	2.0E-26	AI801412.1	EST_HUMAN	M.musculus mRNA for astrocytic phosphoprotein, PEA-15
11704	24701		2.06	2.0E-26	AF050066.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
12989	26276		1.76	2.0E-26	AB037869.1	NT	repetitive element contains element MER20 MER20 repetitive element ;
12989	26276		1.76	2.0E-26	AB037869.1	NT	Homo sapiens MHC class I region
12604	26088	31658	2.35	2.0E-26	BE170371.1	EST_HUMAN	Homo sapiens mRNA for KIAA1438 protein, partial cds
139	13365	28398	8.95	1.0E-26	AL038093.2	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2105	15244	28365	1.42	1.0E-26	AL038093.2	EST_HUMAN	QV4-HT0538-020300-123-a02 HT0538 Homo sapiens cDNA
2751	15868		6.28	1.0E-26	AF261085.1	NT	DKFZp434H1910_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H1910 5'
6980	20208		2.89	1.0E-26	BE105980.1	EST_HUMAN	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
11131	24203		1.95	1.0E-26	AL038487.1	EST_HUMAN	MR3-HT0487-160200-113-g01 HT0487 Homo sapiens cDNA
12855	26178		2.77	1.0E-26	H55093.1	EST_HUMAN	DKFZp566C2148_r1 586 (synonym: hfkid2) Homo sapiens cDNA clone DKFZp566C2148 5'
13175	25763		1.16	1.0E-26	AW408742.1	EST_HUMAN	CHR220332 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
13175	25763		1.16	1.0E-26	AW408742.1	EST_HUMAN	UI-HF-BMO-adv-d-10-UJ.r1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063210 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7757	20816		0.87	9.0E-27	BF371227.1	EST_HUMAN	RC6-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA
9503	22769		5.02	9.0E-27	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
12143	25118		6.6	9.0E-27	BF446566.1	EST_HUMAN	na03c07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3253644 3' similar to contains OFR.I1 OFR repetitive element ;
11	13249	26249	4.22	8.0E-27	AU831482.1	EST_HUMAN	wj48c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.B2 THR repetitive element ;
571	13763		4.57	8.0E-27	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1448	14601	27678	23.84	8.0E-27	AW162737.1	EST_HUMAN	eu87h08.x1 Schmeider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783285 3' similar to gb.K00558
1448	14601	27679	23.84	8.0E-27	AW162737.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);
2236	15369	28499	1.82	8.0E-27	AY864776.1	EST_HUMAN	eu87h08.x1 Schmeider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783285 3' similar to gb.K00558
3254	16428	28448	1.8	8.0E-27	P12238	SWISSPROT	TUBULIN ALPHA-1 CHAIN (HUMAN);
3434	16602	28621	0.76	8.0E-27	AF181897.1	NT	FM2-SN0018-220300-002-a07 SN0018 Homo sapiens cDNA
5812	18002	32308	1.07	8.0E-27	AV732214.1	EST_HUMAN	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
7117	18543		2.66	8.0E-27	BE926660.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
7192	20057	33487	2.49	8.0E-27	N84870.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBCB06 5'
8410	22484	36048	1.63	8.0E-27	AW851579.1	EST_HUMAN	MR4-BT0398-260800-204-408 BT0398 Homo sapiens cDNA
8410	22484	36049	1.63	8.0E-27	AW851579.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to REPETITIVE ELEMENT L1
701	13884		1.77	7.0E-27	Z70864.1	NT	Human endogenous retroviral element HC2
5201	18322		2.19	7.0E-27	AW629172.1	EST_HUMAN	ht51h12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2876879 3' similar to TR:O78040
8058	22137		0.87	7.0E-27	D86984.1	NT	O78040 ORF2: FUNCTION UNKNOWN; ;
10988	24067		3.7	7.0E-27	AJ271735.1	NT	Human mRNA for KIAA0231 gene, partial cds
10984	24045	37679	3.21	6.0E-27	M26697.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12094	25074	38781	1.55	6.0E-27	U93163.1	NT	Human nuclear protein (B23) mRNA, complete cds
7954	21004		0.73	5.0E-27	AL163303.2	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
10442	23477	37081	3.21	5.0E-27	BF666614.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
10442	23477	37082	3.21	5.0E-27	BF666614.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
6883	20035	33444	1.65	4.0E-27	9910569	NT	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
							Mus musculus sperm tail associated protein (Slap), mRNA



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## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8125	21207		0.98	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8172	21254		1.31	4.0E-27	AF078778.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8845	22984	36577	0.81	4.0E-27	AW189085.1	EST_HUMAN	QVO-OT0033-070300-152-b10 OT0033 Homo sapiens cDNA
11803	24891	36592	2.82	4.0E-27	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
13213	26080	31655	1.17	4.0E-27	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
2089	16239	28381	7.1	3.0E-27	X60858.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4388	17528	30510	1.55	3.0E-27	BE071824.1	EST_HUMAN	PMO-BT0527-090100-001-011 BT0527 Homo sapiens cDNA
5482	18682	31641	6.81	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
9505	22771	36342	3.49	3.0E-27	BF036327.1	EST_HUMAN	60145853F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3682086 5'
42	13280	26286	9.28	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1944	15037		24.24	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
3178	16353		13.34	2.0E-27	AW628172.1	EST_HUMAN	h151m12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2875879 3' similar to TR:O76040
3266	16470	29489	1.45	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3296	16470	29490	1.45	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6814	19987	33373	0.79	2.0E-27	H02655.1	EST_HUMAN	X36601.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150840 5' similar to
8282	21384	34883	1.17	2.0E-27	AI866347.1	EST_HUMAN	SP-HMGC_MOUSE Q02591 HOMEOBOX PROTEIN ;
9469	22528		2.6	2.0E-27	AA551927.1	EST_HUMAN	wf28g07.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2429286 3'
8895	23033	36625	0.83	2.0E-27	X60658.1	NT	rh08h05.s1 NCI_CGAP_Thy11 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.13 L1
10241	23276	36868	1.45	2.0E-27	M78590.1	EST_HUMAN	R. rattus RYA3 mRNA for a potential ligand-binding protein
10241	23276	36869	1.45	2.0E-27	M78590.1	EST_HUMAN	EST T00738 Fetal brain, Striatum (cat#535206) Homo sapiens cDNA clone HFBCF07
11197	24266	37801	3.61	2.0E-27	AU121885.1	EST_HUMAN	EST T00738 Fetal brain, Striatum (cat#535206) Homo sapiens cDNA clone HFBCF07
11777	15087		6.43	2.0E-27	AA559345.1	EST_HUMAN	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000746 5'
12107	26087	38791	1.64	2.0E-27	AF216650.1	NT	nk01b10.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
449	13645		2.34	1.0E-27	AL163246.2	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
1021	14192	27251	4.97	1.0E-27	AB026998.1	NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6874	18833	33222	8.61	1.0E-27	6005855	NT	Homo sapiens chromosome 21 segment HS21C049
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
							Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7010	20146	33568	1.65	1.0E-27	F30158.1	EST_HUMAN	HSPD20481 HM3 Homo sapiens cDNA clone e4000095C10
7010	20146	33567	1.65	1.0E-27	F30158.1	EST_HUMAN	HSPD20481 HM3 Homo sapiens cDNA clone e4000095C10
8809	21898	35430	1.16	1.0E-27	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9188	22264		1.69	1.0E-27	BE079780.1	EST_HUMAN	RC6-BT0827-140200-011-E06 BT0827 Homo sapiens cDNA
9923	22963	36551	2.65	1.0E-27	D87449.1	NT	Human mRNA for KIAA0260 gene, partial cds
12003	24950	36694	3.05	1.0E-27	AF111093.1	NT	Bos taurus letraphilin 3 splice variant bsh mRNA, complete cds
144	13368		2.26	9.0E-28	BE348399.1	EST_HUMAN	hw17c11.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
321	13535	26587	2.17	9.0E-28	AU126260.1	EST_HUMAN	SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [3] TR:Q07280 TR:Q07313;
10801	20636	37243	0.47	9.0E-28	AA174078.1	EST_HUMAN	AU126260 NT2P1 Homo sapiens cDNA clone NT2RP1000443 5'
12224	25173		3.04	9.0E-28	BF377859.1	EST_HUMAN	zp18g12.61 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:603662 3'
12565	26003		13.39	8.0E-28	AW157571.1	EST_HUMAN	CM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
1208	14370	27430	11.5	7.0E-28	AU142750.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782011 3' similar to
11463	24522	38192	1.65	7.0E-28	11417856	NT	TR:O60302 O60302 KIAA0555 PROTEIN. contains element MER22 repetitive element;
12181	28141		5.04	7.0E-28	AV795348.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
8119	22198		1.28	6.0E-28	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
12866	25577		5.92	6.0E-28	AA504562.1	EST_HUMAN	aa60e03.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu
328	13542		2.75	5.0E-28	A1921003.1	EST_HUMAN	repetitive element/contains element PTR6 repetitive element;
4116	17270	30269	38.94	6.0E-28	R79782.1	EST_HUMAN	w018c07.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455692 3' similar to contains THR.b1
2889	16809	28926	1.46	4.0E-28	AW195096.1	EST_HUMAN	THR repetitive element;
3177	16352	29358	1.34	4.0E-28	BE409100.1	EST_HUMAN	y89f10.r1 Soares placenta N22HP Homo sapiens cDNA clone IMAGE:148443 5'
7483	20558	34030	3.55	4.0E-28	A1198941.1	EST_HUMAN	xn33a09.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2895504 3' similar to SW:GG85_HUMAN
11105	24177		4.19	4.0E-28	AF029008.1	NT	Q08379 GOLGIN-95;
11255	24324		14.89	4.0E-28	AB038241.1	NT	601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'
11278	20558	34030	4.34	4.0E-28	A1198941.1	EST_HUMAN	qf66f10.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1
12622	25418		1.7	4.0E-28	AW854244.1	EST_HUMAN	REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
12773	26089		1.62	4.0E-28	AW862350.1	EST_HUMAN	RC3-CT0254-240400-210-112 CT0254 Homo sapiens cDNA
							RC0-CT0379-070100-031-h01 CT0379 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1312	14468		2.29	3.0E-28	AF165382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22), mRNA, complete cds
5227	18349		0.84	3.0E-28	AF009680.1	NT	Homo sapiens T cell receptor beta locus, TORBV7S9A2 to TORBV12S2 region
8027	22108	35847	2.28	3.0E-28	BF354030.1	EST_HUMAN	MR3-HT0713-280500-013-109 HT0713 Homo sapiens cDNA
11176	24245	37878	2.09	3.0E-28	U63688.1	NT	Homo sapiens MHC class 1 region
12653	25433		3.77	3.0E-28	AI831891.1	EST_HUMAN	wj08f07.x1 NCJ CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element ;
12803	28536		3.29	3.0E-28	BE082801.1	EST_HUMAN	RC2-BT0842-210200-013-603 BT0842 Homo sapiens cDNA
12865	28576	31883	1.22	3.0E-28	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12866	28676	31884	1.22	3.0E-28	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
91	13326	26354	12.76	2.0E-28	BE062167.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1181	14353	27411	9.24	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
2546	15671	28795	2.16	2.0E-28	AI348834.1	EST_HUMAN	qc35b06.x1 NCJ CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element;
3448	16614	26632	0.81	2.0E-28	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
6437	18604	32668	1.48	2.0E-28	BF224402.1	EST_HUMAN	h76c03.x1 NCJ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element;
8460	19827		3	2.0E-28	BF212805.1	EST_HUMAN	601814196F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
8234	21316	34837	0.83	2.0E-28	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
9783	22823		2.23	2.0E-28	AW872305.1	EST_HUMAN	EST384934 MAGE resequences, MAGL Homo sapiens cDNA
11913	24900	36603					Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12631	25424		2.52	2.0E-28	AF224669.1	NT	(UBE2D3) genes, complete cds
1508	14661	27744	1.74	2.0E-28	H06376.1	EST_HUMAN	y76c09.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:44300 5'
2294	15428	28560	2.85	1.0E-28	D38044.1	NT	Human gene for Ah-receptor, exon 7-9
4691	17826		3.91	1.0E-28	BF333238.1	EST_HUMAN	QV1-BT0821-120900-360-503 BT0821 Homo sapiens cDNA
8044	21127		0.95	1.0E-28	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
8208	21290		1.95	1.0E-28	11428885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63091), mRNA
			3.03	1.0E-28	8822763	NT	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA
9478	22535	36089					EST1176615 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR
10080	23118	36720	4.75	1.0E-28	AA308744.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
10080	23118	36721	5.91	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGT1A1), mRNA
12186	25145		7.68	1.0E-28	AA054182.1	EST_HUMAN	z55.c01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380448 5'
13013	25881		4.56	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expressio Signal:	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13135	26122	31543	1.8	9.0E-29	AW063997.1	EST_HUMAN	h176g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978288 3'
12752	25498		2.57	8.0E-29	Q00130	SWISSPROT	HYPOPHYSAL GENE 50 PROTEIN
1632	14784	27870	1.98	7.0E-29	AW968447.1	EST_HUMAN	EST378521 IMAGE ressequences, MAGI Homo sapiens cDNA
13187	26779		9.03	7.0E-29	AJ132352.1	NT	Reatus nonvagus mRNA for 45 kDa secretory protein, partial
608	13797	26817	9.39	8.0E-29	AI936748.1	EST_HUMAN	wp69501.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O18475
12495	25342		5.19	6.0E-29	BE940438.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN; contains LTR7 b1 LTR7 repetitive element;
12587	25395		2.1	6.0E-29	BF688097.1	EST_HUMAN	RC3-UT0062-210800-021-c05 UT0062 Homo sapiens cDNA
5113	18241		2.39	5.0E-29	AL163203.2	NT	802184092F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300079 6'
8929	22008		8.35	5.0E-29	AW887641.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12785	25531		1.49	6.0E-29	BE812449.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
3304	16478		2.28	4.0E-29	AI752387.1	EST_HUMAN	601451827F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855728 5'
6133	16312		7.06	4.0E-29	BE164930.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cello Homo sapiens cDNA clone NHTBC_cn15c02 random
8272	21354	34870	0.64	4.0E-29	AI678101.1	EST_HUMAN	QV1-HT0471-280300-121-405 HT0471 Homo sapiens cDNA
8272	21354	34871	0.64	4.0E-29	AI678101.1	EST_HUMAN	wd335g08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
8944	22023	35553	3.59	4.0E-29	JD4988.1	NT	MER29.12 MER29 repetitive element;
4538	17674	30658	1.31	3.0E-29	AB042297.1	NT	wd335g08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains
4855	17988	30978	1.1	3.0E-29	BF333238.1	EST_HUMAN	Human 90 kD heat shock protein gene, complete cds
6053	19235	32560	0.83	3.0E-29	BE314018.1	EST_HUMAN	Homo sapiens PTS gene for 5-pyruvyltetrahydropterin synthase, complete cds
8931	22010	35548	3.23	3.0E-29	D38044.1	NT	QV1-BT0821-120900-360-403 BT0821 Homo sapiens cDNA
9500	22566	38119	1.22	3.0E-29	AW303317.1	EST_HUMAN	601162657F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508627 5'
9731	22786		1.49	3.0E-29	AL163249.2	NT	Human gene for Ah receptor, exon 7-9
10164	23201		0.61	3.0E-29	BE350127.1	EST_HUMAN	xx17703.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813408 3' similar to contains Alu
11546	24602	38278	2.26	3.0E-29	AA403053.1	EST_HUMAN	repetitive element; contains MER19.12 MER19 repetitive element;
12385	25272		1.36	3.0E-29	D63882.1	NT	Homo sapiens chromosome 21 segment HS21C046
13092	26132		1.62	3.0E-29	D63882.1	NT	h08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
505	13699	26727	0.98	2.0E-29	AF084869.1	NT	MER29 repetitive element;
505	13699	26728	0.98	2.0E-29	AF084869.1	NT	z62b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1563	14718	27794	7.8	2.0E-29	AI93804.1	EST_HUMAN	wr65d10.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15548 O15548 HERV-E ENVELOPE GLYCOPROTEIN;
1563	14718	27795	7.8	2.0E-29	AI93804.1	EST_HUMAN	wr65d10.x1 NCI CGAP_UH1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15548 O15548 HERV-E ENVELOPE GLYCOPROTEIN;
1782	14931	28024	2.31	2.0E-29	X84900.1	NT	H sapiens mRNA for laminin-5, alpha3b chain
1782	14931	28025	2.31	2.0E-29	X84900.1	NT	H sapiens mRNA for laminin-5, alpha3b chain
4394	17537	30516	2.55	2.0E-29	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5946	19132	32446	0.78	2.0E-29	AI082459.1	EST_HUMAN	os71604.x1 NCI CGAP_GC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.12 L1 repetitive element;
6309	19481	32835	1.49	2.0E-29	AI809418.1	EST_HUMAN	wf27g07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element;
7732	19481	32835	1.28	2.0E-29	AI809418.1	EST_HUMAN	wf27g07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element;
8164	21246	34768	1.16	2.0E-29	BE957157.1	EST_HUMAN	601442208F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846648 5' Homo sapiens DNA-binding protein (LOC56242), mRNA
8777	21856	35398	0.81	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
8777	21856	35399	0.81	2.0E-29	10567821	NT	Homo sapiens chromosome 21 segment HS21C048
9708	22757	36327	2.76	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9708	22757	36328	2.76	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10444	23479	37084	3.65	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10444	23479	37085	3.65	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11767	24760	37086	1.67	2.0E-29	11425108	NT	Homo sapiens splicing factor similar to dnal (SPF31), mRNA
8892	22071	35611	8.27	1.0E-29	AW983890.1	EST_HUMAN	RC1-HN0003-220300-021-504 HN0003 Homo sapiens cDNA
10850	23683	37503	2.81	1.0E-29	XG0658.1	NT	Rattus RYA3 mRNA for a potential ligand-binding protein
6712	19870	33261	3.63	9.0E-30	AA761215.1	EST_HUMAN	nt20c07.s1 NCI CGAP_GC31 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 MER4 repetitive element;
12688	26200		4.55	9.0E-30	11422746	NT	Homo sapiens zinc/iron regulated transporter-like (ZIRT), mRNA
8449	19816		10.5	8.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8465	21546	35076	2.26	8.0E-30	AA333873.1	EST_HUMAN	EST197317 Thymus (Homo sapiens cDNA 5' and similar to EST containing O family repeat
8882	21961	35495	2.79	8.0E-30	AI557072.1	EST_HUMAN	PT2.1_13_B11.r tumor2 Homo sapiens cDNA 3'
1646	14687		1.07	7.0E-30	BE091133.1	EST_HUMAN	PM4-B10724-150400-004-d11 BT0724 Homo sapiens cDNA
1814	14963	29058	1.67	6.0E-30	D26303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3259	18433	29450	3.15	6.0E-30	BE008028.1	EST_HUMAN	QV0-BN0147-280400-214-f12 BN0147 Homo sapiens cDNA
4881	18433	29450	1.02	6.0E-30	BE008028.1	EST_HUMAN	QV0-BN0147-280400-214-f12 BN0147 Homo sapiens cDNA
10760	23793	37412	0.76	6.0E-30	AF177227.1	NT	Homo sapiens CTCL tumor antigen se20-10, mRNA, partial cds

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Single Exon Probes Expressed In Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13161	18485		1.75	6.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4121	17275	30274	43.22	5.0E-30	AI395992.1	EST_HUMAN	ig2g03.x1 NCI_CGAP_OLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element;
5353	25928		5.79	5.0E-30	U87931.1	NT	Human aconitate hydratase (ACO2) gene, exon 7
11126	24198		2.12	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11423	24484	38148	2.76	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11423	24484	38148	2.76	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2210	16344	28470	2.38	4.0E-30	AW837471.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
2210	16344	28471	2.38	4.0E-30	AW837471.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
9106	22185	35728	1.56	4.0E-30	AW812488.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
1175	14338		4.56	3.0E-30	AI338551.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
3863	17013	30013	1.16	3.0E-30	AF128893.1	NT	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
8138	21220		0.53	3.0E-30	AF078779.1	NT	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
8883	21783		0.45	3.0E-30	AF078779.1	NT	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
10849	23683	37294	0.74	3.0E-30	BE350127.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
11482	24541	38217	1.52	3.0E-30	P34056	SWISSPROT	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
692	13876	26908	1.42	2.0E-30	AW857315.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
1108	14273		2.53	2.0E-30	F08688.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
1509	14662	27745	5.5	2.0E-30	BE175877.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
2779	15895	25005	9.93	2.0E-30	BE765232.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
2986	18162	28179	6.83	2.0E-30	AF114756.1	NT	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
3889	17048	30048	1.95	2.0E-30	AW206581.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
4900	18030	31018	2.02	2.0E-30	BE298945.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
4900	18030	31019	2.02	2.0E-30	BE298945.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
8734	21814	36349	4.69	2.0E-30	C18939.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
8836	21915	35452	1.71	2.0E-30	BE670617.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
8836	21915	35453	1.71	2.0E-30	BE670617.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA
10201	23238	36528	3.78	2.0E-30	AW971568.1	EST_HUMAN	QV3-DT0043-080200-080-c08 DT0043 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10287	23322	36924	8.31	2.0E-30	AW470791.1	EST_HUMAN	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3
287	13514	26548	10.87	1.0E-30	C16939.1	EST_HUMAN	TH-R repetitive element:
551	13744	26769	1.62	1.0E-30	AW468897.1	EST_HUMAN	G16939 Human placenta cDNA (7Fujiviera) Homo sapiens cDNA clone GEN:570C01 5'
734	13916	26866	5.16	1.0E-30	AL163203.2	NT	ha30b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains
2286	15418	28550	11.56	1.0E-30	AA664377.1	EST_HUMAN	MER1.13 MER1 MER1 repetitive element:
2633	16658	28782	2.15	1.0E-30	BF347728.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
3120	16296	29310	0.91	1.0E-30	AA315045.1	EST_HUMAN	ac77b08.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:888599 3'
7801	20953	34460	1.96	1.0E-30	BF183230.1	EST_HUMAN	60202260F1 NCI_CGAP_Bn07 Homo sapiens cDNA clone IMAGE:4157991 5'
8176	21258	34780	0.49	1.0E-30	BE061588.1	EST_HUMAN	EST168888 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end
12789	26117		1.57	1.0E-30	AA299214.1	EST_HUMAN	601809832F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040694 5'
12837	26025		5.31	1.0E-30	H55593.1	EST_HUMAN	MRO-BT0249-091289-101-g01 BT0248 Homo sapiens cDNA
3862	17022	30020	0.8	8.0E-31	T73025.1	EST_HUMAN	EST11698 Uterus Homo sapiens cDNA 5' end
3862	17022	30021	0.8	8.0E-31	T73025.1	EST_HUMAN	CHR220632 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
8518	21600	35135	0.88	8.0E-31	R18214.1	EST_HUMAN	yc65e06.r1 Stratagene liver (#837224) Homo sapiens cDNA clone IMAGE:85570 5'
8518	21600	35136	0.88	8.0E-31	R18214.1	EST_HUMAN	yc65e06.r1 Stratagene liver (#837224) Homo sapiens cDNA clone IMAGE:85570 5'
8825	21904		1.99	9.0E-31	Z38293.1	EST_HUMAN	yc65e06.r1 Stratagene liver (#837224) Homo sapiens cDNA clone IMAGE:85570 5'
8827	21906	35445	0.65	9.0E-31	AF078779.1	NT	yc65e06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30565 5' similar to gbX12953 RAS-
13193	25776	31934	1.29	9.0E-31		NT	RELATED PROTEIN RAB-2 (HUMAN):
1102	14267	27325	2.52	8.0E-31		NT	yc65e06.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30565 5' similar to gbX12953 RAS-
2484	18611		7.93	8.0E-31	AL163208.2	NT	RELATED PROTEIN RAB-2 (HUMAN):
728	13911		1.59	7.0E-31	AA372637.1	EST_HUMAN	HS005F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3'
2733	15650	28982	2.1	7.0E-31	BE328517.1	EST_HUMAN	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
2733	16550	28983	2.1	7.0E-31	BE328517.1	EST_HUMAN	Mus musculus syndecan 4 (Sdc4), mRNA
8595	21678	35212	1.02	7.0E-31	AF208541.1	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
8595	21678	35213	1.02	7.0E-31	AF208541.1	NT	Homo sapiens chromosome 21 segment HS21C008
9468	22523		1.03	7.0E-31	BE408611.1	EST_HUMAN	EST84555 Cdon adenocarcinoma IV Homo sapiens cDNA 6' end
3769	16930		3.42	6.0E-31	AF223391.1	NT	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8347	21428		1.39	6.0E-31	AF05068.1	NT	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
							Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
							Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
							601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							Homo sapiens MHC class 1 region

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8528	21607	35148	0.75	6.0E-31	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3
10978	24055	37689	1.43	6.0E-31	AU19105.1	EST_HUMAN	MER29 repetitive element ;
12327	25236	32108	3.7	6.0E-31	AW372888.1	EST_HUMAN	AU19105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'
12459	25947		2.54	6.0E-31	BE894488.1	EST_HUMAN	RC5-BT0377-091299-031-D12 BT0377 Homo sapiens cDNA
197	13420	26450	3.38	6.0E-31	M50694.1	NT	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
197	13420	26451	3.39	6.0E-31	M50694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8640	21720		1.29	6.0E-31	BF0569540.1	EST_HUMAN	Homo sapiens type I DNA topoisomerase gene, exon 8
609	13798		3.02	4.0E-31	AJ271735.1	NT	7106004.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR:Q13537 Q13537
							SIMILAR TO POGO ELEMENT ; contains L1 L1 repetitive element ;
1642	14794	27878	1.14	4.0E-31	Q10473	SWISSPROT	Homo sapiens Xq pseudautosomal region, segment 1/2
1861	15007		2.09	4.0E-31	AL163280.2	NT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP
2849	15963		1.57	4.0E-31	5730038	NT	ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-
10764	23787	37402	0.46	4.0E-31	AF084484.1	NT	ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
12787	25526		1.55	4.0E-31	11430273	NT	Homo sapiens chromosome 21 segment HS21C080
12924	25609		2	4.0E-31	AB008681.1	NT	Homo sapiens SET domain and mafin transferase fusion gene (SETMAR) mRNA
2660	15782	28897	1.75	3.0E-31	6009871	NT	Rattus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds
7494	20569	34041	8.04	3.0E-31	4828853	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
7683	20730	34208	1.23	3.0E-31	11420329	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8355	21436		1.61	3.0E-31	AL163206.2	NT	Homo sapiens SEC63, endoplasmic reticulum translocon component (S. cerevisiae) like (SEC63L), mRNA
9779	22819	36397	2.59	3.0E-31	D14523.1	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) (NDUFB8) mRNA
10822	23855	37477	0.65	3.0E-31	AA421242.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
10867	23852	37582	2.03	3.0E-31	P11174	SWISSPROT	Homo sapiens chromosome 21 segment HS21C006
1967	24482		3.47	3.0E-31	BF035327.1	EST_HUMAN	Horse mRNA for ferritin L-chain, complete cds
1967	15110	28211	1.58	2.0E-31	AW898171.1	EST_HUMAN	2106004.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:731047 5'
2288	15420	28552	1.03	2.0E-31	A1393383.1	EST_HUMAN	40S RIBOSOMAL PROTEIN S15 (R16 PROTEIN)
2416	15545	28674	2.22	2.0E-31	AL119245.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
							QV2-LT0051-260300-111-033 LT0051 Homo sapiens cDNA
							tg44g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
							DKFZp761G1513.t1 701 (synonym: ham12) Homo sapiens cDNA clone DKFZp761G1513 5'
							ea89f11.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains
2511	15637	28758	4.63	2.0E-31	AA458924.1	EST_HUMAN	THR12 THR repetitive element ;
5389	18591	31583	0.76	2.0E-31	AW444368.1	EST_HUMAN	U1-H-B19-akb-T-09-0-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733833 3'



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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5829	19020	32326	3.43	2.0E-31	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kic13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29.b3
9277	22363		1.53	2.0E-31	AA877784.1	EST_HUMAN	MER29 repetitive element;
9408	22482	36046	3.46	2.0E-31	7661536	NT	h06104.61 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13637 Q13637
10110	23148	36748	1.1	2.0E-31	AV710948.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
10110	23148	36749	1.1	2.0E-31	AV710948.1	EST_HUMAN	Homo sapiens B9 protein (B9), mRNA
10280	23315	36914	2.75	2.0E-31	BE408811.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
10280	23315	36915	2.75	2.0E-31	BE408811.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
12430	25305		3.49	2.0E-31	AF148512.1	NT	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3838310 5'
12578	26202		2.59	2.0E-31	AI114527.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3838310 5'
17	13255	26256	9.91	1.0E-31	U93163.1	NT	Homo sapiens hexokinase II gene, promoter region
1698	14848	27632	2.68	1.0E-31	O95371	SWISSPROT	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
1698	14848	27633	2.68	1.0E-31	O95371	SWISSPROT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1
1698	14848	27634	2.68	1.0E-31	O95371	SWISSPROT	(MAGE-B1) genes, complete cds
6407	18609	31681	3.97	1.0E-31	AW391679.1	EST_HUMAN	OLFACTORY RECEPTOR 2C1
6261	19435	32781	2.57	1.0E-31	AF048727.1	NT	OLFACTORY RECEPTOR 2C1
7441	20518	33990	0.84	1.0E-31	AF126145.1	NT	MRS-ST0220-151299-028-a08_1 ST0220 Homo sapiens cDNA
8006	21055	34587	1.35	1.0E-31	BE972818.1	EST_HUMAN	Homo sapiens minisatellite cebT repeat region
10441	23476	37080	0.5	1.0E-31	U93183.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
11156	24227	37857	2.35	1.0E-31	AI086434.1	EST_HUMAN	601652052F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935293 5'
6778	19931	33327	2.19	8.0E-32	AV723976.1	EST_HUMAN	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1
7530	20603	34077	0.88	9.0E-32	L31770.1	NT	(MAGE-B1) genes, complete cds
7768	20825	28387	0.91	9.0E-32	11430822	NT	q21h03.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1750709 3' similar to TR:Q16595
2139	15275	28387	5.1	8.0E-32	AI056770.1	EST_HUMAN	Q16595 FRATAXIN.;
5569	18794	31843	0.77	8.0E-32	AW997214.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAAG01 5'
12408	25285		2.38	7.0E-32	X17283.1	NT	Bos taurus vacuolar H <sup>+</sup> -ATPase subunit mRNA, complete cds
7523	20586		1.32	6.0E-32	BE888016.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA
							Human chromosome 22 immunoglobulin V(K) gene, part with 5' breakpoint between orphion and neighbouring non-amplified region
							601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12669	26181		2.5	6.0E-32	AA864653.1	EST_HUMAN	oh37c03.a1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459672 3' similar to contains L1.13 L1 repetitive element;
1056	14225	27282	10.42	5.0E-32	AF116827.1	NT	Homo sapiens PRO1181 mRNA, complete cds
854	14127		1.64	4.0E-32	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7779	20835	34328	3.4	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7779	20835	34327	3.4	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8554	21635		0.93	4.0E-32	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-R06 BT0311 Homo sapiens cDNA
468	13663	26698	2.84	3.0E-32	Y17283.1	NT	Homo sapiens FLI-1 gene, partial
1484	14637	27721	15.82	3.0E-32	AV731500.1	EST_HUMAN	AV731500 HTF Homo sapiens cDNA clone HTFAKC07 5'
2973	16149	29168	0.75	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
2873	16149	29168	0.76	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
9594	22649	36221	3.1	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
9594	22649	36222	3.1	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBBH12 5'
11166	24237	37898	3.43	3.0E-32	AA777621.1	EST_HUMAN	215507.31 Soares fetal_liver_spleen_11NPLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR13 THR repetitive element;
12433	25307		7.95	3.0E-32	BE278086.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
12843	16149	29168	4.95	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
12843	16149	29168	4.95	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
13020	25671		6.47	3.0E-32	BE278086.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
6382	19551	32807	0.89	2.0E-32	M35418.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6808	19768	33166	5.55	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
6808	19768	33157	5.55	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
8473	21554	35085	3.34	2.0E-32	AA114294.1	EST_HUMAN	215508.1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
8473	21554	35086	3.34	2.0E-32	AA114294.1	EST_HUMAN	215508.1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
13154	25750	31923	1.28	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
13154	25750	31924	1.28	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBFBIA08 5'
3163	16338		1.25	1.0E-32	BE743269.1	EST_HUMAN	601573207F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834433 5'
7200	20085	33470	6.64	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
8785	21874	35413	4.53	1.0E-32	AA720574.1	EST_HUMAN	nv21g02.a1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13 THR repetitive element;

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3570	16735		4.8	9.0E-33	BE327112.1	EST_HUMAN	hw07c05.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11.;
6650	16712		3.17	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8988	22067	36607	1.81	9.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCL CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4156870 5'
11038	24117		4.55	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
62	13300	26320	2.73	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
62	13300	26321	2.73	7.0E-33	5031736	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2228	15362	28491	3.04	7.0E-33	AI680115.1	EST_HUMAN	to12608.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.11 OFR repetitive element;
2714	15832		7.85	7.0E-33	AV730056	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTF-AVE08 5'
3314	16487		15	7.0E-33	AW971307.1	EST_HUMAN	EST388396 MAGI2 Homo sapiens cDNA clone IMAGE:4156870 5'
9147	22226		0.87	7.0E-33	X54890.1	NT	Human hLPR mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphatase) (EC 3.1.3.48)
11067	24142	37777	1.88	7.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCL CGAP_Brm87 Homo sapiens cDNA clone IMAGE:4156870 5'
11526	24592	38258	1.58	7.0E-33	AW971688.1	EST_HUMAN	EST388396 MAGI2 Homo sapiens cDNA clone IMAGE:4156870 5'
12413	26292	32082	9.74	7.0E-33	AA601416.1	EST_HUMAN	no16h01.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.1 L1 repetitive element;
3830	18930		0.93	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
6192	19368	32717	0.91	6.0E-33	F30831.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
6192	19368	32718	0.91	6.0E-33	F30831.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H06
8778	21857	35400	1.86	6.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
8899	21978	35517	3.12	6.0E-33	11429188	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
10214	23250	36839	2.03	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
10214	23250	36840	2.03	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1818	14967		1.8	5.0E-33	BF373515.1	EST_HUMAN	QV1-FT0169-100700-271-ac2 FTO169 Homo sapiens cDNA
1931	15074		1.32	6.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC6A7), mRNA
1947	15090	28180	1.63	6.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1947	15090	28181	1.63	6.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
2346	15477		2.92	5.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C086
4169	17316	30312	0.66	5.0E-33	AB014599.1	NT	Homo sapiens mRNA for KIAA0899 protein, partial cds
10454	23469	37097	0.82	5.0E-33	AW264678.1	EST_HUMAN	xs3311.x1 NCL CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
10454	23469	37098	0.82	5.0E-33	AW264679.1	EST_HUMAN	xs3311.x1 NCL CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12212	25165		1.45	5.0E-33	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1162	14316		2.25	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2184	15328	28454	3.37	4.0E-33	4768887	NT	Homo sapiens RAB1, member RAS oncogene family (RAB1) mRNA
2491	15618		1.16	4.0E-33	AA626621.1	EST_HUMAN	ab51b1.11 Stragene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element contains MER28.b2 MER28 repetitive element;
2810	15734	28850	4.78	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4806	17743	30722	2.38	4.0E-33	AW283349.1	EST_HUMAN	UHH-B12-ah-c-03-OUI.s1 NCI_CGAP.Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5518	18717	31731	24.75	4.0E-33	AA05053.1	EST_HUMAN	z171a08.11 Stragene colon (#937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gbX12871_mna1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
5522	18687	33060	0.79	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
5522	18687	33061	0.79	4.0E-33	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1113	14278		6.62	3.0E-33	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3 MER28 repetitive element;
1114	14278		5.83	3.0E-33	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3 MER28 repetitive element;
2522	16084		1.16	3.0E-33	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLCFCF09 3'
10655	23689	37298	0.87	3.0E-33	AA881510.1	EST_HUMAN	ak32b12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407847 3' similar to TR:Q13579 Q13579 MARINER TRANSPOSASE.;
18	13256		1.57	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF.t1 ORF repetitive element.;
107	13286		5.53	2.0E-33	AI160189.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF.t1 ORF repetitive element.;
4539	17877		4.53	2.0E-33	BE158039.1	EST_HUMAN	qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF.t1 ORF repetitive element.;
5100	18228	31199	8.64	2.0E-33	AA626683.1	EST_HUMAN	MFO-HT0405-160300-202-408 HT0405 Homo sapiens cDNA
5204	18325	31294	1.6	2.0E-33	11421332	NT	ab51g11.11 Stragene lung carcinoma 337218 Homo sapiens cDNA clone IMAGE:844388 5' similar to gbX00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5204	18325	31295	1.6	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5553	18715	33091	1.39	2.0E-33	AI277492.1	EST_HUMAN	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
6301	22377		2.15	2.0E-33	AI052256.1	EST_HUMAN	q186401.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1680161 3'
9	13247		1.61	1.0E-33	AF003528.1	NT	oz21d03.x1 Soares_fetal_liver_spleen_1NFL3_S1 Homo sapiens cDNA clone IMAGE:1675973 3' similar to gbM29536 TRANSLOCATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
7585	20537	34113	0.86	1.0E-33	M13975.1	NT	gbM29536 TRANSLOCATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
							Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds

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10227	26229		1.4	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11602	24656	38340	1.56	1.0E-33	AV99818.1	EST_HUMAN	QV3-BND047-230200-102403 BND047 Homo sapiens cDNA
11982	24947	38662	2.44	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12768	25511		1.25	1.0E-33	AV004491.1	EST_HUMAN	RC5-N1055-260400-021-G03 N11055 Homo sapiens cDNA
12928	13247		5.7	1.0E-33	AF003528.1	NT	Homo sapiens X-linked embryonic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12980	25626	31879	2.19	1.0E-33	AV727808.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCCNC12.5
13178	26766		4.77	8.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2240	16373	28501	0.96	8.0E-34	8922751	NT	Homo sapiens hypothetical protein FLJ10900 (FLJ10900), mRNA
4620	17767	30739	1.83	8.0E-34	BE062570.1	EST_HUMAN	QV2-B10288-071299-019-g07 BT0268 Homo sapiens cDNA
7874	21024	34537	0.87	8.0E-34	BE039882.1	EST_HUMAN	NR4-B10389-200100-001-h03 BT0399 Homo sapiens cDNA
1476	14828	27714	2.5	7.0E-34	TT0845.1	EST_HUMAN	Yd16505.t1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:108320 5'
10204	14829	27714	0.54	7.0E-34	TT0845.1	EST_HUMAN	Yd16505.t1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:108320 5'
12482	26394		3.85	7.0E-34	H12986.1	EST_HUMAN	Y14610.t1 Soares placenta Nb21p Homo sapiens cDNA clone IMAGE:148722 5'
483	13677	28711	1.74	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
483	13677	28711	1.74	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
5247	18368	31335	1.68	6.0E-34	AV09811.1	EST_HUMAN	PM0-BND065-100300-001-c08 BND065 Homo sapiens cDNA
12280	25215	32089	2.22	6.0E-34	U03986.1	NT	Mus musculus DAB2J hair-specific (hadr-1) gene
1928	16072		3.15	5.0E-34	U06500	NT	Human splicing factor SRP55-1 (SRP-55) mRNA, complete cds
5173	18285	31287	5.24	5.0E-34	U00883.1	NT	Homo sapiens Npw48-binding protein NpwBP (LOC51729), mRNA
8067	22146	35693	1.17	5.0E-34	AF078778.1	NT	Human splicing factor SRP55-1 (SRP-55) mRNA, complete cds
10880	23974	37605	2.02	5.0E-34	AB037856.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11632	24588		1.83	5.0E-34	AL163209.2	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
2034	16195	28309	2.09	4.0E-34	AI004667.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
3241	18415	29430	0.9	4.0E-34	5803168	NT	HS4408.x1 NC1_CGAP_P728 Homo sapiens cDNA clone IMAGE:2249184 3'
6981	19168	32489	0.82	4.0E-34	AA064773.1	EST_HUMAN	Homo sapiens splicing factor 3a, subunit 3, 60KD (SF3A3), mRNA
9238	22315	35857	0.83	4.0E-34	BF20878.1	EST_HUMAN	AK3501.61 Soares testis N4T Homo sapiens cDNA clone IMAGE:1407639 3'
6361	18531	32880	0.88	3.0E-34	M31277.1	NT	601874850.F1 NIH_MGC_34 Homo sapiens cDNA clone IMAGE:4102213 5'
11420	24481		2.66	3.0E-34	BF035327.1	EST_HUMAN	Human 1q germline H-chain D-region genes, partial cds
9152	22230	35774	0.75	2.0E-34	AI678101.1	EST_HUMAN	601458531.F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
9152	22230	35775	0.75	2.0E-34	AI678101.1	EST_HUMAN	Wd33g08.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains Wd33g08.x1 Soares_NFL_T_G8C_S1
11431	24492	38156	8.64	2.0E-34	P51895	SWISSPROT	Wd33g08.x1 Soares_NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains Wd33g08.x1 Soares_NFL_T_G8C_S1

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11431	24492	38157	8.54	2.0E-34	P51805	SWISSPROT	PLEXIN 4 PRECURSOR (TRANSMEMBRANE PROTEIN SEX)
1634	14697	27767	10.13	1.0E-34	P12236	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
1738	14897		7.18	1.0E-34	AU136024.1	EST_HUMAN	AU136024 PLACE1 Homo sapiens cDNA clone PLACE1003383 5'
3764	16825	29927	2.51	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4181	17331	30323	0.79	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4181	17331	30324	0.79	1.0E-34	AY008397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4602	17739		8.28	1.0E-34	BE071414.1	EST_HUMAN	RC2-B10508-240400-018-h08 B10508 Homo sapiens cDNA
6268	18440	32787	2.26	1.0E-34	BE974052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3866999 5'
6268	19440	32788	2.28	1.0E-34	BE974052.1	EST_HUMAN	601484430F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3866999 5'
9527	22592	38163	0.64	1.0E-34	P23268	SWISSPROT	OLFACTOR RECEPTOR-LIKE PROTEIN F5
9898	22638	38523	8.07	1.0E-34	AU036635.1	EST_HUMAN	DKFZ554A1553.1 564 (synonym: hbr2) Homo sapiens cDNA clone DKFZ554A1553 5'
11459	24518	38186	1.51	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11459	24518	38187	1.51	1.0E-34	BE781790.1	EST_HUMAN	601470592F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873478 5'
11473	24532	38202	2.82	1.0E-34		NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12660	26125		2.44	1.0E-34	AA807097.1	EST_HUMAN	cc31c11.s1 NCL_CGAP_G031 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb: X68203
12950	26660		5.84	1.0E-34	AL163210.2	NT	TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN);
3735	16868	28800	1.3	9.0E-35	AW663302.1	EST_HUMAN	hbt7b06.y1 NCL_CGAP_G01 Homo sapiens cDNA clone IMAGE:2968787 5'
232	13453		7.21	8.0E-35	6031190	NT	Homo sapiens prohibitin (PHB), mRNA
1776	14925	28019	3.63	8.0E-35	BF389937.1	EST_HUMAN	ne83408.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
1776	14926	28020	3.63	8.0E-35	BF389937.1	EST_HUMAN	ne83408.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912
4989	18118	31097	2.51	8.0E-35	BF183195.1	EST_HUMAN	O75912 DIACYLGLYCEROL KINASE IOTA.;
10828	24011	37645	1.53	8.0E-35	BE379480.1	EST_HUMAN	601230488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608513 5'
12404	26283		5.89	8.0E-35	BF66282.1	EST_HUMAN	602184624T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300860 3'
6813	19773	33164	1.01	7.0E-35	11423417	NT	Homo sapiens phosphatidylinositol glycan, class C (PIGC), mRNA
1445	14598	27675	1.06	6.0E-35	AA175716.1	EST_HUMAN	at63h03.s1 Soares_teste_NHT Homo sapiens cDNA clone 1309397 3'
2025	16166	28271	4.63	6.0E-35	6005975	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
4184	17314	30309	0.8	6.0E-35	AV297191.1	EST_HUMAN	UHLHBW-afid-d-090-UJ.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731433 3'
8081	21163	34880	4.03	6.0E-35	6005921	NT	Homo sapiens triple functional domain (PTPase interacting) (TRIO), mRNA
8906	21985	35524	0.57	6.0E-35	X61232.1	NT	H. sapiens mRNA for novel T-cell activation protein

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8808	21885	35525	0.57	6.0E-35	X64232.1	NT	H. sapiens mRNA for novel T-cell activation protein
9867	22907	38492	0.61	6.0E-35	AB002384.1	NT	Human mRNA for KIAA0386 gene, partial cds
10107	23145	38743	2.97	6.0E-35	AF037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
148	13373	20406	0.61	5.0E-35	AF164830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
1746	14895	27989	2.25	9.0E-35	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2844	16568	29087	0.99	5.0E-35	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
3074	16280	28271	2.87	6.0E-35	6972639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
4528	17667	30653	1.72	6.0E-35	AF023268.1	NT	Homo sapiens cdk2 kinase (CLK2), profilin, cofilin, glucocorticoid-induced pseudogene, and thrombospondin 3 (THBS3) gene, partial cds
8378	21459		4.25	6.0E-35	BE090982.1	EST_HUMAN	601431884F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
8405	21486	35016	2.17	5.0E-35	AI208765.1	EST_HUMAN	qg38c05.x1 Soares_Jestis_NHT Homo sapiens cDNA clone IMAGE:1837448 5' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249.:
8405	21486	35016	2.17	5.0E-35	AI208765.1	EST_HUMAN	qg38c05.x1 Soares_Jestis_NHT Homo sapiens cDNA clone IMAGE:1837448 5' similar to SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249.:
11451	24511		2.54	5.0E-35	AA001786.1	EST_HUMAN	z784112.t1 Soares_Totol liver_spleen_TNFLS_S1 Homo sapiens cDNA clone IMAGE:428016 5'
1465	14619	27703	20.48	4.0E-35	BE267807.1	EST_HUMAN	601109719F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350405 5'
1862	15008	28114	11.21	4.0E-35	H01193.1	EST_HUMAN	YU88A07.t1 Soares fetal liver spleen TNF.LS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element:
7358	20437		1.67	4.0E-35	BE350127.1	EST_HUMAN	hm09d01.x1 NCJ_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29B3
8715	21795	35332	8.05	4.0E-35	AI046586.1	EST_HUMAN	MER29 repetitive element: DKFZp434L148.t1 434 (synonym: hla3) Homo sapiens cDNA clone DKFZp434L148 5'
12088	25078	38786	2.5	4.0E-35	AF114196.1	NT	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
1610	14763	27843	33.82	3.0E-35	BE268182.1	EST_HUMAN	601128260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345083 5'
2408	15539		2.64	3.0E-35	AF224482.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
5456	18656	31634	23.43	3.0E-35	BF433100.1	EST_HUMAN	7p28a08.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7
5456	18656	31634	23.43	3.0E-35	BF433100.1	EST_HUMAN	Q8QZH7.F-BOX PROTEIN FBL2.:
8899	22738		1.45	3.0E-35	AF223391.1	NT	7p28a08.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q9QZH7
10378	23413	37022	1.5	3.0E-35	AW003063.1	EST_HUMAN	Q9QZH7.F-BOX PROTEIN FBL2.:
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
							wf03a05.x1 NCJ_CGAP_G08 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW:POL1_HUMAN P-10266 RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE:]

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
111	16005	26372	1.25	2.0E-36	N88665.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
1215	14376	27439	1.89	2.0E-35	T19009.1	EST_HUMAN	REPTITIVE ELEMENT
2282	16424	28558	4.56	2.0E-35	AB018413.1	NT	AB71F Heart Homo sapiens cDNA clone AB71
2748	16865	28976	1.13	2.0E-35	AY665005.1	EST_HUMAN	h86a12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979166 3' similar to
3386	16558	28570	1.08	2.0E-35	6912459	NT	SW:TR12_HUMAN Q14689 THYROID RECEPTOR INTERACTING PROTEIN 12:
3386	16558	28571	1.08	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (K1AA0571), mRNA
3847	16810		0.77	2.0E-35	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4019	17176	30184	0.85	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Bay61-HIGSC project:TCBA Homo sapiens
4019	17176	30185	0.85	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Bay61-HIGSC project:TCBA Homo sapiens
4792	17927		3.01	2.0E-35	H49239.1	EST_HUMAN	cdna clone TCBAP4328
6700	18894	32186	1.93	2.0E-35	BF33247.1	EST_HUMAN	Wt18a12.1 Scores fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:274079 5'
7263	20336	33785	0.6	2.0E-35	BE932636.1	EST_HUMAN	QV0-BT0701-210400-189-b04 BT0701 Homo sapiens cDNA
7263	20336	33786	0.6	2.0E-35	BE932636.1	EST_HUMAN	CM2-MT0125-280700-287-G02 MT0125 Homo sapiens cDNA
11036	24116	37749	2.93	2.0E-35	X68417.1	NT	H. sapiens PROS-27 mRNA
12157	16566	28570	1.22	2.0E-35		NT	Homo sapiens Grb2-associated binder 2 (K1AA0571), mRNA
12157	16566	28571	1.22	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (K1AA0571), mRNA
12342	25247	32111	1.33	2.0E-35	BE934978.1	EST_HUMAN	601486774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:389869 5'
12342	25247	32112	1.33	2.0E-35	BE934978.1	EST_HUMAN	601486774F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:389869 5'
12831	26814		7.22	2.0E-35	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
13066	16005	26372	1.74	2.0E-35	N88665.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to
47	13288	26295	5.76	1.0E-36	AA631846.1	EST_HUMAN	REPTITIVE ELEMENT
47	13288	26296	5.76	1.0E-35	AA631846.1	EST_HUMAN	fric16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
771	13952	27000	35.82	1.0E-35	AW389473.1	EST_HUMAN	fric16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
771	13952	27001	35.82	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131099-006-412 ST0162 Homo sapiens cDNA
832	14107		1.28	1.0E-35	TE947.1	EST_HUMAN	y639a01.1 Scores fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:115752 5' similar to
2807	15730	28847	1.86	1.0E-35	7705994	NT	SP-A44282 A44282 RETROVIRUS-RELATED POL YPROTEIN - HUMAN:
2826	15940	28050	1.34	1.0E-35	BE50127.1	EST_HUMAN	Homo sapiens hypodermal protein (LOC51233), mRNA
							h10901.x1 NCL_CGAP_K1413 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28 b3
							MER29 repetitive element:



Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2826	16940	29051	1.34	1.0E-35	BE350127.1	EST_HUMAN	h06g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.B3
3212	16386	28397	1.87	1.0E-35	6006030	NT	MER29 repetitive element;
3232	16406	29418	1.67	1.0E-35	AV650422.1	EST_HUMAN	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCBF1L) mRNA
3232	16406	29419	1.67	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GIC Homo sapiens cDNA clone GICCEF06 3'
4542	17680	30661	4.82	1.0E-35	7656905	NT	AV650422 GIC Homo sapiens cDNA clone GICCEF06 3'
4542	17680	30662	4.82	1.0E-35	7656905	NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
6827	18821	31896	1.48	1.0E-35	11526236	NT	Mus musculus actin receptor interacting protein 1 (Arip1-pending), mRNA
7135	18561	31475	0.74	1.0E-35	AW808665.1	EST_HUMAN	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7135	18561	31476	0.74	1.0E-35	AW808665.1	EST_HUMAN	MR1-ST0111-111189-011-d07 ST0111 Homo sapiens cDNA
7652	20720	34196	0.89	1.0E-35	AB033105.1	NT	MR1-ST0111-111189-011-d07 ST0111 Homo sapiens cDNA
7819	20874	34373	0.91	1.0E-35	11418002	NT	Homo sapiens mRNA for KIAA1279 protein, partial cds
8742	26861	36383	2.48	1.0E-35	AU158595.1	EST_HUMAN	Homo sapiens KIAA0645 gene product (KIAA0645), mRNA
8742	26861	36384	2.48	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLAC3 Homo sapiens cDNA clone PLACE300382 3'
10805	23838	37462	0.72	1.0E-35	BF598594.1	EST_HUMAN	nan06d06.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
10805	23838	37463	0.72	1.0E-35	BF598594.1	EST_HUMAN	O31341 BETA-GALACTOSIDASE 1
12055	26036	38743	1.49	1.0E-35	AB028980.1	NT	nan06d06.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
12055	26036	38744	1.49	1.0E-35	AB028980.1	NT	O31341 BETA-GALACTOSIDASE 1
12062	26043		2.04	1.0E-35	AI525119.1	EST_HUMAN	Homo sapiens mRNA for KIAA1057 protein, partial cds
12188	26077		6.35	1.0E-35	11418274	NT	Homo sapiens mRNA for KIAA1057 protein, partial cds
12406	26284		1.26	1.0E-35	11418110	NT	primase-7 DBP1 bifurcar Homo sapiens cDNA 5'
12806	26539		2.49	1.0E-35	BE792832.1	EST_HUMAN	Homo sapiens fibulin 1 (FBLN1), mRNA
6131	18310	32650	0.67	8.0E-36	XV8478.1	NT	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
9430	22504	36070	0.79	8.0E-36	AA348480.1	EST_HUMAN	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
2897	16173	28192	1.53	7.0E-36	AB87678.1	EST_HUMAN	Homo sapiens casein kinase 1, epsilon (CSNK1E), mRNA
3188	16363		5.26	7.0E-36	4557498	NT	60T584833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3838985 5'
6273	18392	31360	1.09	7.0E-36	C21409	SWISSPROT	B.ova BBSc mRNA for schlerin
6273	18392	31361	1.09	7.0E-36	C21409	SWISSPROT	EST54628 Hippocampus II Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 9, 5' LTR
7832	20887	34389	6.31	7.0E-36	U06872.1	NT	CM1-CT0315-091298-083-d07 CT0315 Homo sapiens cDNA
7832	20887	34389	6.31	7.0E-36	U06872.1	NT	Homo sapiens C-terminal binding protein 2 (CTBP2) mRNA
12570	25388	32040	27.38	7.0E-36	AF052051.1	NT	ADHESIVE PLAQUE MATRIX PROTEIN PRECURSOR (FOOT PROTEIN 1) (MGFP1) (MGFP-1)

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2060	16201	28315	1.92	6.0E-36	7706622	NT	Homo sapiens nhlh2 2 (NHLH2), mRNA
2490	16917		5.59	6.0E-36	AB035346.1	NT	Homo sapiens TOL8 gene, exon 12
3729	16990	29894	0.59	6.0E-36	BF518101.1	EST_HUMAN	U4H-BW1-amy-c-12-O-UL1, NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
6448	18648	31824	7.17	6.0E-36	AI435159.1	EST_HUMAN	083005.x1 Soares, NSF, 78_9W_OT_PA_P_31 Homo sapiens cDNA clone IMAGE:2126185 3' similar to
7258	20341	33792	3.03	6.0E-36	AW780143.1	EST_HUMAN	083005.x1 NCI_CGAP_C014 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMAZ_HUMAN
8853	21832	36471	4.62	6.0E-36	AF208161.1	NT	P52292 IMPORTIN ALPHA-2-SUBUNIT
10430	23465		0.63	6.0E-36	CT6927.1	EST_HUMAN	Homo sapiens synaptophysin precursor, mRNA, complete cds
11841	24630	38521	3.49	6.0E-36	AI380499.1	EST_HUMAN	08509.x1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:2107024 3' similar to contains MERR9.b2
140	13366	26399	16.16	6.0E-36	AJ271735.1	NT	MERR9 repetitive element
2809	15923	28033	21.08	5.0E-36	BE398436.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
3700	16861	29863	3.24	5.0E-36	AL163209.2	NT	601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
4809	18039	31028	1.31	5.0E-36	5729729	NT	Homo sapiens chromosome 21 segment HS21C009
4909	18039	31028	1.31	5.0E-36	5729729	NT	Homo sapiens AP15-like 1 (AP15L1), mRNA
7669	21016	34528	0.59	6.0E-36	11078227	NT	Homo sapiens AP15-like 1 (AP15L1), mRNA
12166	13366	26399	8.11	5.0E-36	AJ271735.1	NT	Homo sapiens N-ethylmaleimide-sensitive factor (NSF), mRNA
12458	26322	32095	2.56	5.0E-36	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1252	14411	27473	1.57	4.0E-36	BE010038.1	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1677	14829	27913	1.36	4.0E-36	BE362574.1	EST_HUMAN	PM3-BN0176-100400-001-904 BN0176 Homo sapiens cDNA
2287	15428		4.14	4.0E-36	AW247772.1	EST_HUMAN	601289574F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3628386 5'
3435	16603	29622	1.1	4.0E-36	BE362599.1	EST_HUMAN	2820020 SpHme NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3435	16603	29623	1.1	4.0E-36	BE362599.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
4877	18008	30892	0.59	4.0E-36	AL163204.2	NT	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
5833	18024		0.99	4.0E-36	RF6423.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
6180	18368	32704	2.49	4.0E-36	11497041	NT	Y1905.r1 Soares placenta NB24P Homo sapiens cDNA clone IMAGE:138713 5'
7831	20888	34388	1.78	4.0E-36	M33320.1	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
8752	21831	35369	1.45	4.0E-36	C87675.1	NT	Human placenta Glycoprotein IIb (GPIIb) gene, exons 2-29
8752	21831	35370	1.45	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
11235	24304	37941	3.13	4.0E-36	AA400370.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
12476	25328		1.61	4.0E-36	11420516	NT	z08c10.r1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:743250 5'
12520	25951		4.27	4.0E-36	AV753629.1	EST_HUMAN	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
714	13889	28934	2.93	3.0E-36	AF098910.1	NT	AV753629 TP Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMAZ_HUMAN

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2373	15504	28630	1.19	3.0E-36	7662401	NT	Human sapiens KIAA0952 protein (KIAA0952), mRNA
4624	17761	30743	7.5	3.0E-36	10161139	NT	Mus musculus Junctophilin 1 (Jp1-pending), mRNA
11368	24426	38086	1.84	3.0E-36	BE036327.1	EST_HUMAN	601459531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3238	16412	29427	2.5	2.0E-36	BE259267.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342706 5'
5074	18202	31174	10.78	2.0E-36	AW880376.1	EST_HUMAN	QV0-Q10030-240300-174-R04 OT0030 Homo sapiens cDNA
5603	18768	31848	2.88	2.0E-36	AF267747.1	NT	Mus musculus P47-phox gene, complete cds
5870	19156	32471	3.75	2.0E-36	T08756.1	EST_HUMAN	EST06648 Infant Brain, Banto Scores Homo sapiens cDNA clone HIBB128 5' end
6706	19864	33254	13.94	2.0E-36	T63629.1	EST_HUMAN	yc44407.1 Stralagene liver (#837224) Homo sapiens cDNA clone IMAGE:83508 5'
9588	22643	36212	0.94	2.0E-36	BF512704.1	EST_HUMAN	U1-H-BW1-enu-e-11-0-U1.s1 NCL_CGAP_SubD Homo sapiens cDNA clone IMAGE:3071132 3'
9749	22687	36258	0.74	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP-13), mRNA
9749	22687	36259	0.74	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP-13), mRNA
908	14053	27148	1.74	1.0E-36	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2212	15346	28474	1.71	1.0E-36	BE146523.1	EST_HUMAN	RC1-H10217-131199-021-h07 HT0217 Homo sapiens cDNA
2212	15346	28475	1.71	1.0E-36	BE146523.1	EST_HUMAN	RC1-H10217-131199-021-h07 HT0217 Homo sapiens cDNA
2279	16408	28538	1.83	1.0E-36	BF073761.1	EST_HUMAN	602136483F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:427288 5'
3425	16564		3.33	1.0E-36	AF156882.1	NT	Homo sapiens human endogenous retrovirus W prov6-18 protease (pro) gene, partial cds
5847	19037	32344	0.94	1.0E-36	AI044446.1	EST_HUMAN	DKFZp434G022.1 434 (synonym: hsc3) Homo sapiens cDNA clone DKFZp434G022 5'
6020	19203	32523	1.23	1.0E-36	4827064	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147), mRNA
6312	19484		4.27	1.0E-36	AB6774.1	EST_HUMAN	wb37c12.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element
6519	19884	33055	1.9	1.0E-36	RC25012.1	EST_HUMAN	yg38g10.1 Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:34529 5' similar to SP-CAHP_HUMAN P35218 CARBONIC ANHYDRASE-RELATED PROTEIN 1
6519	19884	33056	1.9	1.0E-36	RC25012.1	EST_HUMAN	yg38g10.1 Scores Infant brain 1NIB Homo sapiens cDNA clone IMAGE:34529 5' similar to SP-CAHP_HUMAN P35218 CARBONIC ANHYDRASE-RELATED PROTEIN 1
6820	19973	33361	0.72	1.0E-36	AI120542.1	EST_HUMAN	SP-CAHP_HUMAN P35218 CARBONIC ANHYDRASE-RELATED PROTEIN 1
8147	21228	34747	4.06	1.0E-36	AA148034.1	EST_HUMAN	DKFZp761A228.1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZp761A228 5'
8147	21228	34748	4.06	1.0E-36	AA148034.1	EST_HUMAN	z051a12.1 Stralagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:560398 5'
8243	21325	34841	0.78	1.0E-36	AA220467.1	EST_HUMAN	z051a12.1 Stralagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:560398 5'
8243	21325	34842	0.78	1.0E-36	AA220467.1	EST_HUMAN	ncb0608.1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8373	21454	34977	0.88	1.0E-36	AI141688.1	EST_HUMAN	ncb0608.1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8373	21454	34978	0.88	1.0E-36	AI141688.1	EST_HUMAN	AIU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
9226	22307	35850	3.33	1.0E-36	AV103698.1	EST_HUMAN	AIU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
10320	23355	36984	3.83	1.0E-36	BF584189.1	EST_HUMAN	ys2b507.x1 NCL_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614357 3'
10534	23559	37176	0.84	1.0E-36	AV1855868.1	EST_HUMAN	QV3-NN1023-010600-199-H01 NN1023 Homo sapiens cDNA
							RC3-CT0278-040500-017-a10 CT0278 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10534	23569	37177	0.64	1.0E-36	AW856883.1	EST_HUMAN	RC3-C10279-040500-017-a10 CT0279 Homo sapiens cDNA
11190	24269	37895	2.55	1.0E-36	AW897633.1	EST_HUMAN	GM3-NN0061-140400-147-h12 NN0061 Homo sapiens cDNA
11662	24741	38432	3.55	1.0E-36	AW504143.1	EST_HUMAN	U1-HF-BN0-ale-c-03-0-U1.1 NH_MGC_50 Homo sapiens cDNA clone IMAGE:307927 5'
12048	25028		10.8	1.0E-36	11648901	NT	Homo sapiens PP3227 protein (PP3227), mRNA
12340	25245		2.83	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12836	25566		5.76	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
13131	25737		2.76	1.0E-36	AF202723.1	NT	Homo sapiens Sact1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7539	20612	34087	2.27	8.0E-37	AW009277.1	EST_HUMAN	was00b07.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
7539	20612	34088	2.27	8.0E-37	AW009277.1	EST_HUMAN	was00b07.x1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245 3'
12618	25417		3.57	8.0E-37	W22618.1	EST_HUMAN	73D4 Human retina cDNA Tsp509-cleaved sublibrary Homo sapiens cDNA not directional
3436	16604	29824	1.4	8.0E-37	4757879	NT	Homo sapiens chimerin (chimerin) 2 (CHN2) mRNA
6363	18566		1.7	8.0E-37	BE698077.1	EST_HUMAN	CM0-UT0003-050800-503-d09 UT0003 Homo sapiens cDNA
5949	19135	32448	3.48	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:3140266 3' similar to contains MER29 b3
5949	19135	32448	3.48	8.0E-37	BE350127.1	EST_HUMAN	MER29 repetitive element:
5949	19135	32448	3.48	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:3140266 3' similar to contains MER29 b3
5996	19183	32505	7.08	8.0E-37	AW840840.1	EST_HUMAN	MER29 repetitive element:
8089	21150	34870	6.2	8.0E-37	X37344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14
1313	14469		4.82	7.0E-37	AL042800.1	EST_HUMAN	genes
5226	18350	31320	3.04	7.0E-37	AW868823.1	EST_HUMAN	DKFZp434E0422.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434E0422 5'
10994	24073	37706	8.66	7.0E-37	AI817700.1	EST_HUMAN	EST380699 IMAGE: resseques, MAG1 Homo sapiens cDNA
11134	24206	37831	1.89	7.0E-37	AI536702.1	EST_HUMAN	wk26b11.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.12
8634	21714	35251	0.59	6.0E-37	AF168889.1	NT	PTR5 repetitive element:
12864	25576		2.3	6.0E-37	U78308.1	NT	tm87g03.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2185140 3' similar to contains L1.b3 L1
12864	25576		2.3	6.0E-37	U78308.1	NT	repetitive element:
12864	25576		2.3	6.0E-37	U78308.1	NT	Homo sapiens protocadherin alpha 10 alternative isoform (PCDH-10) mRNA, complete cds
12864	25576		2.3	6.0E-37	U78308.1	NT	Homo sapiens olfactory receptor olfr17-201.1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo olfr17-01 (OR17-01) pseudogene, complete cds
12864	25576		2.3	6.0E-37	U78308.1	NT	Homo sapiens Sact1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
12864	25576		2.3	6.0E-37	U78308.1	NT	EST1178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8218	18383	32741	4.3	5.0E-37	AA307123.1	EST_HUMAN	EST1178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8218	18383	32742	4.3	5.0E-37	AA307123.1	EST_HUMAN	AV750211 NPC Homo sapiens cDNA clone NPC8GH08 5'
8956	22035	35576	1.03	5.0E-37	AV750211.1	EST_HUMAN	Homo sapiens glycine C-acetyltransferase 2 (amilo-3-hydrobutyrate-CoA ligase) (GCAT), mRNA
1160	24231		4.02	5.0E-37	7857117	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
12335	25242		3.63	5.0E-37	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2485	15622	28741	2.87	4.0E-37	AA702794.1	EST_HUMAN	Z80b04.e1 Soares fetal liver spleen, INFUS_S1 Homo sapiens cDNA clone IMAGE:448018.3
6416	16685	32847	0.88	4.0E-37	AW794502.1	EST_HUMAN	RC8-UM0014-210200-021-H05 UM0014 Homo sapiens cDNA
9559	22921	36192	0.56	4.0E-37	AA843806.1	EST_HUMAN	RA096022.5 Soares parathyroid tumor NBHFA Homo sapiens cDNA clone IMAGE:1405442.3
2074	15214	28332	3.42	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418.t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
2074	15214	28333	3.42	3.0E-37	AL048956.1	EST_HUMAN	DKFZp434L2418.t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L2418
2581	15706		1.54	3.0E-37	AW681150.1	EST_HUMAN	EST373222 IMAGE resequences, MAGF Homo sapiens cDNA
3030	16206		4.02	3.0E-37	AW681150.1	EST_HUMAN	EST373222 IMAGE resequences, MAGF Homo sapiens cDNA
5985	18170	32492	0.7	3.0E-37	AL138274.1	EST_HUMAN	DKFZp547G067.t1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547G067.5
7728	20780	34279	0.72	3.0E-37	AI749952.1	EST_HUMAN	AI84605.X1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373896.3 similar to TR:Q13537
392	13629	26688	0.89	2.0E-37	DB9780.1	NT	Homo sapiens mRNA for AML1, complete cds
392	13629	26687	0.89	2.0E-37	DB9780.1	NT	Homo sapiens mRNA for AML1, complete cds
1105	14270	27328	2.53	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2R3 Homo sapiens cDNA clone NT2R3002186.5
1105	14270	27329	2.53	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2R3 Homo sapiens cDNA clone NT2R3002186.5
2021	15162	28287	1.32	2.0E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3989	17156	30162	6.71	2.0E-37		4503210 NT	Homo sapiens chromosome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
4360	17603	30485	0.6	2.0E-37		4826885 NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
6504	18703		0.9	2.0E-37	BF035327.1	EST_HUMAN	601458531.F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086.5
6076	19835	33224	0.6	2.0E-37		11800617 NT	Homo sapiens mouse thiamin pyrophosphokinase homolog (TPK1), mRNA
6789	19953	33393	3.72	2.0E-37	AA346720.1	EST_HUMAN	EST2831.Fetal heart II Homo sapiens cDNA 5' end
8185	21267	34780	0.47	2.0E-37	BE53764.1	EST_HUMAN	601067534.F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657.5
8185	21267	34781	0.47	2.0E-37	BE53764.1	EST_HUMAN	601067534.F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453657.5
8227	21309	34829	2.32	2.0E-37	BE204032.1	EST_HUMAN	601869157.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111406.5
11856	24844	38541	10.07	2.0E-37	AF176013.1	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
12797	26770		1.44	2.0E-37		11417972 NT	Homo sapiens pescadillo (zabratish) homolog 1, containing BRCT domain (PEST1), mRNA
13184	26770		4.19	2.0E-37		11417972 NT	Homo sapiens pescadillo (zabratish) homolog 1, containing BRCT domain (PEST1), mRNA
2154	15290	28417	6.95	1.0E-37	AI163282.1	NT	Homo sapiens chromosome 21 segment HS21C081
3267	16441		1.03	1.0E-37	AB62082.1	EST_HUMAN	RC3-CT0347-210400-016-h03 CT0347 Homo sapiens cDNA
5055	18163	31158	2.34	1.0E-37	BF37719.1	EST_HUMAN	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
6127	19306		0.89	1.0E-37		7305960 NT	Mus musculus cdcgellin (Clog), mRNA
8409	21490	35019	1.12	1.0E-37	BE54032.1	EST_HUMAN	601072419.F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458308.5
8933	22012	35551	3.59	1.0E-37	AA171408.1	EST_HUMAN	zcp21b02.1 Shalagene neurophilinellum (#937231) Homo sapiens cDNA clone IMAGE:610059.5 similar to contains L11L2L1 repetitive element.

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10937	24018	37652	2.19	1.0E-37	M22878.1	NT	Human somatic cytochrome c (Hc1) processed pseudogene, complete cds
12871	25447		1.84	1.0E-37	BE71814.1	EST_HUMAN	CA3-FT0066-140700-243-d07 FT0066 Homo sapiens cDNA
5898	19088	32298	1.72	9.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC56768), mRNA
1249	14408	27470	1.98	8.0E-38	11436985	NT	Homo sapiens Grn2-associated binder 2 (KIAA0571), mRNA
2967	15692	28617	1.21	8.0E-38	BF346221.1	EST_HUMAN	602018401F1 NCI_CGAP_Bri87 Homo sapiens cDNA clone IMAGE:4153992.5
12735	14408	27470	1.37	8.0E-38	11436985	NT	Homo sapiens Gln2-associated binder 2 (KIAA0571), mRNA
13210	26049		1.44	8.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
2254	18387	28515	1.7	7.0E-38	AW872825.1	EST_HUMAN	EST384920 IMAGE:ressequences, MAGL Homo sapiens cDNA
3107	16283	28289	1.98	6.0E-38	BF033033.1	EST_HUMAN	601456722F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3858348.5
5708	18899	32192	0.88	6.0E-38	11426114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5708	18899	32193	0.98	6.0E-38	11426114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
7482	20567	34029	0.59	6.0E-38	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
12189	25147		4.27	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12704	25468	32025	6.66	6.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
13160	25913	31861	1.79	6.0E-38	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
745	13928	28987	0.8	5.0E-38	AW871819.1	EST_HUMAN	EST383908 IMAGE:ressequences, MAGL Homo sapiens cDNA
2525	15650	28774	4.57	5.0E-38	AI237740.1	NT	Homo sapiens RIBIR gene (partial), exon 8
3786	16957	28981	0.94	5.0E-38	7849804	NT	Homo sapiens telodirase, lodothyronine, type II (DIO2), transcript variant 2, mRNA
3974	16957	28981	0.77	5.0E-38	7849804	NT	Homo sapiens telodirase, lodothyronine, type II (DIO2), transcript variant 2, mRNA
6288	15650	28774	0.88	6.0E-38	AI237740.1	NT	Homo sapiens RIBIR gene (partial), exon 8
7172	20305	33748	1.53	5.0E-38	BE871610.1	EST_HUMAN	601450148F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854074.5
121	13351	26380	4.28	4.0E-38	Z25466.1	NT	B. leuvis mitochondrial aspartate aminotransferase mRNA, complete CDS
121	13351	26381	4.28	4.0E-38	Z25466.1	NT	B. leuvis mitochondrial aspartate aminotransferase mRNA, complete CDS
1183	14348	27403	1.15	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2167	15302		4.42	3.0E-38	AF003530.1	NT	Homo sapiens homobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3787	16948		1.48	3.0E-38	7649807	NT	Homo sapiens HIRA interacting protein 4 (hnal-like) (HIRIP4), mRNA
3858	17116	30118	2.48	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3958	17116	30120	2.46	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4736	17871		0.61	3.0E-38	BE279901.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272.5
6893	26836	33453	6.89	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7393	20471	33937	0.88	3.0E-38	AW302461.1	EST_HUMAN	XMG4d01 x1 NCI_CGAP_Bri53 Homo sapiens cDNA clone IMAGE:2827009.5
7783	20822	34313	8.53	3.0E-38	BF373684.1	EST_HUMAN	CA3-FT0181-140700-241-d07 FT0181 Homo sapiens cDNA
8851	21930	35459	2.11	3.0E-38	H85499.1	EST_HUMAN	Y888b04.1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:249775.5
8851	21930	35470	2.11	3.0E-38	H85499.1	EST_HUMAN	Y888b04.1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:249775.5

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10177	23214		1.84	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11598	24551		1.88	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12990	14346	27403	1.23	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
51	13260	28303	1.06	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1411	14565	27639	3.56	2.0E-38	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA
1678	14830	27914	13.95	2.0E-38	AA437353.1	EST_HUMAN	SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ; Z600401.1 Soares very tumor NBH0T Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ; Z600401.1 Soares very tumor NBH0T Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1678	14830	27915	13.95	2.0E-38	AA437353.1	EST_HUMAN	SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ; Z600401.1 Soares very tumor NBH0T Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
3622	16795		0.92	2.0E-38	AJ070670.1	NT	Homo sapiens protein phosphatase 2C alpha 2 mRNA, complete cds
4704	17639	30824	18.59	2.0E-38	4557987	NT	Homo sapiens keratin 18 (KRT18) mRNA
5252	18339	31312	0.68	2.0E-38	AA437181.1	EST_HUMAN	Z61409.1 Soares, Jasius, NHT Homo sapiens cDNA clone IMAGE:758128 5' similar to TR:G817957
5836	19026	32331	0.75	2.0E-38	Z26634.2	NT	G817957 GLYCINE RECEPTOR SUBUNIT ALPHA 4 ; C817957 GLYCINE RECEPTOR SUBUNIT ALPHA 4 ;
5836	19026	32332	0.75	2.0E-38	Z26634.2	NT	Homo sapiens mRNA for ankyrin B (440 kDa)
7897	20949	34467	1.47	2.0E-38	AV721103.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
8680	21760		4.47	2.0E-38	BE168980.1	EST_HUMAN	NR3-HT0487-150200-113-901 HT0487 Homo sapiens cDNA
8096	22175	35719	0.49	2.0E-38	F08450.1	EST_HUMAN	HSC18FC31 normalized infant brain cDNA Homo sapiens cDNA clone c-18103
9165	22243	35788	1.28	2.0E-38	AF069755.1	NT	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
9422	22496		1.36	2.0E-38	BE222258.1	EST_HUMAN	h08902.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3168130 3' similar to TR:002710 002710 GAG POLYPEPTIDE ;
10665	23659	37308	1.67	2.0E-38	D83478.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
11781	24771	38467	4.89	2.0E-38	BE112790.1	EST_HUMAN	QV2-HT0698-080800-293-405 HT0698 Homo sapiens cDNA
11939	24925	38826	2.86	2.0E-38	AF180501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
11939	24925	38827	2.86	2.0E-38	AF180501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
12244	25186		6.21	2.0E-38	AV726988.1	EST_HUMAN	AV726988 HTB Homo sapiens cDNA clone HTCAH107 5'
12246	25187		1.26	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
12546	25370		3.38	2.0E-38	M55630.1	NT	Human topoisomerase I pseudogene 2
12559	25381	32073	4.81	2.0E-38	H55631.1	EST_HUMAN	CH220560 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
12632	25426		2.87	2.0E-38	S74906.1	NT	E1 beta-pp/uvrta dehydrogenase beta (promoter) [human, placenta, Genomic, 1280 nt]
13174	25762		1.35	2.0E-38	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1117	14282		1.98	1.0E-38	AA401570.1	EST_HUMAN	z62602.1 Soares, taste, NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element
2055	15196	28310	2.62	1.0E-38	4885288	NT	MER19 repetitive element;
2077	15217	28330	1.33	1.0E-38	7661969	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA
2664	15689	28815	1.99	1.0E-38	AI270831.1	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
4271	17416	30405	0.93	1.0E-38	AB303783.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
4439	17579	30569	0.6	1.0E-38	4505018	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4444	17684	30563	2.15	1.0E-38	AL163203.2	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4719	17854	30837	1.08	1.0E-38	8922543	NT	Homo sapiens chromosome 21 segment HS21C003
5268	18367	31365	1.89	1.0E-38	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
6161	18327	32872	4.59	1.0E-38	7305360	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
7563	20635	34110	2.93	1.0E-38	AB014512.1	NT	Mus musculus cdcgeln (Cdcg), mRNA
9364	22429	35987	0.58	1.0E-38	11422250	NT	Mus musculus cdcgeln (Cdcg), mRNA
9610	22665	36236	6.31	1.0E-38	BE350127.1	EST_HUMAN	Homo sapiens mRNA for KIAA0612 protein, partial cds
12403	25877		4.79	1.0E-38	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
12116	26096	38801	1.64	8.0E-39	AA112438.1	EST_HUMAN	z62707.1 Striatogene pancreas (8937208) Homo sapiens cDNA clone IMAGE:326883 5'
55	13294	26309	4.83	8.0E-39	4502312	NT	Homo sapiens ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) 16KD (ATP6C) mRNA
1425	14579	27852	1.3	8.0E-39	4758228	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
1876	16020		1.8	8.0E-39	AI323404.1	EST_HUMAN	W63870.X1 NC1_CGAP_K1411 Homo sapiens cDNA clone IMAGE:2384491 5' similar to TR:P87890 P87890
2160	15298	28421	7.08	7.0E-39	AL163227.2	NT	MER29 repetitive element;
11047	24124	37758	2.4	6.0E-39	BF331829.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
13064	26697		2.24	6.0E-39	BE070394.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
1032	14201	27259	1.64	5.0E-39	AF003528.1	NT	Homo sapiens X-linked arylsulfatase ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
3050	16226	28247	9.33	5.0E-39	AI750184.1	EST_HUMAN	at8604.x1 Barstead cotton HPLR87 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
12720	25479		1.53	6.0E-39	11420288	NT	Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ;contains LTR7.1 LTR7 repetitive element ;
							Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA



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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
564	13756	26782	4.39	4.0E-39	AA015610.1	NT	Chlorocephus aethiops mRNA for ribosomal protein S4X, complete cds
3663	16826	29835	0.9	4.0E-39	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010.
5950	19139	32450	0.6	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA
5950	19139	32451	0.6	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100KD) (p100), mRNA
8267	21349	34864	1.02	4.0E-39	AA082949.1	EST_HUMAN	es2g04.s1 Stralagene ech2a brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains
9530	22595	36165	0.46	4.0E-39	D34116.1	NT	ORF.b1 ORF repetitive element.
9530	22595	36166	0.46	4.0E-39	D34116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12744	25494	-	6.36	4.0E-39	11418177	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12884	28588	-	2.56	4.0E-39	BE83452.1	EST_HUMAN	OV0-FN0063-260600-278-c08 FN0063 Homo sapiens cDNA
48	13287	28297	11.96	3.0E-39	AA631949.1	EST_HUMAN	fm1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	13287	28298	11.96	3.0E-39	AA631949.1	EST_HUMAN	fm1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
48	13287	28299	11.96	3.0E-39	AA631949.1	EST_HUMAN	fm1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
12236	25190	38348	6.59	3.0E-39	AI094557.1	EST_HUMAN	ox63a10.s1 Soares NIH-MPU, S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
12236	25190	38349	6.59	3.0E-39	AI094557.1	EST_HUMAN	ox63a10.s1 Soares NIH-MPU, S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT
12284	25212	-	5.72	3.0E-39	H37803.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
620	14095	-	7.78	2.0E-39	BE409203.1	EST_HUMAN	yp51c08.s1 Soares retina ND24HR Homo sapiens cDNA clone IMAGE:190954 3'
535	14110	-	11.55	2.0E-39	AI525119.1	EST_HUMAN	601301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
1057	14223	-	3.8	2.0E-39	AF000573.1	NT	prom1a-7.D01.r bVimurc1 Homo sapiens cDNA 5'
1560	14713	-	33.59	2.0E-39	AW372318.1	EST_HUMAN	Homo sapiens homogenitase 1,2-dioxygenase gene, complete cds
2030	16171	28278	4.48	2.0E-39	AA720574.1	EST_HUMAN	PM0-BT0340-211296-003-d02 BT0340 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.G
2692	15812	28928	1.89	2.0E-39	AL163246.2	NT	THR repetitive element ;
4523	17662	30849	1.74	2.0E-39	BF370207.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
8608	18803	31868	4.45	2.0E-39	AA509890.1	EST_HUMAN	RC4-FN0037-290700-011-a10 FN0037 Homo sapiens cDNA
7526	20599	34073	2.08	2.0E-39	AA080867.1	EST_HUMAN	ng88f03.s1 NCJ CGAP_P18 Homo sapiens cDNA clone IMAGE:941693
7702	20767	34251	0.66	2.0E-39	AL163202.2	NT	zno8f02.r1 Stralagene IN1T neuron (6537233) Homo sapiens cDNA clone IMAGE:546561 5'
7702	20767	34252	0.66	2.0E-39	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
8505	21686	35120	0.63	2.0E-39	AF078770.1	NT	Homo sapiens chromosome 21 segment HS21C002
8626	22866	-	0.78	2.0E-39	AI696600.1	EST_HUMAN	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
11716	24766	38452	2.13	2.0E-39	D88964.1	NT	U35603.x1 NCJ CGAP_P128 Homo sapiens cDNA clone IMAGE:2253052 3'
1543	14695	27774	2.83	1.0E-39	AI003346.1	NT	Human mRNA for KIAA0205 gene, partial cds
							Homo sapiens KVLQ11 gene

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1643	14685	27775	2.83	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQ11 gene
1661	14714	27791	6.98	1.0E-39	7637020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
1763	14912	28007	1.14	1.0E-39	H65224.1	EST_HUMAN	CHR220163 Chromosome 22 exon Homo sapiens cDNA clone C22_205 5'
4782	17917	30903	9.32	1.0E-39	AW651895.1	EST_HUMAN	EST384065 MAGB resequences, MAGB Homo sapiens cDNA
4782	17917	30904	9.32	1.0E-39	AW651895.1	EST_HUMAN	EST384065 MAGB resequences, MAGB Homo sapiens cDNA
4824	17957	30943	9.13	1.0E-39	7637020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
5474	18673	31686	0.82	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semahectin) 5A (SEMA5A), mRNA
5474	18673	31687	0.82	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semahectin) 5A (SEMA5A), mRNA
5747	18939	32239	1.2	1.0E-39	T60876.1	EST_HUMAN	Alu repetitive element; contains LTR1 repetitive element:
6791	18973	32278	4.65	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
5781	18973	32276	4.65	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
6865	20183		1.85	1.0E-39	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7521	20694	34069	2.15	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8762	21841	36382	1.04	1.0E-39	O46530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNASE K6)
1166	24236	37867	1.4	1.0E-39	4759051	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS6KA5) mRNA
669	13761	26785	2	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1263	14420	27484	16.02	9.0E-40	4756145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1263	14420	27485	16.02	9.0E-40	4756145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1480	14633	27718	15.75	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Soreby fundus dystrophy, pseudoinflammation) (TIMP3), mRNA
3885	17044	30043	1.18	9.0E-40	4503764	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
4081	18467	30242	3.89	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4466	17608	30684	5.63	9.0E-40	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3106	18282	28288	1.04	8.0E-40	AA078165.1	EST_HUMAN	7H15A04 Chromosome 7 Hela cDNA Library Homo sapiens cDNA clone 7H15A04
4033	17189		3.43	8.0E-40	BE396541.1	EST_HUMAN	601288958F NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619168 5'
7894	20946	34452	2.21	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7894	20946	34453	2.21	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
11136	24208	37834	2.63	7.0E-40	AI183246.2	NT	Homo sapiens chromosome 21 segment HS21C048

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2788	18904	29011	9.91	6.0E-40	AA361273.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
2788	18904	29012	9.91	6.0E-40	AA361276.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
6060	18242		1.85	6.0E-40	BE504703.1	EST_HUMAN	h249g01.x1 NCI_CGAP_B14 Homo sapiens cDNA clone IMAGE:3210480 3'
6276	18449		1.38	6.0E-40	7691998	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
7076	20128	33544	3.04	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7076	20128	33545	3.04	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
10182	23219	36811	6.08	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDDF04 3'
10182	23219	36812	6.08	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDDF04 3'
2670	19791	28907	2.75	5.0E-40	AI163285.2	NT	Homo sapiens chromosome 21 segment HS210085
1926	16068	28173	3.81	4.0E-40	AI886005.1	EST_HUMAN	h91b01.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:224873 3' similar to TR:O73505 O73505 POL PROTEIN.
2175	15310		6.81	4.0E-40	AI003628.1	NT	Homo sapiens X-linked arylidrol ectodermal dysplasia protein gene (EDA), exon 2 end flanking repeat regions
4508	17647	30835	7.2	4.0E-40	7692117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8070	2152	34672	0.84	4.0E-40	AU127831.1	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
8181	21263	34785	6.98	4.0E-40	AA742809.1	EST_HUMAN	md4et01.t NCI_CGAP_B14 Homo sapiens cDNA clone IMAGE:1222122
9265	22332	35881	5.84	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0187-070500-002-n12 BN0187 Homo sapiens cDNA
9235	22332	35882	5.84	4.0E-40	BE009416.1	EST_HUMAN	PMO-BN0187-070500-002-n12 BN0187 Homo sapiens cDNA
10955	24036	37671	1.85	4.0E-40	AW841585.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4260	17398	30385	0.9	3.0E-40	AI928949.1	EST_HUMAN	wh12807.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
4983	18122		0.83	3.0E-40	AA055118.1	EST_HUMAN	z16h09.st Soares_fetal_heart_NBH118W Homo sapiens cDNA clone IMAGE:377163 3'
6592	19752	33137	0.89	3.0E-40	4508736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1), mRNA
6777	18932	33328	7.06	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8576	21656	35187	3.86	3.0E-40	6464167	NT	Homo sapiens HBV associated factor (XAP4), mRNA
9169	22247	35780	1.27	3.0E-40	AF078779.1	NT	Homo sapiens HBV associated factor (XAP4), mRNA
9412	22486	36050	1.6	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10899	23983	37615	1.49	3.0E-40	D83684.1	NT	Human mRNA for KIAA0209 gene, partial cds
11544	24600	38278	8.12	3.0E-40	6005813	NT	Homo sapiens serine threonine protein kinase (NDR), mRNA
335	13548		3.91	2.0E-40	AI223039.1	EST_HUMAN	qg52h06.x1 Soares_testis_NH1 Homo sapiens cDNA clone IMAGE:1838847 3'
817	13896		5.56	2.0E-40	AW303888.1	EST_HUMAN	xx24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RSS_MOUSE P87481 40S RIBOSOMAL PROTEIN S6.

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1872	15016		2.33	2.0E-40	AV731601.1	EST_HUMAN	AV731601 HTF Homo sapiens cDNA clone HTFAZE05.5
1888	15130	28233	2.6	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1888	15130	28234	2.8	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2133	16269	28389	1.39	2.0E-40	A1988562.1	EST_HUMAN	w80611.x1 NCI CGAP GC6 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91929 Q91929
2238	15371	28500	2.21	2.0E-40	5453592	NT	ZINC FINGER PROTEIN, .
2754	16871		1.68	2.0E-40	BE276932.1	EST_HUMAN	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
3186	16371	28378	5.27	2.0E-40	5453592	NT	Homo sapiens adenyl cyclase-associated protein 2 (CAP2) mRNA
6021	18150	31128	1.43	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5021	18150	31129	1.43	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
808	14081		1.2	1.0E-40	AA235894.1	EST_HUMAN	nc09809.s1 NCI CGAP P3 Homo sapiens cDNA clone IMAGE:3863803 5'
2889	16306	28922	1.82	1.0E-40	BF038881.1	EST_HUMAN	601460375F1 NIH_MGC_08 Homo sapiens cDNA clone IMAGE:3863803 5'
2750	15897		3.88	1.0E-40	BE018348.1	EST_HUMAN	bb78410.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q92168 Q92168
3370	16542		2.14	1.0E-40	4507142	NT	SYNTAXIN 17, .
4733	17868	30951	3.69	1.0E-40	4508012	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
6385	19554	32912	0.69	1.0E-40	W92708.1	EST_HUMAN	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
6385	19554	32913	0.69	1.0E-40	W92708.1	EST_HUMAN	217911.s1 Soares fetal liver, spleen, 1NF.S, S1 Homo sapiens cDNA clone IMAGE:418317 3'
7236	20320	33763	1.83	1.0E-40	AA573201.1	EST_HUMAN	217911.s1 Soares fetal liver, spleen, 1NF.S, S1 Homo sapiens cDNA clone IMAGE:418317 3'
7236	20320	33764	1.83	1.0E-40	AA573201.1	EST_HUMAN	nc42804.s1 NCI CGAP AAT Homo sapiens cDNA clone IMAGE:395187 3'
7381	20459	33922	0.82	1.0E-40	P26808	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RUBONUCLEASE H]
11157	24226	37858	8.41	1.0E-40	AU148345.1	EST_HUMAN	AU148345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
11893	24978	38893	1.46	1.0E-40	AA614255.1	EST_HUMAN	nc08003.s1 NCI CGAP P3 Homo sapiens cDNA clone IMAGE:1115881 similar to TR:G1136406
11893	24978	38894	1.46	1.0E-40	AA614255.1	EST_HUMAN	G1136406 KIAA0173 PROTEIN, .
12079	25059		1.86	1.0E-40	AL163346.2	NT	nc08003.s1 NCI CGAP P3 Homo sapiens cDNA clone IMAGE:1115881 similar to TR:G1136406
12687	26032		6.94	1.0E-40	EF334112.1	EST_HUMAN	G1136406 KIAA0173 PROTEIN, .
3906	17065	30064	0.58	9.0E-41	V01568.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
8106	21188	34708	1.6	8.0E-41	AL163303.2	NT	MR2-CT0222-211089-002-e10 CT0222 Homo sapiens cDNA
851	18024	27089	2.62	7.0E-41	A183484.1	EST_HUMAN	z636a02.l1 Soares fetal liver, spleen, 1NF.S Homo sapiens cDNA clone IMAGE:284802 5'
851	18024	27090	2.52	7.0E-41	A183484.1	EST_HUMAN	nc08003.s1 NCI CGAP P3 Homo sapiens cDNA clone IMAGE:2463885 3'
							w044004.x1 NCI CGAP Kid1 Homo sapiens cDNA clone IMAGE:2463885 3'
							w044004.x1 NCI CGAP Kid1 Homo sapiens cDNA clone IMAGE:2463885 3'

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6379	18381	31450	0.9	7.0E-41	11545770	NT	Homo sapiens hypothalamic protein FLJ13188 (FLJ13188) mRNA
6132	16311	32651	2.71	7.0E-41	11418208	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22) mRNA
6463	19690	33012	1.04	7.0E-41	11433010	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
7133	18559	31473	0.96	7.0E-41	U72335.1	NT	Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIS1) gene, exons 3 and 4
11718	24758	38453	2.08	7.0E-41	4758445	NT	Homo sapiens guanine nucleotide binding protein 10 (GNNG10) mRNA
11931	24917	38920	1.41	7.0E-41	A1223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
13182	26028		8.58	7.0E-41	11417972	NT	Homo sapiens pascadiclo (zabratish) homolog 1, containing BRCT domain (PES1) mRNA
291	13508	26543	1.13	6.0E-41	A3037163.1	NT	Homo sapiens DSCRB5 mRNA, complete cds
2179	15314	28443	3.09	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1) mRNA
8166	21240	34760	1.31	6.0E-41	B-513783.1	EST_HUMAN	U1-HBW1-amp-b-03-0-U1.s1 NCJ CGAP Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'
13186	25952		1.25	6.0E-41	AW873897.1	EST_HUMAN	h04408.x1 Soares, NFE_L_T_GBC, S1 Homo sapiens cDNA clone IMAGE:3042183 3' similar to contains MER32.33 MER32 repetitive element:
1845	14591	28092	1.37	5.0E-41	T62628.1	EST_HUMAN	yc03610.s1 Straligene lung (8837210) Homo sapiens cDNA clone IMAGE:79828 3'
4223	17371		1.17	5.0E-41	4885898	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1) mRNA
6678	18837		2.34	5.0E-41	BE087042.1	EST_HUMAN	PM4-B10341-251189-002-F11 B10341 Homo sapiens cDNA
402	13659		1.59	4.0E-41	B5158318.1	EST_HUMAN	GV6-H10367-150200-114-408 HT0367 Homo sapiens cDNA
1122	14267	27342	2.37	4.0E-41	AU118344.1	EST_HUMAN	AU118344 HEMIBA1 Homo sapiens cDNA clone HEMIBA1005583 5'
1442	14595	27670	14.6	4.0E-41	A1027117.1	EST_HUMAN	ow45606.c1 Soares, parathyroid tumor, NBHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR5 repetitive element:
1442	14595	27671	14.6	4.0E-41	A1027117.1	EST_HUMAN	ow45606.s1 Soares, parathyroid tumor, NBHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:000597 000597 CYTOCHROME C-LIKE POLYPEPTIDE, contains LTR5.b1 LTR5 repetitive element:
1434	14607	27697	3.34	4.0E-41	AB008881.1	NT	Homo sapiens gene for actin receptor type IIb, complete cds
1685	14817	27900	7.72	4.0E-41	A1500408.1	EST_HUMAN	trn6604.x1 NCJ CGAP Brn25 Homo sapiens cDNA clone IMAGE:216556 3' similar to contains ORF.b1 ORF repetitive element:
2953	16130	28144	5.02	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
2853	16130	28145	5.02	4.0E-41	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
4282	17407	30383	2.13	4.0E-41	X92638.1	NT	H.sapiens DNaseI hypersensitive site (HSS-3) enhancer element
6638	18787		1.8	4.0E-41	AV758295.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMFBHC08 5'
6895	22835	36519	5.06	4.0E-41	BF30483.1	EST_HUMAN	60188809671 NIH MGC, 17 Homo sapiens cDNA clone IMAGE:4122119 5'
11959	24954		7.36	4.0E-41	AV710490.1	EST_HUMAN	AV710490 CU Homo sapiens cDNA clone CUAAC07 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12800	25917		1.3	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
13110	25725	31942	1.51	4.0E-41	BE887118.1	EST_HUMAN	601508315F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910059 5'
870	14143	27203	1.8	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase Type II, complete cds
4435	17393	30873	4.03	3.0E-41	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
6609	18804	31869	11.76	3.0E-41	X37699.1	NT	H. sapiens mRNA for putative p64 CLOP protein
6511	19876	33048	1.23	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
7887	21017	34329	0.71	3.0E-41	RS4765.1	EST_HUMAN	y75d08.t1 Scores breast 2NBH81 Homo sapiens cDNA clone IMAGE:154575 5'
12116	25099	38804	1.38	3.0E-41	AW694941.1	EST_HUMAN	QV0-BND040-170300-160-108 BND040 Homo sapiens cDNA
12116	25099	38805	1.36	3.0E-41	AW694941.1	EST_HUMAN	QV0-BND040-170300-160-108 BND040 Homo sapiens cDNA
12196	25153		1.93	3.0E-41	AA609768.1	EST_HUMAN	ef17f10.c1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1031947 3'
12783	25525		1.43	3.0E-41	BF125922.1	EST_HUMAN	601762940F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026081 5'
1871	14744	27827	31.25	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
2013	15163	28268	2.17	2.0E-41	AA231840.1	EST_HUMAN	EST33818 Embryo, 8 week 1 Homo sapiens cDNA 5' end
2293	15425	28359	1.28	2.0E-41	D86962.1	NT	Human mRNA for KIAA0207 gene, complete cds
2341	15472	28306	5.52	2.0E-41	X39631.1	NT	G.gorilla DNA for ZNF80 gene homolog
2889	14744	27827	11.99	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
3406	16576	29501	0.89	2.0E-41	AA449549.1	EST_HUMAN	z08b04.r1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:786839 5'
3941	17100	30097	0.59	2.0E-41	AA163287.2	NT	Homo sapiens son of sevenless (Drosophila) homolog 1 (SOS1) mRNA
4744	17879	30862	1.23	2.0E-41	AA163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4744	17879	30863	1.23	2.0E-41	AA163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
5656	18850	32132	0.6	2.0E-41	AA594575.1	EST_HUMAN	not2a07.s1 NCICGAP_Pho1 Homo sapiens cDNA clone IMAGE:1100460 3' similar to gb:XS2851_mai
6763	19918	33314	0.98	2.0E-41	AF038404.1	EST_HUMAN	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
7850	20905	34409	9.27	2.0E-41	AF038404.1	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
8259	21341	34858	1.36	2.0E-41	MA6644.1	NT	Homo sapiens homolog of Nedd5 (Nedd5) mRNA, complete cds
8259	21341	34859	1.36	2.0E-41	MA6644.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8288	21370	34891	1.42	2.0E-41	AA338285.1	EST_HUMAN	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8776	22263	35786	1.65	2.0E-41	PS2742	SWISSPROT	EST131723 Embryo, 12 week 1 Homo sapiens cDNA 5' end
9917	22672	36241	0.68	2.0E-41	11417118	NT	ZINC FINGER PROTEIN 135
9917	22672	36242	0.56	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11775	24767	38463	2.87	2.0E-41	AA372637.1	EST_HUMAN	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
13148	25747		1.2	2.0E-41	11420516	NT	EST184555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3276	19450	29470	1.05	1.0E-41	BE869735.1	EST_HUMAN	EST184555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
							Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
							60144564T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3849803 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3276	16450	28471	1.05	1.0E-41	B3689735.1	EST_HUMAN	601445847F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
4689	17824	30811	9.46	1.0E-41	6078468	NT	Mus musculus tubulin alpha 6 (Tub6), mRNA
9018	22673	36243	1.67	1.0E-41	A1217868.1	EST_HUMAN	q756c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1765858 3'
12334	25241		1.67	1.0E-41	11528291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8717	21797		1.19	9.0E-42	BE179191.1	EST_HUMAN	FC0-HT0613-210300-032-g01 HT0613 Homo sapiens cDNA
8376	22450	36011	2.81	9.0E-42	11950151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9376	22450	36012	2.81	9.0E-42	11560151	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
476	13670	28702	5.34	8.0E-42	A1003530.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2176	16311	28439	8.63	8.0E-42	A3028698.1	NT	nt07202.s1 NC1_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:343586 similar to TR:G434304 G434304
12376	26036		30.09	8.0E-42	AA493898.1	EST_HUMAN	397BP EXPRESSED SEQUENCE TAG MRNA:
12396	25904		2.91	8.0E-42	AW088062.1	EST_HUMAN	xc37804.x1 NC1_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2592174 3' similar to contains OFR.12
955	14128		2.23	7.0E-42	AL163285.2	NT	OFR repetitive element:
8668	21746		0.5	7.0E-42	R10883.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
9446	22561	36124	1.32	7.0E-42	A120439.1	EST_HUMAN	Y88g04.r1 Soares fetal liver spleen T1NF.S Homo sapiens cDNA clone IMAGE:129174 5'
1803	16046	28156	3.24	6.0E-42	A1012872.1	NT	qf56g12.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754276 3'
1803	16046	28156	3.24	6.0E-42	A1012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds
2363	15494		3.9	9.0E-42	AW238656.1	EST_HUMAN	Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds
5584	18778	31824	1.68	6.0E-42	AB028880.1	NT	xc28f08.x1 NC1_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741789 3' similar to contains L1.11 L1
5834	18778	31824	1.6	6.0E-42	AB028880.1	NT	repetitive element:
138	13364		8.34	6.0E-42	AJ271735.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
451	13647	26893	1.56	5.0E-42	BE217913.1	EST_HUMAN	Homo sapiens mRNA for KIAA1067 protein, partial cds
499	13694		3.06	6.0E-42	5730038	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
500	13695		1.14	5.0E-42	5730038	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
6825	18978	33385	0.94	5.0E-42	11433063	NT	h331e1.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
6825	18978	33386	0.94	5.0E-42	11433063	NT	Homo sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
6941	20254	33691	2.57	5.0E-42	11417957	NT	Homo sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
7351	20430	33892	1.55	5.0E-42	A1071589.1	NT	Homo sapiens SET domain and marker transposase fusion gene (SETMAR) mRNA
							Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
							Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
							Homo sapiens myotubularin related protein 3 (MTMR3), mRNA
							Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8878	22057	35599	2.88	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1284 protein, partial cds
10832	23865	37487	0.55	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10832	23865	37488	0.55	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
11246	24915	37855	1.77	6.0E-42	8023162	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
772	13953	27002	5.0	4.0E-42	AFO5006.1	NT	Homo sapiens MHC class I region
772	13953	27003	5.6	4.0E-42	AFO5006.1	NT	Homo sapiens MHC class I region
1091	14256	27312	1.82	4.0E-42	AF188011.1	NT	Homo sapiens ribonuclease II (RN3) mRNA, complete cds
4311	17454	30442	1.39	4.0E-42	X69417.1	NT	H. sapiens PROS-27 mRNA
4343	17486	30469	1.1	4.0E-42	AF246219.1	NT	Homo sapiens SNARE protein kinase SNK mRNA, complete cds
4364	17507	30488	4.87	4.0E-42	4506496	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4706	17941	30825	17.04	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
5285	18404	31372	0.93	4.0E-42	7661635	NT	Homo sapiens DKFZP564O2082 protein (DKFZP564O2082), mRNA
10701	23734	37339	0.57	4.0E-42	AW371201.1	EST_HUMAN	CGC-BT0282-171289-127403 BT0282 Homo sapiens cDNA
10884	23868	37687	2.32	4.0E-42	AW818830.1	EST_HUMAN	RC1-ST0278-04040-018-h11 ST0278 Homo sapiens cDNA
10884	23868	37998	2.32	4.0E-42	AW818830.1	EST_HUMAN	RC1-ST0278-04040-018-h11 ST0278 Homo sapiens cDNA
11240	24309	37946	1.43	4.0E-42	AK35225.1	EST_HUMAN	B11602.x1 NCL CGAP Part1 Homo sapiens cDNA clone IMAGE:2130147 3'
11698	24695	38387	1.69	4.0E-42	BF035327.1	EST_HUMAN	6014683f1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3862086 5'
1512	14885	27750	3.79	2.0E-42	BF378834.1	EST_HUMAN	RCO-TN0079-110900-024-507 TN0079 Homo sapiens cDNA
2468	16593	28718	1.6	2.0E-42	AV690218.1	EST_HUMAN	AV690218 GKC Homo sapiens cDNA clone GKCGB08 5'
2483	15910		4.24	2.0E-42	AW888344.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2496	15623	28742	3.0	2.0E-42	AW350059.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
5875	19065	32972	11.82	2.0E-42	AW85386.1	EST_HUMAN	EST367438 IMAGE:2819283 3'
6876	19065	32973	11.82	2.0E-42	AW85386.1	EST_HUMAN	EST367438 IMAGE:2819283 3'
6892	23084	39462	0.9	2.0E-42	AU052586.1	EST_HUMAN	bw63405.x1 Soares, fetal liver, spleen, 1NF.LS, S1 Homo sapiens cDNA clone IMAGE:1853417 3'
10046	23084	39462	1.28	2.0E-42	BE538918.1	EST_HUMAN	801081294f1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
10260	23285	38892	0.84	2.0E-42	PS1649	SWISSPROT	RIBONUCLEASE K3 (RNAse K3)
10260	23285	38893	0.84	2.0E-42	PS1649	SWISSPROT	RIBONUCLEASE K3 (RNAse K3)
12037	25019	38723	1.53	2.0E-42	AL168246.2	NT	Homo sapiens chromosome 21 segment HS21C046
762	13932	28677	1.75	1.0E-42	X57147.1	NT	Human endogenous retrovirus pHE-1 (ERV9)
1067	14233	27292	2.2	1.0E-42	AW295809.1	EST_HUMAN	U1-H-B1-eth-e-04-0-L11 NCL CGAP Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1125	14280	27345	1.74	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1125	14280	27346	1.74	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1271	18033	27498	11.99	1.0E-42	AF067166.1	NT	Homo sapiens NADH-dependent oxidoreductase AGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds



Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1271	16033	27499	11.99	1.0E-42	AF067166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene
1735	14884	27077	1.15	1.0E-42	11423219	NT	encoding mitochondrial protein, complex ccs
2087	15227	28349	1.18	1.0E-42	AF110296.1	NT	Homo sapiens rec (LOC51207), mRNA
2693	15733	28849	1.42	1.0E-42	5174458	NT	Homo sapiens PDNP1 gene, exon 17
							Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
							Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3028	16205	29228	9.15	1.0E-42	4505524	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3798	16960	29984	3.31	1.0E-42	7682027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3895	17054	30054	1.11	1.0E-42	5031610	NT	Homo sapiens Gcdg vesicular membrane trafficking protein p18 (BET1) mRNA
4036	17182	30202	0.89	1.0E-42	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4361	17504	30486	3.47	1.0E-42	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4716	17851	30834	0.61	1.0E-42	AW813617.1	EST_HUMAN	RC3-ST0197-161099-012-403 ST0197 Homo sapiens cDNA
4867	18000	30984	2.37	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (P31), mRNA
4867	18000	30984	2.37	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (P31), mRNA
4867	18000	30984	2.37	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (P31), mRNA
4801	18031	31020	6.13	1.0E-42	4505759	NT	Homo sapiens ryanodine receptor 3 (RyR3), mRNA
11440	24501	38168	1.39	1.0E-42	BE408611.1	EST_HUMAN	601304128F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
10291	23326	36929	6.16	9.0E-43	4767969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
689	13855	26883	20.77	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
689	13855	26884	20.77	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
718	13900	26838	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
718	13900	26838	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
718	13900	26838	5.12	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20287 (FLJ20287), mRNA
5816	18006	32312	0.72	8.0E-43	H13952.1	EST_HUMAN	Homo sapiens placenta NB3HP Homo sapiens cDNA clone IMAGE:2822251 5'
5731	16892	29898	7.48	7.0E-43	AV246442.1	EST_HUMAN	2822251 Splice NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822251 5'
8868	22047		3.88	7.0E-43	AI336748.1	EST_HUMAN	wp69601 x1 NCI CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2468985 3' similar to TR:O15475
1374	14528		11.62	6.0E-43	AA491890.1	EST_HUMAN	O16475 UNIMED HEVY-H PROTEIN, contains LTR7.b1 LTR7 repetitive element;
2857	15780		4.03	6.0E-43	AV708201.1	EST_HUMAN	ne72406 s1 NCI CGAP_Ewt1 Homo sapiens cDNA clone IMAGE:309803 similar to gb:U05095 60S
4983	18092	31068	252.27	6.0E-43	AI421540.1	EST_HUMAN	RIBOSOMAL PROTEIN L30 (HUMAN);
6441	19808	32971	2.63	6.0E-43	BB55973	NT	AV708201 ADC Homo sapiens cDNA clone ADCAC10 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7046	20101	33518	1.8	6.0E-43	AW468937.1	EST_HUMAN	hnd30504.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810981 3' similar to contains
10056	23094	36998	1.77	6.0E-43	AA195184.1	EST_HUMAN	MER1.13 MER1 MER1 repetitive element;
11363	24424		2.45	6.0E-43	AL119158.1	EST_HUMAN	z35508.t1 Soares_NHMP1.S1 Homo sapiens cDNA clone IMAGE:695410 5' similar to TR:G529641
146	13370		1.82	6.0E-43	AL163213.2	NT	G529641 DB1, COMPLETE CDS, contains element PTR7 repetitive element;
515	13709	26736	3.4	6.0E-43	AA382780.1	EST_HUMAN	DKFZp7611712.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7611712 5'
2808	16086	28100	1.59	6.0E-43	AV732578.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
6435	20096	33512	0.9	6.0E-43	AI613509.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HTFANG06 5'
7043	20096	33512	0.69	6.0E-43	AI613509.1	EST_HUMAN	hw22607.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2280452 3'
8381	21462	34985	0.64	6.0E-43	AA442271.1	EST_HUMAN	hw22607.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2280452 3'
8381	21462	34986	0.64	6.0E-43	AA442271.1	EST_HUMAN	hw22607.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2280452 3'
9080	22169		0.73	5.0E-43	HW4277.1	EST_HUMAN	z64603.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
9564	22706	36272	4.09	5.0E-43	AA465288.1	EST_HUMAN	z64603.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757420 5'
10609	23643	37251	2.6	5.0E-43	AI733244.1	EST_HUMAN	y49912.t1 Soares fetal liver spleen INFLS1 Homo sapiens cDNA clone IMAGE:226510 5'
10651	23655	37256	1.02	8.0E-43	AI049110.1	EST_HUMAN	aa33d08.t1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'
11001	24080	37715	4.53	5.0E-43	AW863007.1	EST_HUMAN	co52e10.x5 NCI_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1569810 3' similar to TR:P90591 P90591
11213	24282	37821	2.24	6.0E-43	W28011.1	EST_HUMAN	PV14 GENE;
895	15987	27227	4.4	4.0E-43	AF003628.1	NT	DKFZp4344D0119.t1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp4344D0119
5373	18576	31444	1.09	4.0E-43	AI056338.1	EST_HUMAN	MR2_SN0007-280400-004-002 SN0007 Homo sapiens cDNA
6499	18665	33028	0.88	4.0E-43		EST_HUMAN	55a4 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7280	20363		1.6	4.0E-43	11416783	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
8371	21452	34976	5.18	4.0E-43	AI244341.1	EST_HUMAN	regions
8371	21452	34976	5.18	4.0E-43	AI244341.1	EST_HUMAN	cy47h03.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1669013 3'
10621	23556	37164	1.02	4.0E-43		EST_HUMAN	Homo sapiens glycyl-tRNA synthetase (GARS) mRNA
12311	26227		2.7	4.0E-43	R30950.1	EST_HUMAN	Homo sapiens protocadherin beta 6 (PCDH6), mRNA
13030	26898		1.33	4.0E-43	AI436083.1	EST_HUMAN	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1240	14399		3.46	3.0E-43	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1730	14930	27971	2.52	3.0E-43	X07869.1	NT	H. sapiens gene encoding L8 aubp antigen
2120	16053	28377	1.1	3.0E-43	R33422.1	EST_HUMAN	Yp82D1.1 Scores fetal liver spleen 1NFUS Homo sapiens cDNA clone IMAGE:193945 5' similar to contains MSR1 repetitive element;
3692	16825	28834	1.22	3.0E-43	S69002.1	NT	AML1-EV1-1-AML1-EV1-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
4405	17549	30532	0.9	3.0E-43	AA548154.1	EST_HUMAN	nk55d06.s1 NCI_CGAP_P77 Homo sapiens cDNA clone IMAGE:1017419
6014	18168	32515	0.94	3.0E-43	D34613.1	NT	Human TBXAS1 gene for thromboxane synthase, promoter region and exon 1
6487	18654	33016	1.66	3.0E-43	7305360	NT	Mus musculus obogelin (Olog), mRNA
6487	18654	33017	1.56	3.0E-43	7305360	NT	Mus musculus obogelin (Olog), mRNA
6867	20019	33428	5.09	3.0E-43	U95467.1	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
8357	21438		4.39	3.0E-43	AA458824.1	EST_HUMAN	aa86t11.s1 Strelagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR12 THR repetitive element;
8020	22059	36639	1	3.0E-43	7661721	NT	Homo sapiens hypothetical protein (HSA011916), mRNA
10068	23106	36709	0.88	3.0E-43	11420217	NT	Homo sapiens similar to ornithine carbamoyltransferase (H. sapiens) (LOC63648), mRNA
12026	25010	38712	1.42	3.0E-43	5730038	NT	Homo sapiens SET domain end marker transposase fusion gene (SETMAR) mRNA
186	13410		7.24	2.0E-43	A1190764.1	EST_HUMAN	cd81c09.x1 Source: Jastic_NHT Homo sapiens cDNA clone IMAGE:1733968 3' similar to contains PTR713 PTR7 PTR7 repetitive element;
6604	18764	33152	1.2	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element;
6604	18764	33153	1.2	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element MER40 repetitive element;
7426	20503	33973	1.29	2.0E-43	AY207860.1	EST_HUMAN	MER40 repetitive element;
8503	21594		3.16	2.0E-43	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
11476	24535		4.75	2.0E-43	TC0007.1	EST_HUMAN	Human ribosomal protein L23a mRNA, complete cds
1681	14833	27917	2.95	1.0E-43	AF154933.1	NT	FB1G5 fetal brain, Striatogene Homo sapiens cDNA clone FB1G5 3' end similar to LINE-1
1681	14833	27918	2.95	1.0E-43	AF154933.1	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
1742	14891	27985	4.12	1.0E-43	AF154933.2	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
2789	15902	28009	4.73	1.0E-43	BF348283.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
5526	18723	31740	0.88	1.0E-43		NT	602022315F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157666 5'
6744	19900	33291	6.84	1.0E-43	4507169	NT	Homo sapiens p17veta dehydrogenase kinase, isoenzyme 3 (PDK3) mRNA
6744	19900	33292	8.84	1.0E-43	4507169	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7106	18533	31488	1.19	1.0E-43	R19751.1	EST_HUMAN	HY40601.1 Soares infant brain (NIB Homo sapiens cDNA clone IMAGE:34732 5' similar to SP:BD38_MOUSE P28656 BRAIN PROTEIN DN38;
8117	21189	34720	0.6	1.0E-43	AF176265.1	NT	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
8256	21338		2.17	1.0E-43	AF188490.1	NT	Homo sapiens Bq22.1 region and MTG8 (CBFA2T1) gene, partial cds
9037	22116	35659	28.54	1.0E-43	AW963676.1	EST_HUMAN	EST1375749 IMAGE: ressequencs, MACH Homo sapiens cDNA
10498	23533	37143	0.66	1.0E-43	AW963229.1	EST_HUMAN	EST1365299 IMAGE: ressequencs, MACH Homo sapiens cDNA
11206	24275	37912	5.81	1.0E-43	AI984951.1	EST_HUMAN	wt87h01.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494708 3'
11647	24728	38418	3.05	1.0E-43	AI137984.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E) mRNA
12248	25189		2.29	1.0E-43	AI1424378	NT	DKFZ6761D1015.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZ6761D1015 5'
12530	25373	32071	3.16	1.0E-43	AI675416.1	EST_HUMAN	W59B04.x1 NC1_CGAP_P128 Homo sapiens cDNA clone IMAGE:2313775 3'
12805	25539	32013	3.21	8.0E-44	AI222985.1	EST_HUMAN	Homo sapiens cathenin EGF LAG seven-pass G-type receptor 1 (CELSR1) mRNA
913	14086	27154	5.32	8.0E-44	AI222985.1	EST_HUMAN	q123g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1945552 3'
8736	21815	35350	2.89	8.0E-44	X94354.1	NT	H. sapiens DNA for Cone cGMP-P-DE gene 1x;
10545	23580	37189	0.5	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C) mRNA
10545	23580	37189	0.5	8.0E-44	11423497	NT	Homo sapiens small proline-rich protein 2C (SPRR2C) mRNA
11436	24497	38164	2.87	8.0E-44	Y10488.2	NT	Homo sapiens mRNA for tyrosine kinase, partial cds
11887	24972	39877	1.76	8.0E-44	L29139.1	NT	Homo sapiens myosin mRNA, partial cds
12501	25345	32065	2.89	8.0E-44	11527389	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F) mRNA
12544	25735	31760	2.17	8.0E-44	11418089	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP) mRNA
12845	25938		1.85	8.0E-44	11418089	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP) mRNA
13126	25735	31946	2.29	8.0E-44	11418089	NT	Homo sapiens putative nuclear protein (HNF1FB2122) mRNA
676	13862		1.13	7.0E-44	R06035.1	EST_HUMAN	Y68901.1 Soares fetal liver spleen tINF5 Homo sapiens cDNA clone IMAGE:124620 5'
2307	15439	28573	1.19	7.0E-44	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
3031	16207	29229	4.44	7.0E-44	AF048729.1	NT	Homo sapiens multisatellite ms32 repeat region
3031	16207	29230	4.44	7.0E-44	AF048729.1	NT	Homo sapiens multisatellite ms32 repeat region
3985	17123	30126	2.71	7.0E-44	AF163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4366	17499	30479	0.85	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4366	17499	30480	0.85	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
8379	21480	34983	2.39	7.0E-44	AU156839.1	EST_HUMAN	AU156839 Y79AA1 Homo sapiens cDNA clone Y79AA1000498 3'
6229	19404	32754	0.67	6.0E-44	Z20946.1	EST_HUMAN	HSAAD6VUP_Human foetal Brain Whole tissue Homo sapiens cDNA
314	13530		4.25	5.0E-44	AJ289380.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene
342	13553		2.42	5.0E-44	AJ289380.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZTFL1 gene

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8072	21154	34673	4.12	5.0E-44	AI568523.1	EST_HUMAN	h40d02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.11
9684	22726		1.39	5.0E-44	AU124571.1	EST_HUMAN	OFR OFR repetitive element ;
3501	10689	28678	4.27	4.0E-44	AL163303.2	NT	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
5128	16253		0.89	4.0E-44	AI456225.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
7639	20708	34187	0.87	4.0E-44	B388176.1	EST_HUMAN	h11d02.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
8488	21547	36077	0.89	4.0E-44	L21948.1	NT	601508601F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910152 5'
8079	22158		0.71	4.0E-44	BE176618.1	EST_HUMAN	Human fibrillin (FBN1) locus polymorphism
11513	24570	38247	5.64	4.0E-44	U30378.1	NT	RC3-H170585-010400-023-408 HT0585 Homo sapiens cDNA
1827	14976		1.5	3.0E-44	6912477	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
3167	16342	28350	5.11	3.0E-44	AA189851.1	EST_HUMAN	Homo sapiens keratophen alpha 6 (imporin alpha 7) (KPNAB), mRNA
7870	21020	34533	0.65	3.0E-44	BE894820.1	EST_HUMAN	zp18b05.1 Streptococcus felis retina 837202 Homo sapiens cDNA clone IMAGE:608777 5'
9719	22784	36355	0.63	3.0E-44	AI7005273.1	NT	601510647F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912010 5'
1074	14240	27286	1.43	2.0E-44	4826689	NT	3us scrofa domestica submaxillary apomucin mRNA, complete cds
1074	14240	27297	1.43	2.0E-44	4826689	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp-His) box polypeptide 1 (DDX1) mRNA
1234	14393	27456	3.61	2.0E-44	5803200	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp-His) box polypeptide 1 (DDX1) mRNA
1234	14393	27456	3.61	2.0E-44	5803200	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp-His) box polypeptide 1 (DDX1) mRNA
1340	14468	27568	8.82	2.0E-44	AI7133688.1	NT	Homo sapiens RAB36 (RAB36) mRNA, complete cds
1400	14554	27628	1.5	2.0E-44	BE465325.1	EST_HUMAN	hwt4q06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182898 3' similar to SW:OXYB_HUMAN
2219	16353	28484	3.07	2.0E-44	AF070671.1	NT	P22059 OXYSTEROL-BINDING PROTEIN ;
2605	16728		1.28	2.0E-44	4507592	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
2642	16765	28879	0.94	2.0E-44	D25303.1	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
2676	16786		2.3	2.0E-44	5801893	NT	Human mRNA for integrin alpha subunit, complete cds
3558	16724	29740	1.34	2.0E-44	D87675.1	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAP34), mRNA
4692	17827	30813	1.75	2.0E-44	AW864378.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
6220	19395	32744	1.75	2.0E-44	11449901	NT	PMA-SIN0016-120500-003-cd4 SIN0016 Homo sapiens cDNA
6998	18515	31507	2.18	2.0E-44	AF038988.1	NT	Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA
7572	20844	34121	3.8	2.0E-44	11419228	NT	Homo sapiens general transcription factor 2i (GTF2i) mRNA, alternatively spliced product, complete cds
7572	20844	34122	3.8	2.0E-44	11419228	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRIK3), mRNA
8623	21703	35238	0.7	2.0E-44	7706370	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRIK3), mRNA
8623	21703	35239	0.7	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0917), mRNA
8819	21898	35437	1.8	2.0E-44	BE389058.1	EST_HUMAN	6012865014F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3813588 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12152	26122		4.59	2.0E-44	BE244902.1	EST_HUMAN	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2795
12730	26094		1.56	2.0E-44	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
63	13262	26306	5.24	1.0E-44	7657334	NT	Homo sapiens Misschappen/NIK-related kinase (MINK) mRNA
53	13282	26307	5.24	1.0E-44	7657334	NT	Homo sapiens Misschappen/NIK-related kinase (MINK) mRNA
594	13784	26804	1.53	1.0E-44	AW683192.1	EST_HUMAN	RC1-CT0249-030300-026-112 CT0249 Homo sapiens cDNA
1224	14384		1.96	1.0E-44	AW994803.1	EST_HUMAN	RC1-BN0039-110300-012-501 BN0039 Homo sapiens cDNA
1605	14759		8.05	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2289	15431	28563	6.17	1.0E-44	AA434554.1	EST_HUMAN	zW53d02.r1 Soares fetal, Nb2HF8_gw Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR3 THR repetitive element;
2299	15431	28564	6.17	1.0E-44	AA434554.1	EST_HUMAN	zW53d02.r1 Soares fetal, Nb2HF8_gw Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR3 THR repetitive element;
2818	16932	29043	1.74	1.0E-44	AF198779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptohyacin genes, complete cds, and L-type calcium channel $\alpha 2$
3819	16975		3	1.0E-44	AA455869.1	EST_HUMAN	aa07c09.s1 Soares NIH/MPU_S1 Homo sapiens cDNA clone IMAGE:811984 3'
5221	18343	31314	0.68	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5221	18343	31315	0.68	1.0E-44	AJ130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
8460	21541	35070	0.91	1.0E-44	AW967073.1	EST_HUMAN	EST1378147 MAGE resequences, MAGE Homo sapiens cDNA
8460	21541	35071	0.91	1.0E-44	AW967073.1	EST_HUMAN	EST1378147 MAGE resequences, MAGE Homo sapiens cDNA
8648	21927	35468	0.66	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C1009
8648	21927	35468	0.66	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C1009
9227	22305	35848	0.56	1.0E-44	AI337183.1	EST_HUMAN	q888g07.x1 NC1 CGAP_G06 Homo sapiens cDNA clone IMAGE:2009028 3'
11264	24333		4.13	1.0E-44	AV174608.1	EST_HUMAN	AV174608.DCB Homo sapiens cDNA clone DCBBYE03 5'
11820	24809	39505	3.47	1.0E-44	10082684	NT	Homo sapiens Sush1 domain (SCR repeat) containing (BK65A6.2), mRNA
11890	24878	38574	3.21	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150899-011-C08 CT0198 Homo sapiens cDNA
11890	24878	38575	3.21	1.0E-44	AW846967.1	EST_HUMAN	RC1-CT0198-150899-011-C08 CT0198 Homo sapiens cDNA
4701	17839	30821	0.98	8.0E-46	BB22391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4701	17839	30822	0.98	8.0E-46	BB22391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
6787	18842	33340	1.41	9.0E-46	AB032121.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
2891	15716	28534	3.9	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5183	18315	31283	9.63	8.0E-46	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
8298	21380	34902	1.03	8.0E-46	AA377985.1	EST_HUMAN	EST190893 Synovial sarcoma Homo sapiens cDNA 5' and
1563	14735		2.36	6.0E-46	AI875425.1	EST_HUMAN	wb89-c08.x1 NC1 CGAP_P728 Homo sapiens cDNA clone IMAGE:2313902 3' similar to contains L1 (L1 repetitive element);

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4087	17242		3.77	6.0E-48	AW157670.1	EST_HUMAN	eu83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782909 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A;
12911	26164		1.89	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARF-GAP1) mRNA
916	14090		1.71	6.0E-46	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2068	15189	28313	4.42	5.0E-48	BF333827.1	EST_HUMAN	GM4-CH0044-180200-515-01 CN0044 Homo sapiens cDNA
3281	18455	29477	2.87	6.0E-46	AI523766.1	EST_HUMAN	tg94h07.x1 NC1 CGAP CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1.;
5629	18823	31897	8.95	6.0E-46	AA397781.1	EST_HUMAN	z172d03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TARI repetitive element;
6143	19321	32884	1.09	5.0E-46	Y18833.1	NT	Homo sapiens MCP-1 gene and enhancer region
6143	19321	32865	1.09	5.0E-46	Y18833.1	NT	Homo sapiens MCP-1 gene and enhancer region
6180	19366	32714	0.92	5.0E-48	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, oocyte ods
6180	19366	32715	0.92	6.0E-46	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6318	19480	32847	0.87	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277) mRNA
6318	19490	32849	0.87	5.0E-45	11496268	NT	Homo sapiens zinc finger protein 277 (ZNF277) mRNA
8471	21552	35082	1.12	5.0E-45	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5) mRNA
8241	22318	35861	1.46	6.0E-46	4769223	NT	Homo sapiens programmed cell death 5 (PDCD5) mRNA
11897	24982	38888	2.5	5.0E-45	8923698	NT	Homo sapiens golgin-like protein (GLP) mRNA
1187	14330	27385	6.3	4.0E-46	X95825.1	NT	H. sapiens ART4 gene
2385	15488	28622	2.16	4.0E-46	BE286622.1	EST_HUMAN	801194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3358429 5'
9167	22235		0.81	4.0E-46	AA228220.1	EST_HUMAN	no28e07.c1 NC1 CGAP_P1 Homo sapiens cDNA clone IMAGE:1009284 similar to contains element L1 repetitive element;
12166	26089	31659	1.36	4.0E-45	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3) mRNA
3411	16580		0.83	3.0E-45	U71480.1	EST_HUMAN	W35107.r1 Soares fetal liver spleen TINF5 Homo sapiens cDNA clone IMAGE:110245 5'
4189	16580		1.03	3.0E-45	U71480.1	EST_HUMAN	W35107.r1 Soares fetal liver spleen TINF5 Homo sapiens cDNA clone IMAGE:110245 5'
6368	18536	32895	1.34	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnalc11), mRNA
6368	18536	32896	1.34	3.0E-45	6753651	NT	Mus musculus dynein, axon, heavy chain 11 (Dnalc11), mRNA
8645	21725		1.76	3.0E-45	AV723976	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
8645	22070	35610	4.31	3.0E-45	4758451	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
10515	23560	37169	7.62	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10515	23560	37160	7.62	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
13040	26078		3.45	3.0E-45	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2572	15697		3.12	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
3097	18273	29287	0.92	2.0E-45	AL243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6651	19810	33198	5.45	2.0E-45	U01655.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7786	20942	34394	1.1	2.0E-45	BE782184.1	EST_HUMAN	801467793F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870838 6'
8610	21690	35228	0.91	2.0E-45	AW834834.1	EST_HUMAN	RCCLT0001-150200-032-311 L170001 Homo sapiens cDNA
8784	22824	36402	0.51	2.0E-45	AB367186.1	EST_HUMAN	1656a01.x1 NCI_CGAP_K168 Homo sapiens cDNA clone IMAGE:2232352 3'
11042	25867	37754	12.68	2.0E-45	BE834350.1	EST_HUMAN	MF0-H10923-190800-201-e02 HT0923 Homo sapiens cDNA
11450	24510	38177	2.71	2.0E-45	AA458770.1	EST_HUMAN	aa8712.11 Stratigene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838319 5' similar to
11784	24784	38481	3.35	2.0E-45	AW270280.1	EST_HUMAN	TR.G1144589 G1144689 R-SLY1.1
11784	24784	38482	3.35	2.0E-45	AW270280.1	EST_HUMAN	XP72603.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
13087	25710		2.73	2.0E-45	11418157	NT	XP72603.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
13617			1.22	1.0E-45	BE389856.1	EST_HUMAN	XP72603.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
422	13617		1.09	1.0E-45	BE389856.1	EST_HUMAN	XP72603.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
485	13679	20714	1.02	1.0E-45	4508412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1201	14363	27423	1.66	1.0E-45	7667280	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3172	16347	29354	10.41	1.0E-45	U02169.1	NT	Homo sapiens pro- $\alpha 2$ chain of collagen type XI (COL11A2) gene, complete cds
3581	16748	29784	0.85	1.0E-45	8659358	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
3664	16827	29836	0.69	1.0E-45	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
4689	17736	30716	6.4	1.0E-45	BE396833.1	EST_HUMAN	601284350F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608183 5'
4848	17981		1.05	1.0E-45	H07443.1	EST_HUMAN	601284350F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608183 5'
5081	18209	31181	1.56	1.0E-45	11545786	NT	Y05502.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:204363 5'
8220	21302	34822	0.7	1.0E-45	11422236	NT	Homo sapiens ribben protein (NIBAN), mRNA
8220	21302	34823	0.7	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
8806	21885	35425	0.9	1.0E-45	087675.1	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
9321	22397	35950	3.92	1.0E-45	BE87843.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
9722	22787	36358	0.99	1.0E-45	AB002297.1	NT	601511226F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912535 5'
12369	25263	32117	3.5	1.0E-45	11418089	NT	Human mRNA for KIAA0299 gene, partial cds
12582	25384		19.43	1.0E-45	11502821	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
12668	25697		6.42	1.0E-45	11418177	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
13047	25696	31963	4.02	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
8423	21504	35037	2.71	8.0E-46	8910283	NT	Homo sapiens cadherin complex 2, gene 6g (K12-6g), mRNA
8836	21914		6.82	8.0E-46	AL163209.2	NT	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
10697	23730	37335	6.89	8.0E-46	AW246904.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
							2822449.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822449 5'



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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2513	15639	28760	7.67	8.0E-46	AI433261.1	EST_HUMAN	IC3208.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:U00314_mn2 TUBULIN BETA-1 CHAIN (HUMAN);
2513	15639	28761	7.67	8.0E-46	AI433261.1	EST_HUMAN	IC3208.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gb:U00314_mn2 TUBULIN BETA-1 CHAIN (HUMAN);
8244	21328		2.72	8.0E-46	BE167244.1	EST_HUMAN	RC54H10508-280200-012-C12 HT10508 Homo sapiens cDNA
4703	17838		4.79	7.0E-46	BE366165.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
4928	18068		1.33	7.0E-46	BE064398.1	EST_HUMAN	RC4-B10310-110300-016-f10 BT0310 Homo sapiens cDNA
6167	19343	32689	4	7.0E-46	8922708	NT	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
6623	19783	33171	1.8	7.0E-46	BF105946.1	EST_HUMAN	601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042736 5'
12706	25489		2.6	7.0E-46	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2812	15926	29037	6.87	6.0E-46	AI684381.1	EST_HUMAN	MER19 repetitive element; MIR19 repetitive element;
2812	15926	29038	6.87	6.0E-46	AI684381.1	EST_HUMAN	MIR19 repetitive element; MIR19 repetitive element;
8257	19431	32778	11.57	6.0E-46	AI635448.1	EST_HUMAN	ts5bh10.x1 NCI_CGAP_Ki68 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 CG0363 SA GENE;
7368	20445	33907	0.99	6.0E-46	AW513244.1	EST_HUMAN	x042604.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2706654 3' similar to gb:U08069 DNAJ
7541	20514	34091	0.87	6.0E-46	BE509740.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN);
11873	23801		2.14	6.0E-46	BE784971.1	EST_HUMAN	U14-B14-493-b-06-0-U1.1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3087298 3'
209	13432		6.31	6.0E-46	AL163210.2	NT	601478409F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880995 5'
3017	16781	29788	1.17	5.0E-46	BE677194.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
3617	16781	29787	1.17	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupsel_dorsal_rool_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
6874	20026	33436	1.52	5.0E-46	BE590442.1	EST_HUMAN	na83807.x1 NCI_CGAP_Ki61 Homo sapiens cDNA clone IMAGE:3258767 3' similar to TR:O76202
7050	20174	33598	3.69	6.0E-46	BE347228.1	EST_HUMAN	075202 HOMOLOG OF RAT KIDNEY-SPECIFIC;
7244	20327	33772	0.75	5.0E-46	AW682353.1	EST_HUMAN	802021764F1 NCI_CGAP_Bme7 Homo sapiens cDNA clone IMAGE:4156670 5'
7944	20616	34093	0.59	5.0E-46	BE549744.1	EST_HUMAN	QV44510212-120100-075-109 ST0212 Homo sapiens cDNA
658	13844		3.95	4.0E-46	AA601143.1	EST_HUMAN	7b38805.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230481 3'
1740	14889	27981	2.89	4.0E-46	AW770544.1	EST_HUMAN	no54609.x1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_mn1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
							h88603.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_mn1 LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1740	14889	27082	2.99	4.0E-46	AW770544.1	EST_HUMAN	h186c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008938 3' similar to gb:X14008_Jma1
2798	15913	29021	7.4	4.0E-46	M18048.1	NT	LYSOZYME C PRECURSOR (HUMAN); contains element MER37 repetitive element;
5583	18760	31788	2.1	4.0E-46	M38862.1	NT	Human endogenous retrovirus RTV1-H2
5563	18750	31787	2.1	4.0E-46	M38852.1	NT	Human Ig gamma-3 heavy-chain gene V region, partial cds
12851	25565	31889	1.38	4.0E-46	AB002059.1	NT	Human Ig gamma-3 heavy-chain gene V region, partial cds
2359	15490	28620	0.94	3.0E-46	7657203	NT	Homo sapiens DNA for Human P2XM, complete cds
4513	17552	30840	1.21	3.0E-46	4508376	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU15552), mRNA
4898	18026	31015	1.11	3.0E-46	Z73660.1	NT	Homo sapiens mitogen-activated protein kinase kinase 3 (MAP4K3), mRNA
4898	18026	31015	1.11	3.0E-46	Z73660.1	NT	H sapiens Ig lambda light chain variable region gene (7c.11.2) germ-line, Ig-Light-Lambda; VLambda
4898	18026	31016	1.11	3.0E-46	Z73660.1	NT	H sapiens Ig lambda light chain variable region gene (7c.11.2) germ-line, Ig-Light-Lambda; VLambda
8949	22028	35569	12.45	3.0E-46	A1831482.1	EST_HUMAN	w49604.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406160 3' similar to contains THR.b2
8208	22284	35824	0.61	3.0E-46	U08850.1	NT	THR repetitive element;
8208	22284	35825	0.61	3.0E-46	U08850.1	NT	Human AD amyloid mRNA, complete cds
11873	24851	38558	1.76	3.0E-46	D31765.1	NT	Human mRNA for KIAA0081 gene, partial cds
860	14037	27099	12.65	2.0E-46	AA468848.1	EST_HUMAN	ne08603.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:380408 3' similar to contains THR.b2 THR
1598	14746		3.78	2.0E-46	AA878246.1	EST_HUMAN	(repetitive element);
1871	14823	27908	6.63	2.0E-46	U78027.1	NT	z158602.r1 Scarses Testis, NHT Homo sapiens cDNA clone IMAGE:726850 5' similar to SW-103P1_MOUSE
6089	18217	31188	1.26	2.0E-46	AA399288.1	EST_HUMAN	(L44L) and FTP3 (FTP3) genes, complete cds
7653	20721	34197	7.1	2.0E-46	8910599	NT	Homo sapiens Brulon's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
8260	21342		1.29	2.0E-46	BE866161.1	EST_HUMAN	z158602.r1 Scarses Testis, NHT Homo sapiens cDNA clone IMAGE:726850 5' similar to SW-103P1_MOUSE
11524	24980		1.82	2.0E-46	7657233	EST_HUMAN	z158602.r1 Scarses Testis, NHT Homo sapiens cDNA clone IMAGE:726850 5' similar to SW-103P1_MOUSE
12294	26040		1.4	2.0E-46	BF028854.1	EST_HUMAN	z158602.r1 Scarses Testis, NHT Homo sapiens cDNA clone IMAGE:726850 5' similar to SW-103P1_MOUSE
12555	26331		1.57	2.0E-46	H48391.1	EST_HUMAN	z158602.r1 Scarses Testis, NHT Homo sapiens cDNA clone IMAGE:726850 5' similar to SW-103P1_MOUSE
12568	26401		3.31	2.0E-46	AA001788.1	EST_HUMAN	z158602.r1 Scarses Testis, NHT Homo sapiens cDNA clone IMAGE:726850 5' similar to SW-103P1_MOUSE
12934	26923	31864	4.28	2.0E-46	AW27214.1	EST_HUMAN	z158602.r1 Scarses Testis, NHT Homo sapiens cDNA clone IMAGE:726850 5' similar to SW-103P1_MOUSE
1261	14418	27483	4.31	1.0E-46	4502694	NT	z158602.r1 Scarses Testis, NHT Homo sapiens cDNA clone IMAGE:726850 5' similar to SW-103P1_MOUSE
2356	15487	28619	4.88	1.0E-46	AW978518.1	EST_HUMAN	z158602.r1 Scarses Testis, NHT Homo sapiens cDNA clone IMAGE:726850 5' similar to SW-103P1_MOUSE

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2473	15600	28725	3.53	1.0E-46	U97330.1	EST_HUMAN	EST148b095 WATM1 Homo sapiens cDNA clone 48b095
3321	16494	29511	2.12	1.0E-46	AA631012.1	EST_HUMAN	np78b02.s1 NCI_CGAP_P2 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:U78717 H. sapiens
4895	18124		3.13	1.0E-46	AB023197.1	NT	MT-11 mRNA. (HUMAN):
6817	19007	32313	5.89	1.0E-46	BF194707.1	EST_HUMAN	Homo sapiens mRNA for KIAA0980 protein, partial cds
6098	25818	32809	5.34	1.0E-46	8923762	NT	769b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
6098	25818	32810	5.34	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6746	19902	33285	0.64	1.0E-46	BF196247.1	EST_HUMAN	7n48607.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567852 3' similar to contains element
11102	19007	32313	3.72	1.0E-46	BF194707.1	EST_HUMAN	MER22 repetitive element:
11410	24471	38136	1.61	1.0E-46	AJ245021.1	NT	769b01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
12323	25233	32105	1.39	1.0E-46	BF531102.1	EST_HUMAN	60207224f1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5'
12323	25233	32106	1.39	1.0E-46	BF531102.1	EST_HUMAN	60207224f1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215398 5'
13176	25764		1.89	1.0E-46	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAE03 5'
787	13966		3.7	9.0E-47	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
6047	18175	31152	3.05	9.0E-47	AW770928.1	EST_HUMAN	h83604.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O78703 O78703
6508	19672	33039	0.86	9.0E-47	11425439	NT	HYPOTHETICAL 12.4 KD PROTEIN.
11398	24449	38110	1.4	9.0E-47	11432209	NT	Homo sapiens zinc finger protein ZNF286 (ZNF286), mRNA
12874	28027	31675	1.04	9.0E-47	11417966	NT	Homo sapiens similar to aldo-keto reductase family 1, member B1 (aldose reductase) (H. sapiens)
1851	14937	28100	32.2	8.0E-47	Y18536.1	NT	Homo sapiens SEC14 (S. cerevisiae) like 2 (SEC14L2), mRNA
1851	14937	28101	32.2	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2781	15887	29007	1.5	8.0E-47	5453955	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
3089	16265	29283	2.04	8.0E-47	AJ229043.1	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
3715	18878	29881	0.77	8.0E-47	AB041928.1	NT	Homo sapiens 559 kb contig between MML1 and CBR1 on chromosome 21q22, segment 3/3
3715	18878	29882	0.77	8.0E-47	AB041928.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
12962	25922		1.89	7.0E-47	AB041928.1	EST_HUMAN	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
2613	15737	28831	3.04	6.0E-47	AI163246.2	NT	AV683294 GKC Homo sapiens cDNA clone GKCASH11 5'
8890	21959	35505	0.32	6.0E-47	U77054.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
8476	22533	36097	6.83	6.0E-47	AI696189.1	EST_HUMAN	HSU77054 Human Homo sapiens cDNA clone NT
9013	22953	36538	0.69	6.0E-47	AB042824.1	NT	628102.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296559 3'
9813	22953	36539	0.69	6.0E-47	AB042824.1	NT	Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds
							Homo sapiens RECQL5 beta mRNA for DNA helicase recQ5 beta, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6707	19865	33255	5.73	5.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
11035	24114		5.68	6.0E-47	M78590.1	EST_HUMAN	EST100739 Fetal brain, Strategene (cat#36206) Homo sapiens cDNA clone HFB07
1432	14585	27650	7.03	4.0E-47	4657556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
6971	20199	33825	0.62	4.0E-47	BE93898.1	EST_HUMAN	MRA-TN0108-280600-201-004 TN0108 Homo sapiens cDNA
8677	21757	35292	2.22	4.0E-47	BE016483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:362243 5'
8677	21757	35293	2.22	4.0E-47	BE016483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:362243 6'
8818	21897	35436	0.83	4.0E-47	AW09377.1	EST_HUMAN	RC3-BN0034-220300-015-05 BN0034 Homo sapiens cDNA
11930	24922		1.98	4.0E-47	AW615509.1	EST_HUMAN	xx68b07.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW-INT6_MOUSE
558	13751	26778	2.09	3.0E-47	BE907834.1	EST_HUMAN	Q8422 VIRAL INTEGRATION SITE PROTEIN INT-6, (1):
558	13751	26779	2.09	3.0E-47	BE907834.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898721 5'
841	14019	27075	3.89	3.0E-47	N57483.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898721 5'
868	14141	27202	10.04	3.0E-47	AL163284.2	NT	Y54b04.s1 Soares_multiple_sclerosis_ZN8HNSP Homo sapiens cDNA clone IMAGE:27327 3'
3376	16548	29582	0.97	3.0E-47	4604116	NT	Homo sapiens chromosome 21 segment HS21C084
4073	17229		6.61	3.0E-47	U93181.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4482	17822	30603	1.14	3.0E-47	M112959.1	NT	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
8139	18315	32854	4.68	3.0E-47	AW408800.1	EST_HUMAN	Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds
6136	19316	32855	4.68	3.0E-47	AW408800.1	EST_HUMAN	UHF-BM0-adv-d-07-0-UI11 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
8694	19852		1.71	3.0E-47	AI222413.1	EST_HUMAN	UHF-BM0-adv-d-07-0-UI11 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
7540	20613	34089	0.88	3.0E-47	AI019755.1	EST_HUMAN	q104607.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
8033	22112	35654	0.77	3.0E-47	AW663796.1	EST_HUMAN	w11h08.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
8033	22112	35655	0.77	3.0E-47	AW663796.1	EST_HUMAN	w11h08.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
152	13377	28409	1.21	2.0E-47	AL163209.2	NT	EST137689 MAGe resequences, MAGH Homo sapiens cDNA
890	14162	27221	2.45	2.0E-47	AL163209.2	NT	EST137689 MAGe resequences, MAGH Homo sapiens cDNA
990	14162	27222	2.45	2.0E-47	AL163209.2	NT	EST137689 MAGe resequences, MAGH Homo sapiens cDNA
1598	14751	27659	0.85	2.0E-47	AW98279.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
1823	14775	27659	1.61	2.0E-47	7662709	NT	Homo sapiens chromosome 21 segment HS21C009
1712	14883	27952	4.49	2.0E-47	AA524514.1	EST_HUMAN	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
4467	17607	30585	1.61	2.0E-47	4504868	NT	ng43112.s1 NCI CGAP_Cos3 Homo sapiens cDNA clone IMAGE:937607 3'
4503	17643	30628	1.67	2.0E-47	AA569592.1	EST_HUMAN	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
4503	17643	30629	1.67	2.0E-47	AA569592.1	EST_HUMAN	m23g07.s1 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:914652
4628	17704	30746	2.14	2.0E-47	5174648	NT	m23g07.s1 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:914652
4933	18063	31046	1.25	2.0E-47	AW965188.1	EST_HUMAN	Homo sapiens Rev/Rex activation domain binding protein-related (RAB-R) mRNA
							EST1377239 MAGe resequences, MAGH Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5245	18386		0.71	2.0E-47	AI041128.1	EST_HUMAN	ov61h03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1641845 3'
5904	19093	32407	0.8	2.0E-47	AF073921.1	NT	Homo sapiens regulator of G-protein signaling 6 variant form (RGS6) mRNA, complete cds
6097	19278	32607	1.32	2.0E-47	BE778476.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3607487 5'
6097	19278	32608	1.32	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3607487 5'
7678	25854		1.34	2.0E-47	U09751.1	NT	Homo sapiens 6-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
8151	21233	34753	1.66	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8151	21233	34764	1.66	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8815	21994	35533	1.76	2.0E-47	AF071771.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
9690	22739	36308	1.27	2.0E-47	U1526136	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
12357	26073	31653	3.36	2.0E-47	F42423.1	EST_HUMAN	Y02608.s1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:29966 3' similar to contains OFFR repetitive element;
12394	26078		1.87	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1437	14590	27683	6.42	1.0E-47	A1333426.1	EST_HUMAN	q959100.x1 Soares_fetal_lung_NbHL18W Homo sapiens cDNA clone IMAGE:1031189 3'
3926	17085	30080	1.1	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3926	17085	30081	1.1	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5187	18309	31275	2.4	1.0E-47	AW813906.1	EST_HUMAN	RC3-ST0197-130400-017402 ST0197 Homo sapiens cDNA
7189	20054	33464	10.76	1.0E-47	AI880886.1	EST_HUMAN	at19e08.x1 Barstead aorta HPLR88 Homo sapiens cDNA clone IMAGE:2365598 3' similar to gb:M22995
8069	22148		4.24	1.0E-47	AW664549.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
10564	22589	37205	2.26	1.0E-47	U30115.1	NT	h18481.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978872 3' similar to gb:M26326
10564	22589	37205	2.26	1.0E-47	U30115.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1643	14785	27879	3.84	9.0E-48	AF223397.1	NT	Pp10 hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
3846	16809	29823	0.73	9.0E-48	BF359947.1	EST_HUMAN	h18481.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978872 3' similar to gb:M26326
6787	18987	32280	1.1	9.0E-48	BE888198.1	EST_HUMAN	keratin, type I cytoskeletal 18 (HUMAN);
6787	18987	32291	1.1	9.0E-48	BE888198.1	EST_HUMAN	Pp10 hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
6226	19401	32751	0.57	9.0E-48	AI833166.1	EST_HUMAN	keratin, type I cytoskeletal 18 (HUMAN);
6355	16625	32882	0.71	9.0E-48	AU123240.1	EST_HUMAN	keratin, type I cytoskeletal 18 (HUMAN);
11378	24439	38098	3.06	9.0E-48	BE393873.1	EST_HUMAN	keratin, type I cytoskeletal 18 (HUMAN);
1278	14436		1.75	8.0E-48	4501800	NT	keratin, type I cytoskeletal 18 (HUMAN);
1280	14436		1.65	8.0E-48	4501800	NT	keratin, type I cytoskeletal 18 (HUMAN);
3205	16390	29390	5.72	8.0E-48	AW768477.1	EST_HUMAN	keratin, type I cytoskeletal 18 (HUMAN);

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3205	16380	29391	5.72	8.0E-48	AW769477.1	EST_HUMAN	h461b03.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gp-X04707
4041	17197	30208	0.68	8.0E-48	4504116	NT	BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
503	13698		2.68	7.0E-48	AB033036.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
504	13698		18.69	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1527	14680	27761	1.98	7.0E-48	6912719	NT	Homo sapiens tousel-like kinase 1 (TLK1) mRNA
1687	14819	27802	5.39	7.0E-48	5730038	NT	Homo sapiens SET domain and methionine transposase fusion gene (SETMAR) mRNA
6885	16843	33233	24.01	7.0E-48	11418831	NT	Homo sapiens histidyl-tRNA synthetase (HARS), mRNA
12125	25105	38809	2.98	7.0E-48	R18623.1	EST_HUMAN	h37b02.1 Sources infant brain T1N8 Homo sapiens cDNA clone IMAGE:34747 5'
3687	16850	29888	0.88	6.0E-48	AJ76111.1	EST_HUMAN	w69h03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:239813 3'
6183	18359	32707	0.84	6.0E-48	AB006956.1	NT	Homo sapiens mRNA for ALE-75, complete cds
6924	20239	33674	0.93	6.0E-48	11420895	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX), mRNA
7628	25849	34172	0.78	6.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
7628	25849	34173	0.78	6.0E-48	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
8323	22399	35953	1.57	6.0E-48	AF028818.1	NT	Homo sapiens putative oncogene protein mRNA, partial cds
9741	22808	36382	1.87	6.0E-48	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
							Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
8860	22830	36514	2.84	6.0E-48	AA189080.1	EST_HUMAN	zq45b06.s1 Striatogene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;
3394	18465	29569	1.48	6.0E-48	4826891	NT	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
8774	21853	35995	1.04	6.0E-48	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-t06 BT0311 Homo sapiens cDNA
2829	15943	25053	1.02	4.0E-48	R45715.1	EST_HUMAN	H4140.f Adult heart, Clontech Homo sapiens cDNA clone a140.f
11200	24289	37905	3.11	4.0E-48	AB020420.1	EST_HUMAN	h47d02.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2254154 3'
12050	25031	38737	1.76	4.0E-48	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-t06 BT0311 Homo sapiens cDNA
1418	14570	27843	1.91	3.0E-48	AV690984.1	EST_HUMAN	AV690984 GKC Homo sapiens cDNA clone GKCDRE12 5'
2032	15173	28282	31.61	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2032	15173	28283	31.61	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3505	16872	28882	0.93	3.0E-48	AF172453.1	NT	Homo sapiens cytidyl transfer factor receptor mRNA, complete cds
3721	16882	28888	0.9	3.0E-48	AW664531.1	EST_HUMAN	h14b12.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872256 3' similar to SW:DCRB_HUMAN
4362	17605		0.83	3.0E-48	AA009541.1	EST_HUMAN	P59555 DOWN SYNDROME CRITICAL REGION PROTEIN B.1
6015	19189	32516	2.08	3.0E-48	BE084571.1	EST_HUMAN	z04q03.1 Sources fetal liver, spleen, TINF5_S1 Homo sapiens cDNA clone IMAGE:429844 6'
7159	20282	33735	1.07	3.0E-48	AF087913.1	NT	Human endogenous retrovirus HERV-P-1470
8685	21669		3.73	3.0E-48	AA689930.1	EST_HUMAN	h03f05.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1210137 3' similar to contains PTR5.S1 PTR5 repetitive element.1

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11114	24188	37818	8.1	3.0E-48	BF514170.1	EST_HUMAN	UHH-BW1-anti-10-Q.U.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267.3'
5	13244	28245	0.66	2.0E-48	AA465007.1	EST_HUMAN	z80c03.t1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:810052.5'
49	13285	28294	1.7	2.0E-48	AA631040.1	EST_HUMAN	hm67 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-26
4654	17780	30774	0.89	2.0E-48	EE240035.1	EST_HUMAN	TCBAP-ID3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project-TCBA Homo sapiens cDNA clone TCBAP3842
5935	19121	32433	0.64	2.0E-48	AA613171.1	EST_HUMAN	not8g01.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1101072.5'
5935	19121	32434	0.64	2.0E-48	AA613171.1	EST_HUMAN	not8g01.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1101072.3'
7688	20753	34236	3.89	2.0E-48	AB040394.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7688	20753	34237	3.89	2.0E-48	AB040394.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7703	20768	34253	3.54	2.0E-48	11486238	NT	Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p85)) (RELA) mRNA
8550	21631	35168	1.13	2.0E-48	AV743451.1	EST_HUMAN	AV743451 OB Homo sapiens cDNA clone CBCCG310.5'
12109	25089		1.38	2.0E-48	AW281799.1	EST_HUMAN	UHH-B12-egf-b-11-Q.U.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724453.3'
12320	13244	28245	2.88	2.0E-48	AA465007.1	EST_HUMAN	z80c03.t1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:810052.5'
12674	25890	31771	1.25	2.0E-48	BE737164.1	EST_HUMAN	601305064.f1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639782.5'
57	13285	28311	2.33	1.0E-48	7708534	NT	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747) mRNA
886	14072	27137	4.67	1.0E-48	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (precursor medn-11, Alzheimer disease) (APP), mRNA
1101	14266	27323	1.52	1.0E-48	7667430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1101	14268	27324	1.52	1.0E-48	7667430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1324	14481	27348	4.01	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 8 (RBM8) mRNA
1868	15111	28212	13.8	1.0E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3577	16742	29769	0.94	1.0E-48	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
5240	18362	31330	1.1	1.0E-48	IM0976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
6417	18686	32848	1.24	1.0E-48	AB89077.1	EST_HUMAN	UHH-BW1-anti-10-Q.U.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267.3'
6417	18686	32849	1.24	1.0E-48	AB89077.1	EST_HUMAN	UHH-BW1-anti-10-Q.U.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267.3'
6628	18788		0.87	1.0E-48	Y18000.1	NT	SIMILARITY TO U73841 :
6727	18883	33274	0.59	1.0E-48	AB028994.1	NT	UHH-BW1-anti-10-Q.U.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267.3'
6727	18883	33275	0.59	1.0E-48	AB028994.1	NT	UHH-BW1-anti-10-Q.U.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267.3'
7407	20485	33984	2.21	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
9031	22110	35651	0.65	1.0E-48	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9031	22110	35652	0.65	1.0E-48	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA

Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9414	22488	36053	0.99	1.0E-48	4502638	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
9468	22525	36089	6.79	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
9781	22821	36399	4.74	1.0E-48	BF304693.1	EST_HUMAN	601888096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
10581	23616	37221	4.23	1.0E-48	11429608	NT	Homo sapiens B cell linker protein (SLP65) mRNA
10581	23616	37222	4.23	1.0E-48	11429608	NT	Homo sapiens B cell linker protein (SLP65) mRNA
12282	28014		1.41	1.0E-48	W26785.1	EST_HUMAN	1368 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
2064	15204	28320	0.97	8.0E-49	AB026497.1	NT	Mus musculus Myosin PDZ domain, complete cds
6178	18354	32701	3.07	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20) mRNA
6178	18354	32702	3.07	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20) mRNA
8491	21572	35109	3.09	8.0E-49	U23850.1	NT	Human inositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
10184	23231	36822	0.93	8.0E-49	AB008891.1	NT	Homo sapiens gene for actinin receptor type IIB, complete cds
11096	24189	37604	3.66	8.0E-49	AI623722.1	EST_HUMAN	is38412x1 NCI CGAP U14 Homo sapiens cDNA clone IMAGE:2230871 3' similar to contains Alu repetitive element; contains element PTR5 repetitive element;
12097	25077	38785	2.08	8.0E-49	AA872183.1	EST_HUMAN	cb78608 s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1337462 3'
142	13602	26637	1.21	7.0E-49	5728990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
142	13602	26638	1.21	7.0E-49	5728990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
405	13602	26637	1.92	7.0E-49	5728990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
405	13602	26638	1.92	7.0E-49	5728990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
408	13602	26637	2.25	7.0E-49	5728990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
408	13602	26638	2.25	7.0E-49	5728990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1248	14407	27469	4.37	7.0E-49	AL183284.2	NT	Homo sapiens chromosome 21 segment HS21CG84
4772	17607	30890	0.9	7.0E-49	OB0811	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.3
5576	18771	31815	2.33	7.0E-49	AB07191.1	EST_HUMAN	W25104.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923
5576	18771	31815	2.33	7.0E-49	AB07191.1	EST_HUMAN	W25104.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923
6586	18781	31826	1.3	7.0E-49	AL120937.1	EST_HUMAN	DKFZ762C033_s1 762 (synonym: hme2) Homo sapiens cDNA clone DKFZ762C033 3'
5926	18771	31815	0.78	7.0E-49	AB07191.1	EST_HUMAN	W25104.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923
							OS4923 RSEC15 ;
							W25104.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923
							DKFZ762C033_s1 762 (synonym: hme2) Homo sapiens cDNA clone DKFZ762C033 3'
							W25104.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923
							OS4923 RSEC15 ;
							bae5g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800504 3' similar to gbX17206 40S
							RIBOSOMAL PROTEIN S4 (HUMAN), gbM20832 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
202	13425	26456	20.33	6.0E-49	AW731740.1	EST_HUMAN	DKFZ761A138_s1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZ761A138 3'
4231	17378	30307	0.94	6.0E-49	AL162091.1	EST_HUMAN	hd44602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:O95696
6854	19140	32456	0.64	6.0E-49	AW511225.1	EST_HUMAN	O95698 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II ;
6572	19734	33113	1.27	6.0E-49	AU140742.1	EST_HUMAN	AU140742 PLACE4 Homo sapiens cDNA clone PLACE4000148 5'



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11557	24612	38291	3.39	6.0E-49	AW452218.1	EST_HUMAN	U1-HB3-elo-e-05-0-J1.s1 NC1 CGAP_Subs5 Homo sapiens cDNA clone IMAGE:30680.48 3'
11681	24646	38650	2.48	6.0E-49	AA366556.1	EST_HUMAN	EST177525 Pancreas tumor III Homo sapiens cDNA 5' end
11681	24948	38651	2.48	6.0E-49	AA366556.1	EST_HUMAN	EST177525 Pancreas tumor III Homo sapiens cDNA 5' end
12670	25897		10.64	6.0E-49	AA707667.1	EST_HUMAN	z28c08.s1 Scares fetal liver spleen INFIL.S.1 Homo sapiens cDNA clone IMAGE:451694.3'
730	13912	26951	5.84	5.0E-49	AL168210.2	NT	Homo sapiens chromosome 21 segment HS21C010
730	13912	26952	5.84	5.0E-49	AL168210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1436	14983	28082	10.18	6.0E-49	AA172121.1	EST_HUMAN	z28c07.r1 StrataGene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610880.5' similar to TR:G333226 G233226 RTVL-H PROTEIN.; contains LTR7.3 LTR7 LTR7 repetitive element.;
2808	15822	29032	7.1	5.0E-49	U17714.1	NT	Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds
3346	16519	28533	7.59	5.0E-49	11436355	NT	Homo sapiens similar to ribosomal protein S27 (metalloprotein 1) (H. sapiens) (LOC63362). mRNA
638	13731	28754	28.39	4.0E-49	AAW189533.1	EST_HUMAN	X08b01.x1 NC1 CGAP_U14 Homo sapiens cDNA clone IMAGE:2676693.3' similar to WP.B0350.2B
7395	20473	33539	0.86	4.0E-49	Z26634.2	NT	CE09703: Homo sapiens mRNA for ankryn B (440 kDa)
7395	20473	33940	0.86	4.0E-49	Z26634.2	NT	Homo sapiens mRNA for ankryn B (440 kDa)
7422	20489	33970	0.68	4.0E-49	11526737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8
7422	20489	33971	0.68	4.0E-49	11526737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8
7892	21042	34534	0.69	4.0E-49	7662209	NT	(GALNAc-1B) (GALNTB). mRNA
8065	22144	35680	0.47	4.0E-49	11425374	NT	Homo sapiens KIAA0623 gene product (KIAA0623). mRNA
8065	22144	35691	0.47	4.0E-49	11425374	NT	Homo sapiens copine III (CPNE3). mRNA
12614	28145		2.74	4.0E-49	AA210788.1	EST_HUMAN	z60f05.r1 NC1 CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682977.5'
12615	25413		2.93	4.0E-49	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
674	13768	28789	0.91	3.0E-49	X68968.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
2713	15831		2.73	3.0E-49	AA010131.1	EST_HUMAN	z631c05.r1 Scares retina N2b-d-HR Homo sapiens cDNA clone IMAGE:360584.5' similar to contains L1.3 L1
6088	18226	31108	2.68	3.0E-49	U46989.1	NT	repetitive element.;
7677	20649	34127	8.83	3.0E-49	H39478.1	EST_HUMAN	Human type IV collagen (COL4A6) gene, exon 40
11562	24836	38316	1.41	3.0E-49	AA331561.1	EST_HUMAN	EST25612 WATM1 Homo sapiens cDNA clone 25612
678	13964		1.83	2.0E-49	BE165980.1	EST_HUMAN	EST42572 Endometrial tumor Homo sapiens cDNA 5' end
3294	18468	29487	1.16	2.0E-49	N28446.1	EST_HUMAN	MR3-H10487-150200-113-801 HT0487 Homo sapiens cDNA
							yz23c08.r1 Scares melanocyte 2N-b-HM Homo sapiens cDNA clone IMAGE:252571.5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit E-VALUE	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3659	16822	28832	0.86	2.0E-49	AF026564.1	NT	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
6876	20027	33437	1.2	2.0E-49	AV717938.1	EST_HUMAN	AV717938 DCB Homo sapiens cDNA clone DCBALB01 5'
8281	21373		1.87	2.0E-49	M86033.1	EST_HUMAN	EST02558 Fetal brain, Striatopons (cat#36209) Homo sapiens cDNA clone HFBGCV50
12826	28008		2.09	2.0E-49	AF163964.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
922	14097		9.1	1.0E-49	BF035327.1	EST_HUMAN	80145833.F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
1584	14736	27816	73.58	1.0E-49	4657887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1844	14890	28091	2.83	1.0E-49	BE255216.1	EST_HUMAN	601820053.F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052052 5'
6476	18674	31688	4.68	1.0E-49	BF131007.1	EST_HUMAN	601115769.F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3368273 5'
6202	19377	32728	0.65	1.0E-49	H16291.1	EST_HUMAN	SP-CBG1 HUMAN Q08447 GUANINE NUCLEOTIDE-BINDING PROTEIN (GTT) GAMMA-1 SUBUNIT ;
6208	19383	32733	1.09	1.0E-49	AW984640.1	EST_HUMAN	EST1376713 MAGE sequences, MAGH Homo sapiens cDNA
7372	20451	33916	2.78	1.0E-49	BE398110.1	EST_HUMAN	601280330.F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7372	20451	33916	2.78	1.0E-49	BE398110.1	EST_HUMAN	601280330.F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7453	20530	34003	2.09	1.0E-49	N25884.1	EST_HUMAN	YW786712.1 Scores, placenta, 8daysweek, 2NBHP8B5W Homo sapiens cDNA clone IMAGE:258406 3'
7453	20530	34004	2.09	1.0E-49	N25884.1	EST_HUMAN	YW786712.1 Scores, placenta, 8daysweek, 2NBHP8B5W Homo sapiens cDNA clone IMAGE:258406 3'
8874	21953		0.71	1.0E-49	8994184	NT	similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
8183	22271	35809	1.48	1.0E-49	BE409340.1	EST_HUMAN	Homo sapiens RNA binding motif protein 7 (LOC51120), mRNA
10331	23366	36975	1.23	1.0E-49	AI043129.2	EST_HUMAN	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds
11304	24369	38010	1.32	1.0E-49	AV751477.1	EST_HUMAN	DKFZp434D2423.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D2423 5'
11580	24643	38325	2.91	1.0E-49	11427366	EST_HUMAN	AV761477 NPB Homo sapiens cDNA clone NPDAWE04 5'
12148	25119		1.26	1.0E-49	BE168343.1	EST_HUMAN	Homo sapiens brefeldin A-ribosylated guanine nucleotide-exchange protein 1 (BIG1), mRNA
12508	25349		1.82	1.0E-49	11418322	NT	MRO-HT0407-010200-005-02 HT0407 Homo sapiens cDNA
6109	18237		0.92	9.0E-50	AF101475.1	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6534	26215		0.63	9.0E-50	BE299798.1	EST_HUMAN	Homo sapiens glycine N-methyltransferase (GNMT) gene, complete cds
174	13398	26426	4.18	8.0E-50	AI183202.2	NT	601176250.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531588 5'
737	13919	26960	1.92	8.0E-50	X85097.2	NT	Homo sapiens chromosome 21 segment HS21C002
1803	14862	28046	4.32	8.0E-50	X85097.2	NT	Homo sapiens mRNA for VIP receptor 2
2552	15677	28800	1.05	8.0E-50	4601880	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2552	15677	28800	1.05	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA
2764	15879	28988	2.42	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51674), mRNA
2891	15160		2.67	8.0E-50	4826858	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
					D80334.1	NT	Homo sapiens hepatocyte growth factor (HGF) gene, exon 18

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
634	13819	26843	1.07	7.0E-50	BE088691.1	EST_HUMAN	QV0-BT0703-280400-211-608 BT0703 Homo sapiens cDNA
6923	20238	33672	0.73	7.0E-50	EF081922.1	EST_HUMAN	RC6-TN0073-150300-011-A12 TN0073 Homo sapiens cDNA
6923	20238	33673	0.73	7.0E-50	EF091922.1	EST_HUMAN	RC6-TN0073-150300-011-A12 TN0073 Homo sapiens cDNA
7457	20533	34008	0.74	7.0E-50	AA627822.1	EST_HUMAN	ng89e12.g1 NCI CGAP C68 Homo sapiens cDNA clone IMAGE:1148206 3' similar to gpX68391 60S RIBOSOMAL PROTEIN L6 (HUMAN);
10893	24072	37705	23.18	7.0E-50	AB872137.1	EST_HUMAN	wnt55g11.x1 NCI CGAP U12 Homo sapiens cDNA clone IMAGE:2439908 3'
4462	17602		0.67	6.0E-50	EE794391.1	EST_HUMAN	601589565f1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943877 5'
8408	21489		3.28	6.0E-50	EE044078.1	EST_HUMAN	h08h04.x1 NCI CGAP U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element;
11053	24130	37765	3.32	6.0E-50	AA312078.1	EST_HUMAN	EST182775 Jurkat T-cell VI Homo sapiens cDNA 5' end
11053	24130	37765	3.32	6.0E-50	AA312078.1	EST_HUMAN	EST182775 Jurkat T-cell VI Homo sapiens cDNA 5' end
1835	14882	28080	1.34	5.0E-50	BF332938.1	EST_HUMAN	CMO-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
1835	14882	28081	1.34	6.0E-50	EF332938.1	EST_HUMAN	CMO-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
8294	22370		5.27	5.0E-50	AA557683.1	EST_HUMAN	n45h10.g1 NCI CGAP P14 Homo sapiens cDNA clone IMAGE:1043983 similar to contains PTR5.b3 PTR5 repetitive element;
12080	25070	38777	1.78	5.0E-50	AA403053.1	EST_HUMAN	z82b01.f1 Soares Jeele NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769
940	14114		2.31	4.0E-50	AA601143.1	EST_HUMAN	G1335769 GAG-POL POLYPROTEIN;
3330	16701	29712	2.06	4.0E-50	AL163248.2	NT	ng54e09.g1 NCI CGAP SS1 Homo sapiens cDNA clone IMAGE:1104620 3' similar to gb:X53741_mat1
6491	18567	33020	0.92	4.0E-50	11440983	NT	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
7383	20491	33924	1.02	4.0E-50	BE081538.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
1892	15134		9.4	3.0E-50	M18048.1	NT	QV1-BT0681-280300-127-f12 BT0681 Homo sapiens cDNA
3371	16543	29557	0.92	3.0E-50	AA748142.1	EST_HUMAN	Human endogenous retrovirus RTVL-H2
3846	17006	30008	0.9	3.0E-50	AW755254.1	EST_HUMAN	h030308.g1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322827 3'
6815	18968	33374	0.88	3.0E-50	11418317	NT	CMYAS Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYAS
6815	18968	33375	0.88	3.0E-50	11419317	NT	Cardiomyopathy associated gene 5
6904	20219	33848	1.71	3.0E-50	11421514	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
7822	20877	34376	5	3.0E-50	AF233436.2	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 12 (PTPN12), mRNA
7822	20877	34377	5	3.0E-50	AF233436.2	NT	Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H sapiens) (LOC83232), mRNA
7822	20877	34377	5	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
7822	20877	34377	5	3.0E-50	AF233436.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8782	21861	35404	0.89	3.0E-50	6601689	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
10023	23061	36657	1.08	3.0E-50	AB048318.1	NT	Homo sapiens mRNA for KIAA1598 protein, partial cds
10032	23070	36670	1.03	3.0E-50	U1418514	NT	Homo sapiens t-complex 10 (a murine top homolog) (TCF10), mRNA
10737	23770	37380	1.04	3.0E-50	AB002287.1	NT	Human mRNA for KIAA0289 gene, partial cds
11364	24429	38080	1.51	3.0E-50	U1436955	NT	Homo sapiens Gbx2-associated binder 2 (KIAA0571), mRNA
11752	23858	37864	8.19	3.0E-50	AJ245621.1	NT	Homo sapiens CTL2 gene
13217	25782	31822	1.95	3.0E-50	AB011399.1	NT	Homo sapiens gene for A-Fc, complete cds
789	13978		7.34	2.0E-50	AF05086.1	NT	Homo sapiens MHC class I region
1104	14269	27327	6.16	2.0E-50	U1457732	NT	Homo sapiens MHC class I region
1474	14687	27713	33.77	2.0E-50	AF138303.1	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
4376	17519	30498	0.76	2.0E-50	D88424.1	NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
5329	18442	31412	1.37	2.0E-50	AB018318.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
7007	20143	33582	0.67	2.0E-50	AU124063.1	EST_HUMAN	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8611	21592	35128	1.03	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8511	21592	35127	1.03	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8650	21730	35288	7.21	2.0E-50	X06986.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8650	21730	35289	7.21	2.0E-50	X06986.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
10086	23128	36728	1.6	2.0E-50	6910293	NT	Mus musculus keratin complex 2, gene Bg [(K12-Bg)] mRNA
10088	23128	36728	1.6	2.0E-50	6910293	NT	Mus musculus keratin complex 2, gene Bg [(K12-Bg)] mRNA
11960	24945		1.38	2.0E-50	AF023561.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
474	13689	26701	2.17	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2438	15566		10.11	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
10396	22431	37038	1.65	1.0E-50	D11078.1	NT	Homo sapiens RGH gene, retrovirus-like element
6104	16294	32817	1.04	9.0E-51	AW511225.1	EST_HUMAN	h444602.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2812378 3' similar to TR.O55636
6354	19624	32881	0.58	9.0E-51	AA744837.1	EST_HUMAN	O86536 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II.;
8672	21951	35467	0.7	9.0E-51	AJ791154.1	EST_HUMAN	n67f003.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283381 3'
9525	22590	36161	1.29	9.0E-51	AA045738.1	EST_HUMAN	SW.PSM_HUMAN O04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN;
9700	22749	35917	0.68	9.0E-51	AJ791154.1	EST_HUMAN	ab23604.s5 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:486352 5'
9700	22749	35917	0.68	9.0E-51	AJ791154.1	EST_HUMAN	SW.PSM_HUMAN O04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN;
9700	22749	35917	0.68	9.0E-51	AJ791154.1	EST_HUMAN	ab23604.s5 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:841866 3' similar to
9700	22749	35917	0.68	9.0E-51	AJ791154.1	EST_HUMAN	SW.PSM_HUMAN O04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN;
11764	23950	37679	1.97	9.0E-51	AB90878.1	EST_HUMAN	yw24908.1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:283210 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11764	23650	37580	1.97	8.0E-51	H89078.1	EST_HUMAN	hw24g06.r1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:253210 5'
12069	25050	38768	1.84	8.0E-51	AA85614.1	EST_HUMAN	am10n02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1466451 3' similar to SW:CAVP_CANFA P10463 CALCYPHOSINE.
4539	17697	30677	1.11	8.0E-51	4503932	NT	Homo sapiens glycine amidotransferase (L-arginine:glycine amidotransferase) (GATM) mRNA
4559	17697	30678	1.11	8.0E-51	4503932	NT	Homo sapiens glycine amidotransferase (L-arginine:glycine amidotransferase) (GATM) mRNA
4690	17825	30812	5.38	8.0E-51	AA610942.1	EST_HUMAN	np89609.s1 NC1_CGAP_Lu1 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gp.X12871_mn1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
7321	20403	33865	0.71	8.0E-51	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
7830	20885	34387	2.11	8.0E-51	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NTV-CO-38), mRNA
8664	22626		1.06	8.0E-51	AU138580.1	EST_HUMAN	AU138590 PLACE1 Homo sapiens cDNA clone IMAGE:1008867 5'
3354	18326	29541	1.27	7.0E-51	AW889219.1	EST_HUMAN	DNA-NT0028-200400-180-d05 NT0028 Homo sapiens cDNA
3447	16615	28633	0.82	7.0E-51	AW774720.1	EST_HUMAN	ms34603.x1 NC1_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TRIC92340
4282	17427	30416	1.37	7.0E-51	AL078828.1	EST_HUMAN	Q92340 ATYPICAL PCP SPECIFIC BINDING PROTEIN.;
4282	17427	30417	1.37	7.0E-51	AL078828.1	EST_HUMAN	DKFZp434B2229_17 434 (synonym: hncs3) Homo sapiens cDNA clone DKFZp434B2229 5'
4376	17618	30488	1.18	7.0E-51	11421695	NT	DKFZp434B2229_17 434 (synonym: hncs3) Homo sapiens cDNA clone DKFZp434B2229 5'
4471	17611	30589	1.44	7.0E-51	AW28903.1	EST_HUMAN	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA
11885	24870	38874	1.36	7.0E-51	AF161448.1	NT	UH-HBW0-sap-b-05-0-ULs1 NC1_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729817 3'
1657	14710	27790	0.94	8.0E-51	6678763	NT	Homo sapiens HSPC331 mRNA, partial cds
2036	15177	28287	5.93	6.0E-51	7657268	NT	Homo sapiens putative DNA binding protein (M66), mRNA
3582	16727	29743	14.85	6.0E-51	7657266	NT	Homo sapiens KIAA0929 protein Msz2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
4426	17568	30547	0.88	6.0E-51	8910553	NT	Homo sapiens KIAA0929 protein Msz2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
4426	17568	30548	0.88	6.0E-51	8910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
6113	19283	32628	1.48	6.0E-51	X01788.1	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
6124	18303	32642	8.16	6.0E-51	AF070083.1	NT	Human haptoglobin related (Hpr) gene exon 3
6124	18303	32642	8.16	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
6800	20215	33845	0.93	6.0E-51	4508736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6K81) mRNA
7032	20168	33580	0.82	6.0E-51	11446751	NT	Homo sapiens non-ribosomal protein Cdc42 effector protein SPEC2 (LOC65990), mRNA
7104	18331	31486	2.15	8.0E-51	11428525	NT	Homo sapiens cerebral cell adhesion molecule (LOC51146), mRNA
8337	22413	35965	0.69	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
8337	22413	35966	0.69	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
8865	22928	36508	2.05	6.0E-51	7681535	NT	Homo sapiens B9 protein (B9), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6964	23003	36568	0.76	6.0E-51	U50093.1	NT	Human ankryn (ANK1) gene, exon 2
11634	24690	38265	1.84	6.0E-51	11528289	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA
914	13983	27047	0.22	5.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
826	14004	27061	1.71	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1016	15028	27247	2.39	5.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1638	14780	27875	1.14	5.0E-51	5031880	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
2658	15781	28894	10.36	5.0E-51	AL007558.1	NT	Homo sapiens mRNA for nucleophorn 155
4055	17211	30221	1.31	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4055	17211	30222	1.31	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5183	18305	31289	1.04	5.0E-51	AB037832.1	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
11568	24613	38292	3.8	5.0E-51	3803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
137	13363	26397	14.26	3.0E-51	AL1587348.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 16 (HUMAN);
1203	14365	27426	48.14	3.0E-51	AL1587348.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 16 (HUMAN);
1876	15119	28220	1.38	3.0E-51	AA211288.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 16 (HUMAN);
4446	17586	30567	1.85	3.0E-51	AL159142.1	NT	Novel human gene mapping to chromosome 22
7733	20813	34304	2.3	3.0E-51	RI5914.1	EST_HUMAN	ye47c08.r1 Soares infant brain 11N1B Homo sapiens cDNA clone IMAGE:53223 5' similar to gb:M14123_cd54
8040	22119		3.83	3.0E-51	M28063.1	NT	RETROVIRUS-RELATED POLYPROTEIN (HUMAN); contains LTR3 repetitive element ;
9268	26227		0.61	3.0E-51	AW583777.1	EST_HUMAN	Human hnRNP C2 protein mRNA
12867	25578		6.56	3.0E-51	AF003528.1	NT	ig04d06.y1 Human Pancreatic Islets Homo sapiens cDNA 5'
377	13595	26619	1.88	2.0E-51	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
706	13889	28921	0.89	2.0E-51	BE391063.1	EST_HUMAN	601285664.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607483 5'
706	13889	28922	0.89	2.0E-51	BE391063.1	EST_HUMAN	601285664.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607483 5'
1723	14873	27865	16.76	2.0E-51	AA233352.1	EST_HUMAN	z30605.r1 Stralagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664880 5' similar
3827	16887	29980	3.05	2.0E-51	AA422416.1	EST_HUMAN	to TR:G232226 G232226 RTV-LH PROTEIN, contains LTR7.12 LTR7 repetitive element ;
4616	17753	30734	1.21	2.0E-51	AW137823.1	EST_HUMAN	U1H-B11-adj4-02-0-U1.s1 NCI CGAP_Sus3 Homo sapiens cDNA clone IMAGE:2718951 3'
6326	18439	31408	0.66	2.0E-51	AB161620.1	EST_HUMAN	h76c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2092622 3' similar to TR:PG3107

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6139	19317	32658	3.54	2.0E-51	BE782015.1	EST_HUMAN	601470446F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5'
7462	20537		0.73	2.0E-51	AF219927.1	NT	Homo sapiens diacylglycerol kinase $\alpha$ (DGK) gene, exon 23
7615	20685	34161	1.29	2.0E-51	7662348	NT	Homo sapiens cell recognition molecule Caspr2 (KIA0689), mRNA
8896	21975	35512	1.61	2.0E-51	EE901994.1	EST_HUMAN	601678787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
8896	21975	35513	1.61	2.0E-51	EE901994.1	EST_HUMAN	601678787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959613 5'
9235	22312	35854	1.03	2.0E-51	11037084	NT	Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA
9712	22777	36347	1.76	2.0E-51	A1917078.1	EST_HUMAN	hs74607.x1 NC1_CGAP_G08 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN
9803	22843	36420	4.86	2.0E-51	BE165880.1	EST_HUMAN	Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR ;
8816	22858	36436	0.69	2.0E-51	AB007926.1	NT	MR3-HT0497-150200-113-g01 HT0487 Homo sapiens cDNA
10848	23682	37283	1.66	2.0E-51	AV682474.1	EST_HUMAN	Homo sapiens mRNA for KIAA0457 protein, partial cds
10690	23723	37329	1.07	2.0E-51	AA378559.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5'
11610	18762	31789	5.82	2.0E-51	AV732851.1	EST_HUMAN	EST181295 Synovial sarcoma Homo sapiens cDNA 5' end
11610	18752	31780	5.82	2.0E-51	AV732851.1	EST_HUMAN	0834709.x5 NC1_CGAP_K05 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
12660	25571	31992	1.62	2.0E-51	11419189	NT	P35436 GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
117	13348	26375	10.94	1.0E-51	4503528	NT	0834709.x5 NC1_CGAP_K05 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
1523	14876		37.16	1.0E-51	AV742248.1	EST_HUMAN	P35436 GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
4918	18048	31039	0.82	1.0E-51	AF111688.2	NT	0834709.x5 NC1_CGAP_K05 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
5505	18704	31720	3.7	1.0E-51	T18862.1	EST_HUMAN	P35436 GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
7827	20882	34384	1.03	1.0E-51	AI572532.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11b)(2)(p15.5)(p11.2)) translocated to, 4
8087	21169	34684	0.51	1.0E-51	BF434359.1	EST_HUMAN	(MLL14), mRNA
12070	26232		1.97	1.0E-51	AV760580.1	EST_HUMAN	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
12610	23409		9.43	9.0E-52	AA777621.1	EST_HUMAN	Homo sapiens translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
156	13391	26412	11.42	8.0E-52	AA720574.1	EST_HUMAN	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1526	14679	27760	2.39	8.0E-52	X84900.1	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1898	14838	27922	2.85	8.0E-52	11669028	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1686	14838	27923	2.65	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4101	14838	27922	6.75	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4101	14838	27923	6.75	8.0E-52	11988028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
7686	20751	34232	0.76	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
7686	20751	34233	0.76	8.0E-52	11416586	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
9216	22293	35836	1.86	7.0E-52	VJ58471.1	EST_HUMAN	z558a06.t1 Scanes_parethyroid_tumor_JhbHPA Homo sapiens cDNA clone IMAGE:326578 5' similar to containe Alu repetitive element
1214	14376		0.63	6.0E-52	EE072409.1	EST_HUMAN	QV8-B10537-271289-049-407 BT0537 Homo sapiens cDNA
1729	14879	27970	7.1	6.0E-62	AF10907.1	NT	Homo sapiens S104 gene, partial cds, PS1 and hypothetical protein genes, complete cds, and S171 gene, partial cds
5845	19035	32341	1.05	6.0E-52	AI208184.1	EST_HUMAN	q944f0.4.x1 Scanes_testis_NHT Homo sapiens cDNA clone IMAGE:1839047 3'
11484	24543	38214	2.36	6.0E-52	BE048172.1	EST_HUMAN	tz46h04.y1 NCI_CGAP_Bms2 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW-IPGBM MOUSE Q06793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE
4362	17700	30882	2.27	6.0E-52	Z78898.1	NT	PROTEOLYCAN CORE PROTEIN PRECURSOR:
8592	22847	36218	0.48	6.0E-52	11437365	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pa18H7
1695	14847	27931	1.66	4.0E-52	AF257318.1	NT	Homo sapiens FSHD region gene 1 (FRG1), mRNA
1829	14977	28072	1.63	4.0E-52	4758843	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
4037	17193	30203	0.77	4.0E-52	4507500	NT	Homo sapiens nucleoporph 155kD (NUP155) mRNA
4862	17895	30980	0.81	4.0E-52	AJ768814.1	EST_HUMAN	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
5401	18603	31574	1.3	4.0E-52	4506132	NT	w88p02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400459 3'
6401	18603	31575	1.3	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
8228	21310	34830	1.19	4.0E-52	BE682032.1	EST_HUMAN	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
8731	21611	35347	5.5	4.0E-52	11417035	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
12429	26304		3.44	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12897	25642		12.70	4.0E-52	AB002059.1	NT	Homo sapiens DNA for Human P2Xv, complete cds
13141	25741		1.3	4.0E-52	AB011399.1	NT	Homo sapiens gene for AF-4, complete cds
4204	17363		11.41	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10975 (FLJ10975), mRNA
576	13768	28780	1.82	2.0E-52	M10976.1	NT	Homo sapiens hypothetical protein FLJ10975 (FLJ10975), mRNA
576	13768	28791	1.82	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2071	15211	28328	1.18	2.0E-52	AB033075.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
							Homo sapiens mRNA for KIAA1249 protein, partial cds



Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2568	15693	28818	1.6	2.0E-52	U6207575.1	EST_HUMAN	b56b07.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gp.X16493 M.musculus mRNA for Zpf-1 zinc finger protein (MOUSE);
2798	15911		11.46	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
5082	18220	31190	3.41	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5126	18251	31216	1.4	2.0E-52	AF141802.1	EST_HUMAN	qa56605.s1 Scores_NhhMFPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
5126	18251	31217	1.4	2.0E-52	AF141802.1	EST_HUMAN	qa56605.s1 Scores_NhhMFPu_S1 Homo sapiens cDNA clone IMAGE:1690784 3'
6821	18011	32317	3.24	2.0E-52	AW648041.1	EST_HUMAN	IL3-CT0214-231289-053.E12 CT0214 Homo sapiens cDNA
6497	19583	33026	1.98	2.0E-52	11141668	NT	Homo sapiens interferon 21 receptor (IL21R), mRNA
6853	20006	33416	0.86	2.0E-52	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7081	20175	33597	0.76	2.0E-52	AF792146.1	EST_HUMAN	os45612.y5 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1608311 5'
7896	21046	34558	0.69	2.0E-52	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
7896	21046	34558	0.69	2.0E-52	5032158	NT	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
8854	21933		8.71	2.0E-52	AF147830.1	NT	Macaca mulatta beta-tubulin mRNA, complete cds
9136	22215	35759	0.96	2.0E-52	AA778765.1	EST_HUMAN	Z45605.s1 Scores_Tetel_liver_spleen_NINF.LS_S1 Homo sapiens cDNA clone IMAGE:453272 3'
9680	22842		1	2.0E-52	4758789	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kd) (NADH-coenzyme Q reductase) (NDUFS5) mRNA
10321	23356	36965	4.6	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10321	23356	36966	4.6	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
11481	24540	38209	3.14	2.0E-52	AB81462.1	EST_HUMAN	w49604.x1 NCI_CGAP_Lut19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2
11481	24540	38210	3.14	2.0E-52	AB81462.1	EST_HUMAN	THR repetitive element :
11491	24550	38225	2.52	2.0E-52	AV715377.1	EST_HUMAN	AV715377 D08 Homo sapiens cDNA clone DGBAEG3 5'
11634	24714		1.46	2.0E-52	W70280.1	EST_HUMAN	zdd49612.1 Scores_Tetel_liver_Nbh-H19W Homo sapiens cDNA clone IMAGE:344038 5'
11918	24904		3.25	2.0E-52	11417980	NT	Homo sapiens LIM domain kinase 2 (LIMK2), mRNA
12234	26194	31541	5.9	2.0E-52	AW236297.1	EST_HUMAN	znt72607.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu
12658	26437		5.72	2.0E-52	AB088935.1	EST_HUMAN	repetitive element, contains element LTR2 repetitive element :
546	13739	28784	1.89	1.0E-52	AA634445.1	EST_HUMAN	wf67d05.x1 Scores_NINF_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360849 3' similar to TR.Q16855
1402	14656	27630	18.76	1.0E-52	4504028	NT	Q16859 CARBOXYL ESTERASE :
2600	15724		1.89	1.0E-52	4502238	NT	znu5112.s1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'
3126	16302	29316	2.6	1.0E-52	SB1070.1	NT	Homo sapiens glutamate-aminomethylase (glutamate synthase) (GLUL) mRNA
							Homo sapiens erythritolase D (ARSD), transcript variant 1, mRNA
							pol=reverse transcriptase homology (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 680 nt]

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5448	18548	31828	4.43	1.0E-52	M29428.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
6523	19588	33062	2.33	1.0E-52	U38684.1	NT	Human PMS2 related (PMSR2) gene, complete cds
7388	20859	34135	2.07	1.0E-52	X07282.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
8014	21084	34576	0.59	1.0E-52	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
8660	21740		1.18	1.0E-52	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
9390	22465	38029	0.77	1.0E-52	AF018779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10804	23837		0.88	1.0E-52	AF020370.1	EST_HUMAN	d108g05.v1 Mordon Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483145 5'
10814	23847		1.06	1.0E-52	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11004	24083	37720	2.12	1.0E-52	U48286.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (PTPCAAX1) mRNA, complete cds
11076	24150		1.72	1.0E-52	U42692.1	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA
12135	25115	38919	1.31	1.0E-52	U421401	NT	Homo sapiens 5'-3' exonuclease 2 (XRN2), mRNA
12135	25115	38920	1.31	1.0E-52	U421401	NT	Homo sapiens 5'-3' exonuclease 2 (XRN2), mRNA
3881	17050	30049	0.69	8.0E-53	U421401	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
4511	17650	30638	3.3	8.0E-53	AF001448.1	NT	Homo sapiens core binding factor alpha1 subunit (CBFA1) gene, exon 3
12480	25332		6.85	7.0E-53	BF238465.1	EST_HUMAN	801904771F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132793 5'
12858	26046		7.06	7.0E-53	U421782.1	EST_HUMAN	tt4407.x1 NCI_CGAP_Bim23 Homo sapiens cDNA clone IMAGE:2088077 3' similar to contains THR11
4214	17363	30351	4.46	5.0E-53	U4768543	NT	THR repetitive element
5283	18411	31377	0.82	5.0E-53	AL163282.2	NT	Homo sapiens heterotrimeric nuclear ribonucleoprotein C (C11C2) (HNRPC) mRNA
12528	25360		1.83	5.0E-53	AW813563.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
50	13289	26301	2.07	4.0E-53	AL163285.2	NT	RC3-ST0197-151088-011-g10 ST0197 Homo sapiens cDNA
50	13289	26302	2.07	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
9816	22671		0.67	4.0E-53	AF013037.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
9816	22671		0.67	4.0E-53	AF013037.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C085
9958	22887		0.84	4.0E-53	F13080.1	EST_HUMAN	HSC3D041 normalized infant brain cDNA Homo sapiens cDNA clone c-310d4
11459	24548	38221	2.99	4.0E-53	BF128701.1	EST_HUMAN	HSC3D041 normalized infant brain cDNA Homo sapiens cDNA clone c-310d4
11459	24548	38222	2.89	4.0E-53	BF128701.1	EST_HUMAN	601810989F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
2726	16844	28955	2.34	3.0E-53	AB028898.1	NT	601810989F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
3826	16985	29989	1.18	3.0E-53	AW060836.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCT4 gene region, position 1/2 (DLEC1, ORCT3, ORCT4 genes, complete cds)
4713	17848	30831	0.75	3.0E-53	AW803563.1	EST_HUMAN	W222607.x1 Soares Dieckgreffe_cclan_NHCD Homo sapiens cDNA clone IMAGE:2558796 3'
5541	18738	31755	0.97	3.0E-53	AF001212.1	NT	IL2.UA0081-240300-055-D03 UA0081 Homo sapiens cDNA
5743	18938	32238	1.01	3.0E-53	U1528287	NT	Homo sapiens 26S proteasome subunit 8 mRNA, complete cds
6323	19495	32851	1.46	3.0E-53	BE180025.1	EST_HUMAN	Homo sapiens MLL1 protein (MLL1), mRNA
							GV1-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7247	20330	33776	0.76	3.0E-63	Y10388.3	NT	H. sapiens gird gene
7247	20330	33777	0.76	3.0E-63	Y10388.3	NT	H. sapiens gird gene
8469	21690	36118	10.87	3.0E-63	S72043.1	NT	GIF=growth inhibitory factor [human, brain, Genomic, 2015 nt]
8060	22139	35683	0.85	3.0E-63	10835090	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
9257	22334		8.77	3.0E-63	5901833	NT	Homo sapiens FGF1 oncogene partner (FOP), mRNA
12361	25259		1.18	3.0E-63	11428423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
470	13665		11.25	2.0E-63	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 6' end
2066	16209	28325	3.29	2.0E-63	7705394	NT	Homo sapiens hyaluronic acid receptor (HAR), mRNA
2404	15535	28662	6.26	2.0E-63	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2601	15725		12.68	2.0E-63	4502319	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31KD; Vacuolar protein-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA
3290	16464	28483	0.78	2.0E-63	7705687	NT	Homo sapiens leucine aminopeptidase (LOC51056), mRNA
3317	16460	28508	1.28	2.0E-63	AF083822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
4170	17320	30313	2.59	2.0E-63	M61879.1	NT	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds
5542	18739	31756	2.46	2.0E-63	BF334740.1	EST_HUMAN	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA
5542	18739	31757	2.46	2.0E-63	BF334740.1	EST_HUMAN	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA
8055	21138	34658	1.01	2.0E-63	AW875598.1	EST_HUMAN	EST138707 MAGE resequenced, MAGN Homo sapiens cDNA
8196	21278		0.48	2.0E-63	AA095852.1	EST_HUMAN	IS429.seq, F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9609	22663		3.47	2.0E-63	AW245678.1	EST_HUMAN	2822665, Splice NIH, MGC, J Homo sapiens cDNA clone IMAGE:3231627 3' similar to TR:Q04009 Q04009
10862	23895	37317	0.69	2.0E-63	BE550195.1	EST_HUMAN	750b02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231627 3' similar to TR:Q04009 Q04009
1477	14630	27715	2.2	1.0E-63	AL271738.1	NT	MYOSIN HEAVY CHAIN.1
3496	16663	28875	2.89	1.0E-63	AB026898.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
5078	16206	31178	1.06	1.0E-63	BE296386.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
6831	18984	33982	1.5	1.0E-63	BE364201.1	EST_HUMAN	601176725F1 NIH, MGC, 17 Homo sapiens cDNA clone IMAGE:3531919 5'
7997	20475	33942	0.87	1.0E-63	BE012071.1	EST_HUMAN	CMA4-NIN1029-160800-543-402 NIN1029 Homo sapiens cDNA
8120	21202	34723	0.6	1.0E-63	AA248072.1	EST_HUMAN	RC6-BN1058-270400-031-DO1 BN1058 Homo sapiens cDNA
9290	22366	35915	4.73	1.0E-63	X79538.1	NT	18571.seq, F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
12228	25176	38345	1.47	1.0E-63	AW245422.1	EST_HUMAN	H. sapiens mRNA for hnRNPC protein A1
3324	16497	29516	0.61	9.0E-64	4504116	NT	2822843 Splice NIH, MGC, 7 Homo sapiens cDNA clone IMAGE:2822843 5'
6417	25803	31593	5.86	9.0E-64	4506786	NT	2822843 Splice NIH, MGC, 7 Homo sapiens cDNA clone IMAGE:2822843 5'
212	13435	28465	1.29	8.0E-64	BE366785.1	EST_HUMAN	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1882	15026	28133	2.08	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
6057	18239	32564	23.39	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABCA1), member 8 (ABCA8), mRNA
395	13632	26669	1.35	7.0E-54	AA812537.1	EST_HUMAN	af79c12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MERR30.13 MERR30 repetitive element;
1877	15021	28128	2.23	7.0E-54	Y10546.1	NT	Homo sapiens mRNA for monocyte chemoattractant protein-2
2278	15410	28541	7.63	7.0E-54	N27177.1	EST_HUMAN	yw68d12.s1 Soares_placenta_8169weeks_2NbhP8169V Homo sapiens cDNA clone IMAGE:257389 3' similar to contains LTR7.b3 LTR7 repetitive element;
10333	23368	38978	2.1	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
11365	24428	38081	1.4	7.0E-54	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11365	24426	38082	1.4	7.0E-54	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11570	24625		3.42	7.0E-54	A1160189.1	EST_HUMAN	qb07603.x1 Soares_fetal_heart_NbhH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR11 OFR repetitive element;
25	13263	26265	0.84	6.0E-54	AB003618.1	NT	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
386	13633	28670	0.77	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
396	13633	28671	0.77	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
3365	16527	29542	0.72	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
4111	17285	30265	22.75	6.0E-54	4502872	NT	Homo sapiens chloride channel 6 (CLCN6) mRNA
4584	17721	30704	1.09	6.0E-54	AV754748.1	EST_HUMAN	AV754746 TP Homo sapiens cDNA clone TPGAAC10 5'
4868	18097	31073	2.15	6.0E-54	4605806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4868	18125		2.04	6.0E-54	X09849.1	NT	H. sapiens shc pseudogene, p58 isoform
6116	18125		3.31	6.0E-54	X09849.1	NT	H. sapiens shc pseudogene, p58 isoform
11741	23927	37552	1.52	6.0E-54	AW813587.1	EST_HUMAN	RC3-STO187-151099-011-08 STO187 Homo sapiens cDNA
2218	16362	28483	1.94	5.0E-54	P51623	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
187	13408		56.19	4.0E-54	AF110103.1	NT	Tupala bengalensis beta-actin mRNA, partial cds
678	14151	27211	14.58	4.0E-54	AA306784.1	EST_HUMAN	EST177698 Jurkat T cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
1848	14894	28096	3.26	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1848	14894	28097	3.26	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3274	16448		1.85	4.0E-54	A1935088.1	EST_HUMAN	wdd28d11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:002711
86	13331	26358	8.12	3.0E-54	AA313487.1	EST_HUMAN	002711 PRO-POL-DUTPASE POLYPROTEIN.
1604	14767		0.86	3.0E-54	AW615742.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
2836	15758	28872	1.18	3.0E-54	AL110383.1	EST_HUMAN	hdb7g08.x1 NCJ CGAP_G08 Homo sapiens cDNA clone IMAGE:2916542 3'
							DKFZp434E0731.1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434E0731 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6024	19207	32527	1.36	3.0E-54	4502434	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA
7548	20620	34098	1.34	3.0E-54	AA844081.1	EST_HUMAN	AB2208.st Soares, parathyroid tumor, NblHPA Homo sapiens cDNA clone IMAGE:1388270.3
7948	20620	34097	1.34	3.0E-54	AA844081.1	EST_HUMAN	AB2208.st Soares, parathyroid tumor, NblHPA Homo sapiens cDNA clone IMAGE:1388270.3
11277	24344		1.77	3.0E-54	11434806	NT	Homo sapiens golgi autubantigen, golgin subfamily a, 5 (GOLGA5) mRNA
11341	24404	38053	4.01	3.0E-54	BF348600.1	EST_HUMAN	602019408F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4155121.5
11650	24728	38421	2.88	3.0E-54	AA393362.1	EST_HUMAN	z7012.r1 Soares, testis, JNH1 Homo sapiens cDNA clone IMAGE:27727.5 similar to TR:G191315
12336	25243	32110	1.32	3.0E-54	AW954559.1	EST_HUMAN	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
12378	26149		3.16	3.0E-54	AW748965.1	EST_HUMAN	EST366629 IMAGE resequences, MAGC Homo sapiens cDNA
659	13845	28871	17.87	2.0E-54	5031900	NT	RC1-BT0313-131199-011-b09 BT0313 Homo sapiens cDNA
1396	14550	27625	1.54	2.0E-54	4507184	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRLG1) mRNA
2604	15727	28846	1.25	2.0E-54	AW163175.1	EST_HUMAN	4492803.yt Schneider, fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783784.5 similar to SW:CU1_HUMAN Q13616 CULLIN HOMOLOG 1. ;
2665	15787	28903	2.25	2.0E-54	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2860	16137	29155	1.95	2.0E-54	AW057524.1	EST_HUMAN	wy60b12.x1 Soares, NSF, F8, GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927.3 similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
3392	16662	29577	0.9	2.0E-54	AL278314.1	NT	Homo sapiens mRNA for phospholipase C-beta-1b (PLCB1 gene)
3638	16802		6.1	2.0E-54	AA632825.1	EST_HUMAN	RI45609.at NCI_CGAP_P19 Homo sapiens cDNA clone IMAGE:995488 similar to gb:K53777.605
4321	17464		1.74	2.0E-54	4502842	NT	RIBOSOMAL PROTEIN L23 (HUMAN);
4563	17701		7.1	2.0E-54	AF208161.1	NT	Homo sapiens chaperonin containing T-complex subunit 9 (CCT9) mRNA
5591	18786	31833	2.65	2.0E-54	4769069	NT	Homo sapiens syncytin precursor, mRNA, complete cds
5720	18913	32209	1.21	2.0E-54	BE047864.1	EST_HUMAN	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
5882	19071	32378	3.99	2.0E-54	11423657	NT	tz43c11.yt NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2281348.5
5982	19167	32487	11.29	2.0E-54	AB046811.1	NT	Homo sapiens KIAA0100 gene product (KIAA0100) mRNA
5982	19167	32488	11.29	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1691 protein, partial cds
6786	19951	33351	1.63	2.0E-54	AF008915.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6950	20263	33701	0.68	2.0E-54	AB023212.1	NT	Homo sapiens EVIS homolog mRNA, complete cds
6950	20263	33702	0.68	2.0E-54	AB023212.1	NT	Homo sapiens mRNA for KIAA0955 protein, partial cds
7273	20356	33810	8.33	2.0E-54	11426544	NT	Homo sapiens mRNA for KIAA0955 protein, partial cds
8828	22869	39451	3.98	2.0E-54	AB001025.1	NT	Homo sapiens neurofilament 1 (neurofilamentosis, von Recklinghausen disease, Watson disease) (NF-1), mRNA
10213	23249	38638	1.14	2.0E-54	11429127	NT	Homo sapiens mRNA for brain tyrosine receptor, complete cds
10328	23381	38971	0.76	2.0E-54	11418762	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2) mRNA
							Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10326	23361	36972	0.76	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
10841	23874	37484	0.48	2.0E-54	AB007631.1	NT	Homo sapiens mRNA for KIAA0492 protein, partial cds
11275	19931	33331	1.40	2.0E-54	AF008945.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
12027	25011		1.72	2.0E-54	7657454	NT	Homo sapiens pascallio (zabrafish) homolog 1, containing BRCT domain (PEST), mRNA
12893	25591	31970	4.38	2.0E-54	8567387	NT	Homo sapiens percid (Drosophila) homolog 3 (PER3), mRNA
4587	17724		1.55	1.0E-54	BF316418.1	EST_HUMAN	601899230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
8927	22008	35545	0.5	1.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA
10459	23494	37105	0.52	1.0E-54	AA412409.1	EST_HUMAN	2410609.t1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:731484 5'
10459	23494	37106	0.52	1.0E-54	AA412409.1	EST_HUMAN	2410609.t1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:731484 5'
13086	25709		2.33	1.0E-54	AL077341.1	EST_HUMAN	AU077341 Sugeno cDNA library Homo sapiens cDNA clone Zm6C880 similar to 5'-end region of Human gamma-glutamyl transpeptidase mRNA, 5' end
10568	23603	37208	1.02	9.0E-56	BE081469.1	EST_HUMAN	QVZ-BT0535-160400-143-112 BT0535 Homo sapiens cDNA
1344	14300		1.59	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1348	14503		2.77	8.0E-56	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
11471	24530		1.83	8.0E-55	AV408714.1	EST_HUMAN	fn02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860907 6'
8004	22083		0.48	7.0E-55	AV103839.1	EST_HUMAN	xd76c02.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:2803522 3' similar to TR:O60365
9383	22456	36021	1.28	7.0E-55	AA89581.1	EST_HUMAN	O60365 FOS39554_1..
9416	22490	35055	1.71	7.0E-55	AU139909.1	EST_HUMAN	ak28a1.s1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:1407260 3'
11485	24544	38215	8.08	7.0E-55	AI561036.1	EST_HUMAN	AU139909 PLAGE1 Homo sapiens cDNA clone PLAGE1011576 5'
11485	24544	38216	8.08	7.0E-55	AI561036.1	EST_HUMAN	iq28f09.x1 NCI_CGAP_Ut Homo sapiens cDNA clone IMAGE:2210249 3'
12726	25911	31860	1.18	7.0E-55	BE670808.1	EST_HUMAN	iq28f09.x1 NCI_CGAP_Ut Homo sapiens cDNA clone IMAGE:2210249 3'
13050	26063		6.37	7.0E-55	H23398.1	EST_HUMAN	7637c01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284640 3'
11804	24794	38492	1.86	6.0E-55	AB040334.1	NT	ym57g07.t1 Soares, infant brain T1NB Homo sapiens cDNA clone IMAGE:52444 5'
1810	14859	28051	1.21	5.0E-55	AA704971.1	EST_HUMAN	Homo sapiens mRNA for KIAA1501 protein, partial cds
1810	14859	28052	1.21	5.0E-55	AA704971.1	EST_HUMAN	z95b09.s1 Soares, fetal liver, spleen, T1NFS, S1 Homo sapiens cDNA clone IMAGE:462617 3'
4994	18024	31010	1.51	5.0E-55	AW208021.1	EST_HUMAN	z95b09.s1 Soares, fetal liver, spleen, T1NFS, S1 Homo sapiens cDNA clone IMAGE:462617 3'
6870	19829	33217	1.49	5.0E-55	4502240	NT	UHH-BT-efp-g-09-0-U.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723536 3'
6805	25833	33360	1.08	5.0E-55	4505952	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
6805	25833	33361	1.08	5.0E-55	4505952	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
7182	20314	33767	1.03	5.0E-55	7382477	NT	Homo sapiens paraoxonase 2 (PON2) mRNA, and translated products
7446	20523	33986	0.72	6.0E-55	11434422	NT	Homo sapiens paraoxonase 2 (PON2) mRNA, and translated products
							Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 5, mRNA
							Homo sapiens speckle-type POZ protein (SPOP), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9244	22321	36865	2.3	5.0E-55	4508302	NT	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA
9520	22585		0.91	5.0E-55	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
10243	23278	36872	1.53	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
10243	23278	36873	1.53	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
10427	23462	37069	1.33	5.0E-55	5453765	NT	Homo sapiens mel (chicken) like 2 (NELL2) mRNA
11502	24560	38236	1.3	5.0E-55	11421649	NT	Homo sapiens SKAP55 homologue (SKAP-HOM), mRNA
11502	24560	38237	1.3	5.0E-55	11421649	NT	Homo sapiens SKAP55 homologue (SKAP-HOM), mRNA
12421	26238		1.73	5.0E-55	11417872	NT	Homo sapiens pascualillo (zabralish) homology 1, containing BRCT domain (PES1), mRNA
56	16004	26310	2.24	4.0E-55	AW817894.1	EST_HUMAN	EST370064 IMAGE reserquence, MAGE Homo sapiens cDNA
688	13873	26906	3.217	4.0E-55	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1472	14626	27710	2.15	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (OS3786), mRNA
1472	14626	27711	2.16	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (OS3786), mRNA
1544	14696		1.72	4.0E-55	BF061411.1	EST_HUMAN	752b10X1 Soares_NSF_F8_9W_OT_PA_P_31 Homo sapiens cDNA clone IMAGE:3380043 3 similar to contains L1.3 L1 repetitive element
2081	15221	28341	2.18	4.0E-55	4306180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2081	15221	28342	2.18	4.0E-55	4306180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2151	15287	28412	8.36	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (DGKD) (DGKG) mRNA
2151	15287	28413	8.36	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (DGKD) (DGKG) mRNA
2384	15515	28444	3.02	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
8539	21620		0.85	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11605	24563		2.31	4.0E-55	W28189.1	EST_HUMAN	43c6 Human retina cDNA randomly primed sublibrary/Homo sapiens cDNA
12937	25244		1.82	4.0E-55	BF30394.1	EST_HUMAN	601886575F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
6731	19867	33278	0.66	3.0E-55	AA077166.1	EST_HUMAN	7809409 Chromosome 7 Fetal Brain cDNA Library/Homo sapiens cDNA clone 7809409
12273	25205		4.18	3.0E-55	BE178519.1	EST_HUMAN	PM1-HT0603-090300-001-g08 HT0603 Homo sapiens cDNA
13103	25719		3.53	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
388	13594	26630	1.69	2.0E-55	X67147.1	NT	Human endogenous retrovirus PHE-1 (ERV9)
666	13757		1.08	2.0E-55	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete proviral segment
666	13852	26880	3.68	2.0E-55	4507286	NT	Homo sapiens synapsin-binding protein 1 (SYBP1) mRNA, and translated products
3023	16199	29222	0.69	2.0E-55	4507286	NT	Homo sapiens ubiquitin protein ligase E3A (human Papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4897	13027	31014	3.51	2.0E-55	BE719898.1	EST_HUMAN	CM1-HT0876-150800-357-g03 HT0876 Homo sapiens cDNA
7673	25851	34217	0.85	2.0E-55	AW501988.1	EST_HUMAN	UH-F-BNO-aka-f-06-0-ULT NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078275 5'
8265	22342	35892	0.48	2.0E-55	BF224452.1	EST_HUMAN	h77608x1 NC1 CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3134463 3'
8265	22342	35893	0.48	2.0E-55	BF224452.1	EST_HUMAN	h77608x1 NC1 CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3134463 3'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8361	22436		4.33	2.0E-55	AI002836.1	EST_HUMAN	am8b105.s1 Striatogene scitzo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains
9442	22319		0.67	2.0E-55	BE007959.1	EST_HUMAN	THR.b2 THR repetitive element :
11182	24231	37897	2.35	2.0E-55	AU118344.1	EST_HUMAN	OV04BN0147-280400-213-qc6 BN0147 Homo sapiens cDNA
13177	16189	28222	1.34	2.0E-55	4507798	NT	AUT18344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
89	13334	28381	1.82	1.0E-55	4505060	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBES3A) mRNA
194	13417	28448	40.5	1.0E-55	U09823.1	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
688	13779	28798	1.38	1.0E-55	AI026718.1	EST_HUMAN	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Pabp1a2) mRNA, complete cds
1173	14336	27392	3.92	1.0E-55	AB020710.1	NT	ov85908.x1 Scarsa testis_NHT Homo sapiens cDNA clone IMAGE:1644160 3'
2008	16146	28251	2.33	1.0E-55	BE277861.1	EST_HUMAN	Human sapiens mRNA for KIAA0903 protein, partial cds
2006	16146	28252	2.33	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2987027 5'
2401	14532		4.65	1.0E-55	5603174	NT	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2987027 5'
2415	15697	28673	1.44	1.0E-55	AF000890.1	NT	Homo sapiens SMA3 (SMA3), mRNA
2586	15711	28829	18.88	1.0E-55	X13111.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
2620	15743	28857	5.51	1.0E-55	AB007686.2	NT	Human sapiens testis-specific Testis Transcript Y 1 (TTY1) molecule (major histocompatibility complex)
2620	16743	28858	5.51	1.0E-55	AB007686.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
2677	15787	28914	3.37	1.0E-55	LS4057.1	NT	Homo sapiens CLP mRNA, partial cds
2830	15984	29073	1.22	1.0E-55	AB033046.1	NT	Homo sapiens mRNA for KIAA1219 protein, partial cds
3485	16862	29874	1.16	1.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary/Homo sapiens cDNA
4097	17262	30253	4.28	1.0E-55	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4409	17551	30596	1.1	1.0E-55	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
4853	17886		0.94	1.0E-55	N72801.1	EST_HUMAN	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
4849	18079	31054	1.15	1.0E-55	AB037633.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
4949	18079	31055	1.15	1.0E-55	AB037633.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
5614	18808	31876	0.65	1.0E-55	AF119358.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
8401	18670	32832	7.26	1.0E-55	11433046	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
8401	18670	32833	7.26	1.0E-55	11433046	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
8178	21260	34782	1.7	1.0E-55	11432894	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
8178	21260	34783	1.7	1.0E-55	11432894	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
8268	21348	34883	0.49	1.0E-55	11421649	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
8273	21365	34872	0.83	1.0E-55	AF224492.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
8273	21365	34873	0.83	1.0E-55	AF224492.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds



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11152	24223	37851	2.41	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11152	24223	37852	2.41	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11733	23919	37544	1.88	1.0E-55	U50950.1	NT	Human infant brain unknown product mRNA, complete cds
11755	23941	37567	1.34	1.0E-55	T10045.1	EST_HUMAN	seq 676 b4HB3MA Co8-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-Ft61 5' similar to similar to Chinese Hamster DHFR-complified protein mRNA
11789	24779	38476	2.67	1.0E-55	8922743	NT	Homo sapiens hypothetical protein FLJ10891 (FLJ10891) mRNA
11876	24854	38560	1.78	1.0E-55	10567821	NT	Homo sapiens DNA-binding protein (LOC66242) mRNA
7522	20556	34070	1.85	9.0E-56	BE379074.1	EST_HUMAN	60123702F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609552 5'
11545	24501	38277	1.34	8.0E-56	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C009
2793	15909	29017	7.08	7.0E-56	H19934.1	EST_HUMAN	Yn62g03.r1 Soares adult brain N25HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains Yn62g03.r1
7818	20873	34371	1.83	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-407 CT0252 Homo sapiens cDNA
7818	20873	34372	1.83	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231099-013-407 CT0252 Homo sapiens cDNA
1727	14877	27868	2.7	5.0E-56	AW897742.1	EST_HUMAN	RC3-BN0053-170200-011-101 BN0053 Homo sapiens cDNA
8362	22437	35995	0.71	5.0E-56	AW015507.1	EST_HUMAN	UH-B10P-asu-a-05-0-UI-61 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2710544 3'
10589	23634		1.35	5.0E-56	W28188.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12513	28137	31860	2.47	5.0E-56	HS5099.1	EST_HUMAN	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_56 5'
28	13266	26268	8.64	4.0E-56	AF141340.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
28	13266	26269	8.64	4.0E-56	AF141340.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2773	15888	28998	3.61	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2773	15888	28998	3.61	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2873	13732	26796	9.22	4.0E-56	AF003526.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
6387	19596	32915	4.94	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
6387	19596	32916	4.94	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
10724	23767	37364	1.68	4.0E-56	AF043346.1	NT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
11163	24234	37863	7.73	4.0E-56	AI498069.1	EST_HUMAN	hne6g12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2763048 3'
11163	24234	37864	7.73	4.0E-56	AI498069.1	EST_HUMAN	hne6g12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2763048 3'
1372	14527	27601	2.69	3.0E-56	8924029	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304) mRNA
1804	14953	28047	1.84	3.0E-56	6912743	NT	Homo sapiens 5'-3' exonuclease 2 (XRN2) mRNA
2217	15351	28482	1.6	3.0E-56	6912697	NT	Homo sapiens oncogene TCC1 (TCC1) mRNA
3185	16370	29376	1.67	3.0E-56	AA329826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3185	16370	29377	1.67	3.0E-56	AA329826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3939	17098		2.81	3.0E-56	AF050066.1	NT	Homo sapiens MHC class I region

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4507	17648	30634	0.87	3.0E-56	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
4544	17682	30894	4.42	3.0E-56	AL163263.2	NT	Homo sapiens chromosome 21 segment HS21C08
4695	17830	30816	2.4	3.0E-50	3902035	NT	Homo sapiens superkiller viralidic activity 2 (S. carvatisa homodog)-like (SKIV2L), mRNA
5801	18991	32283	1.5	3.0E-56	4759163	NT	Homo sapiens speractonecillin, cncv and kezal-like domains proteoglycan (testican) (SPOCK), mRNA
6801	18991	32294	1.5	3.0E-56	4759163	NT	Homo sapiens speractonecillin, cncv and kezal-like domains proteoglycan (testican) (SPOCK), mRNA
7014	20160	33571	5.5	3.0E-59	11421124	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
7476	20551	34023	2.07	3.0E-59	4504970	NT	Homo sapiens LIM binding domain 2 (LDB2), mRNA
7476	20661	34024	2.07	3.0E-59	4504970	NT	Homo sapiens LIM binding domain 2 (LDB2), mRNA
8016	22095	35635	8.11	3.0E-56	11415704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
10018	23035	36852	0.9	3.0E-56	DB3476.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10698	23731	37336	1.39	3.0E-56	11434956	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10880	24059	37693	2.62	3.0E-56	AB042550.1	NT	Homo sapiens mRNA, similar to ret myomegalin, complete cds
11594	24647	38330	4.84	3.0E-56	5802013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11594	24647	38331	4.84	3.0E-56	5802013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
12377	25268	32075	1.62	3.0E-56	11434976	NT	Homo sapiens caveolin 3 (CAV3), mRNA
12377	25268	32076	1.62	3.0E-56	11434976	NT	Homo sapiens caveolin 3 (CAV3), mRNA
537	13730		11.85	2.0E-56	AA169818.1	EST_HUMAN	zgc62a08.s1 Stratiogene neuroepithelium (hs637231) Homo sapiens cDNA clone IMAGE:545208 3'
761	16021	26975	1.18	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
761	16021	26976	1.18	2.0E-56	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
3053	16229	28249	0.84	2.0E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3391	16561		0.84	2.0E-56	AB000891.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3624	16788	28905	1.26	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCG10 5'
7239	20323	33787	1.39	2.0E-56	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR), mRNA
1003	14174		3.01	1.0E-56	AF190390.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1), mRNA, complete cds
3765	18826	29928	1.84	1.0E-56	AW589833.1	EST_HUMAN	h923611.x1 NCI CGAP_G06 Homo sapiens cDNA clone IMAGE:2946452 3'
3765	18826	29929	1.84	1.0E-56	AW589833.1	EST_HUMAN	h923611.x1 NCI CGAP_G06 Homo sapiens cDNA clone IMAGE:2946452 3'
5145	18268	31238	1.42	1.0E-56	AB05162.1	EST_HUMAN	OV-BT077-130199-079 BT077 Homo sapiens cDNA
10161	23198		0.68	1.0E-56	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
10264	23289	36886	1.52	1.0E-56	AV84931.1	EST_HUMAN	RC2-CT0163-220999-001-E02 CT0163 Homo sapiens cDNA
642	13927		1.39	8.0E-57	AW88036.1	EST_HUMAN	QV0-OT0033-070300-152-h03 OT0033 Homo sapiens cDNA
11494	24552	38227	1.72	8.0E-57	AF28497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11494	24552	38228	1.72	8.0E-57	AF28497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11811	24801	38500	2.2	8.0E-57	AB020881.1	NT	Homo sapiens mRNA for cyclin B2, complete cds
14	13262	26262	1.02	8.0E-57	U82334.9	NT	Homo sapiens hypothetical protein FLJ20371, mRNA
308	13524	28556	2.93	8.0E-57	AW816405.1	EST_HUMAN	GV4S10234-181189-037-005 ST0234 Homo sapiens cDNA
907	14082	27147	7.48	8.0E-57	AW264639.1	EST_HUMAN	XP05410.x1 NC1_CGAP_Bms3 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gp.U05875
1859	16006	28112	1.45	8.0E-57	AA489109.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
5355	26034	31879	1.92	8.0E-57	11418185	NT	z51b12.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:757151 5'
6528	19683	33086	0.81	8.0E-57	AB020705.1	NT	Homo sapiens acetylase 2, mitochondrial (ACO2), mRNA
6593	19763	33139	12.82	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0898 protein, partial cds
6593	19763	33139	12.82	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0950 protein, partial cds
7607	20877	34192	0.62	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
7627	20877	34488	1.54	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
7627	20877	34487	1.54	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
11768	13262	28262	3.51	8.0E-57	U82334.9	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
12041	25022	38726	1.74	8.0E-57	11433356	NT	Homo sapiens Rps suppressor protein 1 (RSPU1), mRNA
12102	25022	38789	1.53	8.0E-57	11433356	NT	Homo sapiens Rps suppressor protein 1 (RSPU1), mRNA
12781	25528	32007	1.67	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
12808	25528	32007	1.94	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1246	14405	27487	0.88	7.0E-57	AL003103.1	NT	Homo sapiens GYS2 gene, exon 14
2698	15817	28932	0.97	7.0E-57	U7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2698	15817	28933	0.97	7.0E-57	U7657592	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
3344	16517	28532	0.81	7.0E-57	U605879	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3882	17139	30143	3.14	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
3982	17139	30144	3.14	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
13185	26071		3.99	6.0E-57	AL271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 112
3849	17009	30010	8.03	4.0E-57	AB026858.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
827	14005	27062	0.64	3.0E-57	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1362	14516		12.47	3.0E-57	AA230279.1	EST_HUMAN	nc1307.s1 NC1_CGAP_P11 Homo sapiens cDNA clone IMAGE:1008037 similar to SW_FRS10_HUMAN
2484	15591	28716	1.12	3.0E-57	AA34635.1	EST_HUMAN	P46783.405 RIBOSOMAL PROTEIN S10.1
2768	15883	28992	1.03	3.0E-57	BE076622.1	EST_HUMAN	EST54770 Hippocampus II Homo sapiens cDNA 5' and 783b10.x1 NC1_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:3286443 3' similar to WPIY479C.2

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2768	15883	28993	1.03	3.0E-57	BE076622.1	EST_HUMAN	7/33b10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP.Y477HC.2
3652	16816	28827	1	3.0E-57	AF232703.1	NT	CE20263:
3788	16948		51.29	3.0E-57	AW853984.1	EST_HUMAN	Homo sapiens cell-line tsA201a chloride ion current inducer protein II (Cln) gene, complete cds
6153	19328	32075	1.28	3.0E-57	U1225608	NT	RC3-CT0254-110300-027-410 CT0264 Homo sapiens cDNA
6251	18425	32771	3.25	3.0E-57	BE798637.1	EST_HUMAN	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
8338	21418	34945	3.82	3.0E-57	W28130.1	EST_HUMAN	60158898F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
8363	21444	34866	1.88	3.0E-57	U1545798	NT	42/8 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8363	21444	34866	1.88	3.0E-57	U1545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8476	21557	35080	0.78	3.0E-57	U1427757	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8624	21704	35240	0.62	3.0E-57	J05262.1	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
8624	21704	35240	0.62	3.0E-57	J05262.1	NT	Human farnesyl pyrophosphatase synthetase mRNA, complete cds
9069	22138	35882	5.14	3.0E-57	AU117659.1	EST_HUMAN	AV117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
9451	22667	36132	0.89	3.0E-57	U1545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
9451	22667	36132	0.89	3.0E-57	U1545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
11148	24220	37847	2.34	3.0E-57	AW248374.1	EST_HUMAN	2820473.5prtmc NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
12384	28167	31554	6.37	3.0E-57	W23871.1	EST_HUMAN	ZK5611.1 Soares fetal lung NBHL19W Homo sapiens cDNA clone IMAGE:306549 5'
12882	25640	31994	1.17	3.0E-57	AJ003649.1	EST_HUMAN	AJ003649 Selected chromosome 21 cDNA library Homo sapiens cDNA clone MPI10-1L1
1630	14683	27783	2.89	2.0E-57	AF246213.1	NT	Homo sapiens SNARE protein kinase SNK mRNA, complete cds
1630	14683	27783	2.89	2.0E-57	AF246213.1	NT	Homo sapiens SNARE protein kinase SNK mRNA, complete cds
2780	15906	28014	5.5	2.0E-57	AA845419.1	EST_HUMAN	AK02802.5 Soares Derahyroid tumor NBHFA Homo sapiens cDNA clone IMAGE:1404747 3' similar to
3525	16890		1.4	2.0E-57	AL183204.2	NT	contains Alu repetitive element; contains element MER22 repetitive element:
3641	18805	28818	0.72	2.0E-57	R07702.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
3641	18805	28818	0.72	2.0E-57	R07702.1	EST_HUMAN	Y68b101.1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:125809 5'
4304	17447	30433	0.71	2.0E-57	AA018299.1	EST_HUMAN	Y68b101.1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:125809 5'
4304	17447	30433	0.71	2.0E-57	AA018299.1	EST_HUMAN	Z640C06.1 Soares retina NZB4HR Homo sapiens cDNA clone IMAGE:361450 5'
4304	17447	30433	0.71	2.0E-57	AA018299.1	EST_HUMAN	Z640C06.1 Soares retina NZB4HR Homo sapiens cDNA clone IMAGE:361450 5'
4832	17768	30749	7.42	2.0E-57	AF32831.2	NT	Z640C06.1 Soares retina NZB4HR Homo sapiens cDNA clone IMAGE:361450 5'
6786	18977		1.48	2.0E-57	AA016131.1	EST_HUMAN	Z681C05.1 Soares retina NZB4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1
6158	19334		31.41	2.0E-57	BF116263.1	EST_HUMAN	repetitive element:
6288	19461	32813	6.34	2.0E-57	U1431281	NT	7/8604.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3670966 3' similar to contains TAR1.1
8832	21911	35449	1.03	2.0E-57	AF054522.1	NT	MER22 repetitive element:
10051	23089	36681	1.06	2.0E-57	AF057722.1	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 22 (SCYA22), mRNA
							Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
							Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11548	24904	38281	1.55	2.0E-57	11424034	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11548	24904	38282	1.55	2.0E-57	11424034	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11592	24945	38327	1.76	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
11592	24945	38328	1.76	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
13214	26097	31684	2.59	2.0E-57	AF008663.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
2305	15437	28569	1.88	1.0E-57	AW503208.1	EST_HUMAN	hsc2a08.x1 NCL CGAP_Luz2 Homo sapiens cDNA clone IMAGE:3039062 3' similar to TR:000246
8891	21970		1.87	1.0E-57	BE04303.1	EST_HUMAN	hsc2a08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3
12545	25369		11.29	1.0E-57	AW470791.1	EST_HUMAN	THR repetitive element;
6794	18895	32238	0.83	8.0E-58	AA287847.1	EST_HUMAN	EST11348 Uterus Homo sapiens cDNA 5' and
12854	25567	31990	1.94	8.0E-58	BE395061.1	EST_HUMAN	60130946F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
602	13791		1.69	8.0E-58	BE888716.1	EST_HUMAN	60144548F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'
671	13857	26886	4.24	8.0E-58	A1798376.1	EST_HUMAN	hsc4b07.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475
671	13857	26887	4.24	8.0E-58	A1798375.1	EST_HUMAN	UNNAMED HERV-H PROTEIN;
1804	15047	28157	2.4	8.0E-58	11434921	NT	hsc4b07.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475
1804	15047	28158	2.4	8.0E-58	11434921	NT	UNNAMED HERV-H PROTEIN;
3040	16216		2.76	8.0E-58	17706132	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
7387	20495	33930	0.83	7.0E-58	BE961971.1	EST_HUMAN	Homo sapiens DHHC1 protein (LOC51304), mRNA
11095	24168		4.54	7.0E-58	5174542	NT	hsc4b07.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:3687577 5'
11170	24241	37873	2.61	7.0E-58	AW504109.1	EST_HUMAN	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B)
11170	24241	37874	2.61	7.0E-58	AW504109.1	EST_HUMAN	MEF2B) mRNA
2328	15460	28593	1.63	6.0E-58	BE339031.1	EST_HUMAN	UHF-BNO-alk-9-10-Q-JU1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
2448	15576	28706	5.25	6.0E-58	AU130689	EST_HUMAN	UHF-BNO-alk-9-10-Q-JU1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
2866	16142	29160	1.01	6.0E-58	BE242150.1	EST_HUMAN	60130946F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
2866	16142	29161	1.01	6.0E-58	BE242150.1	EST_HUMAN	AU130689 NT2R23 Homo sapiens cDNA clone NT2R2301263 5'
6268	19472	32827	0.88	8.0E-58	AF106911.1	NT	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baycar-HQSC project=TCAA Homo
10517	23552	37163	1.27	6.0E-58	11434746	NT	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baycar-HQSC project=TCAA Homo
12654	25434		1.22	6.0E-58	11526291	NT	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baycar-HQSC project=TCAA Homo

## Table 4

Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
311	13527	28560	3.08	5.0E-58	1460734	NT	Homo sapiens synaptophysin 1 (SYN1), mRNA
728	13910	28950	6.98	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-180600-016-505 NT0057 Homo sapiens cDNA
1221	14382	27442	2.9	5.0E-58	AW797648.1	EST_HUMAN	CM3-UM0043-240300-127-607 UM0043 Homo sapiens cDNA
1221	14382	27442	2.9	5.0E-58	AW797648.1	EST_HUMAN	CM3-UM0043-240300-127-607 UM0043 Homo sapiens cDNA
1222	14382	27442	2	5.0E-58	AW797648.1	EST_HUMAN	CM3-UM0043-240300-127-607 UM0043 Homo sapiens cDNA
1222	14382	27443	2	5.0E-58	AW797648.1	EST_HUMAN	CM3-UM0043-240300-127-607 UM0043 Homo sapiens cDNA
3400	16570	26565	4.09	5.0E-58	AA888183.1	EST_HUMAN	cr98e07 st NC1 CGAP LU5 Homo sapiens cDNA clone IMAGE:1603908.3'
4373	17616	30466	0.93	5.0E-58	AI636745.1	EST_HUMAN	ts89d07 st NC1 CGAP_G08 Homo sapiens cDNA clone IMAGE:2238468.3' similar to SW:PRO2_ACACA P19894 PROFLIN II ;
5746	18938		1.91	5.0E-58	11406282	NT	Homo sapiens placenta-specific 1 (PLAC1), mRNA
6307	19479	32834	8.55	5.0E-58	H25072.1	EST_HUMAN	Ynt51007 r1 Sources Infant brain t1NB Homo sapiens cDNA clone IMAGE:52071.5'
6824	19889	33053	0.79	5.0E-58	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C086
6800	19760	33148	1.03	5.0E-58	11421330	NT	Homo sapiens apical protein, Xerops lewis-like (APXL), mRNA
6917	20232	33665	0.9	5.0E-58	AF051334.1	NT	Homo sapiens nibrin (NBS), complete cds
6917	20232	33668	0.9	5.0E-58	AF051334.1	NT	Homo sapiens nibrin (NBS), complete cds
7255	20338	33758	0.71	5.0E-58	14886400	NT	Homo sapiens nibrin (NBS), complete cds
8156	21238	34759	9.09	5.0E-58	8822663	NT	Homo sapiens hypothetical protein FLJ10826 (FLJ10826), mRNA
8548	21629	35167	0.68	5.0E-58	AB04683.7.1	NT	Homo sapiens holocytochrome c synthase (cytochrome c heme-lyase) (HCOS), mRNA
10061	23089	36701	0.96	5.0E-58	11430847	NT	Homo sapiens holocytochrome c synthase (cytochrome c heme-lyase) (HCOS), mRNA
10328	23363	36973	1.9	5.0E-58	AL163218.2	NT	Homo sapiens pre-miRNA splicing factor similar to S. cerevisiae Psp18 (PRP18), mRNA
10812	23846	37254	0.65	5.0E-58	AB014511.1	NT	Homo sapiens pre-miRNA splicing factor similar to S. cerevisiae Psp18 (PRP18), mRNA
10812	23846	37255	0.65	5.0E-58	AB014511.1	NT	Homo sapiens pre-miRNA splicing factor similar to S. cerevisiae Psp18 (PRP18), mRNA
12852	26065		4.6	5.0E-58	11526293	NT	Homo sapiens pre-miRNA splicing factor similar to S. cerevisiae Psp18 (PRP18), mRNA
12850	26102		1.47	5.0E-58	11426423	NT	Homo sapiens pre-miRNA splicing factor similar to S. cerevisiae Psp18 (PRP18), mRNA
384	13592	26627	1.71	4.0E-58	4502302	NT	Homo sapiens pre-miRNA splicing factor similar to S. cerevisiae Psp18 (PRP18), mRNA
819	13888	27052	1.87	4.0E-58	1404634	NT	Homo sapiens pre-miRNA splicing factor similar to S. cerevisiae Psp18 (PRP18), mRNA
1498	14649	27731	1.24	4.0E-58	4503648	NT	Homo sapiens pre-miRNA splicing factor similar to S. cerevisiae Psp18 (PRP18), mRNA
2696	15816	28930	2.12	4.0E-58	U36251.1	NT	Homo sapiens pre-miRNA splicing factor similar to S. cerevisiae Psp18 (PRP18), mRNA
3402	18972	29587	1.41	4.0E-58	D16470.1	NT	Homo sapiens pre-miRNA splicing factor similar to S. cerevisiae Psp18 (PRP18), mRNA
3834	18994	29896	0.68	4.0E-58	5031660	NT	Homo sapiens pre-miRNA splicing factor similar to S. cerevisiae Psp18 (PRP18), mRNA
7995	21045	34557	0.8	4.0E-58	BE463857.1	EST_HUMAN	hY18d02.21 NC1 CGAP GC6 Homo sapiens cDNA clone IMAGE:3197842.3'
11624	24975	38396	7.44	4.0E-58	11424059	NT	Homo sapiens E1B-55kDa-associated protein 6 (E1B-AP6), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
345	13556		0.96	3.0E-58	R17878.1	EST_HUMAN	hg10e02.r1 Soares Infant brain (NIH) Homo sapiens cDNA clone IMAGE:31693 5'
1420	14674	27647	2.6	3.0E-58	U758981	NT	Homo sapiens peptide YY (PYY) mRNA
3246	16420	28435	3.07	3.0E-58	BF66848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
3246	16420	28436	3.07	3.0E-58	BF66848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
6390	19559	32918	0.61	3.0E-58	BE089009.1	EST_HUMAN	QV0-810702-170400-104-09 BT0702 Homo sapiens cDNA
6674	18736	33115	1.1	3.0E-58	F07056.1	EST_HUMAN	HSC1T6081 normalized Infant brain cDNA Homo sapiens cDNA clone c-1608
6778	19533	33329	2.48	3.0E-58	AV71297.1	EST_HUMAN	AV71297.7 DCA Homo sapiens cDNA clone DCAAZG04 5'
963	14136	27197	12.47	2.0E-58	AF068624.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds
1318	14474		7.88	2.0E-58	BE206532.1	EST_HUMAN	ba08b07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 6' similar to gb-X69391 60S RIBOSOMAL PROTEIN L6 (HUMAN); gb-X61987 M.musculus mRNA for TAX responsive element binding protein (MOUSE);
6451	18661	31830	0.94	2.0E-58	AW074831.1	EST_HUMAN	xb08a08.x1 Soares NFL_T_G8C_S1 Homo sapiens cDNA clone IMAGE:2567704 3'
6473	25605	31652	2.63	2.0E-58	BE907186.1	EST_HUMAN	601498961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
6473	25605	31685	2.63	2.0E-58	BE907186.1	EST_HUMAN	601498961F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
6182	19358	32706	1.7	2.0E-58	BF513488.1	EST_HUMAN	UH-BW1-ams-g-11-0-UJ.31 NCI_CGAP_Sub07 Homo sapiens cDNA clone IMAGE:3071060 3'
							emb5602.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1639674 3' similar to WP-ZK328.1 CE50605 UBILUTIN CONJUGATING ENZYME; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN;
6249	19423	32769	2.16	2.0E-58	AI124874.1	EST_HUMAN	xb08h08.r1 Soares fetal liver epigen 1NF5S Homo sapiens cDNA clone IMAGE:196379 5'
6283	19456	32806	0.83	2.0E-58	FB2587.1	EST_HUMAN	qm84c01.x1 NCI_CGAP_Lus Homo sapiens cDNA clone IMAGE:1895424 3'
7066	20119	33533	0.83	2.0E-58	AI291407.1	EST_HUMAN	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7307	20389	33848	2.79	2.0E-58	AF134938.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7307	20389	33849	2.79	2.0E-58	AF134938.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
10976	24056	37692	18.01	2.0E-58	BF307745.1	EST_HUMAN	601880812F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131891 5'
11207	24278	37913	1.68	2.0E-58	AW872841.1	EST_HUMAN	hm25708.x1 NCI_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
740	13922	26982	1.06	1.0E-58	IM65134.1	NT	Human complement component C5 mRNA, 3'end
1093	14258	27314	1.33	1.0E-58		NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22KD, B22) (NDUFB9), mRNA
1368	14513	27586	1.12	1.0E-58	AW597182.1	EST_HUMAN	EST3692352 IMAGE_resequences, MAGD Homo sapiens cDNA
1368	14513	27587	1.12	1.0E-58	AW597182.1	EST_HUMAN	EST3692352 IMAGE_resequences, MAGD Homo sapiens cDNA
1427	14581	27654	2.8	1.0E-58	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1697	14849	27935	1.28	1.0E-58	BE466132.1	EST_HUMAN	hy0808.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3196935 3'
2719	16337	28947	1.01	1.0E-58	AT217314.1	NT	Homo sapiens elcrl regulatory element binding transcription factor 2 (SREBF2) mRNA
2863	16977	29087	1.14	1.0E-58		NT	Homo sapiens elcrl regulatory element binding transcription factor 2 (SREBF2) mRNA
2892	16206	28322	1.01	1.0E-58	6174444	NT	Homo sapiens G protein-coupled receptor 69A (GPR69A) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3627	16791	28809	0.83	1.0E-58	4788081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3627	16791	28810	0.83	1.0E-58	4788081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3614	16974	29977	0.66	1.0E-58	4507628	NT	Homo sapiens transition protein 1 (during histone to plectantio replacement) (TNP1) mRNA
6085	18213	31185	7.13	1.0E-58	A1141063.1	EST_HUMAN	024301.x1 Soares_NHMFJ.S1 Homo sapiens cDNA clone IMAGE:1078129 3'
6864	19150	32485	1.37	1.0E-58	BE001830.1	EST_HUMAN	RC1-BT0254-280100-015-001 BT0254 Homo sapiens cDNA
7002	20138	33556	0.87	1.0E-58	J1422031	NT	Homo sapiens hypothetical protein (LOC51260) mRNA
8305	21387	35695	0.48	1.0E-58	AW973537.1	EST_HUMAN	EST385637 MAGE resequences MAGEM Homo sapiens cDNA
8070	22149	35695	0.62	1.0E-58	4505314	NT	Homo sapiens myomesin (M-protein) 2 (16SKD) (MYOM2) mRNA
9182	22260	35602	0.77	1.0E-58	AV751001.1	EST_HUMAN	AV751001 NPC Homo sapiens cDNA clone NPCACH09 5'
9282	22358	35907	0.64	1.0E-58	AA412397.1	EST_HUMAN	z8905.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
9282	22358	35908	0.64	1.0E-58	AA412397.1	EST_HUMAN	z8905.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
10389	23424	37031	0.65	1.0E-58	11432994	NT	Homo sapiens disc large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
12074	25055		2.1	1.0E-58	X63302.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
12100	25080	38787	2.61	1.0E-58	D61405.1	NT	Human MSH3 gene, exon 10
2303	15435	28567	63.38	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
6979	20207	33635	0.74	8.0E-59	AA382291.1	EST_HUMAN	EST56883 Testis 1 Homo sapiens cDNA 5' end
6979	20207	33636	0.74	8.0E-59	AA382291.1	EST_HUMAN	EST56883 Testis 1 Homo sapiens cDNA 5' end
8374	21455	34979	1.55	8.0E-59	AW71963.1	EST_HUMAN	W50006.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384171 3'
182	16005		1.97	6.0E-59	BF036327.1	EST_HUMAN	801458531.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3862086 5'
8015	21066	34579	0.62	6.0E-59	AA982431.1	EST_HUMAN	om81a04.s1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1533530 3' similar to TR:Q13732 Q13732 SA GENE PRODUCT PRECURSOR.
8440	21621	35060	0.69	6.0E-59	AW60910.1	EST_HUMAN	cn08h02.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn08h02 random
3197	16372	28379	7.75	6.0E-59	AW807484.1	EST_HUMAN	W48011.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2858936 3'
4780	17915	30901	9.84	6.0E-59	X63497.1	NT	H. sapiens DNA for ZNF80-linked ERV9 long terminal repeat
7129	18555	31470	8.22	5.0E-59	AW162304.1	EST_HUMAN	au66007.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TARI (repetitive element):
9006	22085	35628	1.03	5.0E-59	J1421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (RPOC39) mRNA
9906	22946	36632	1.44	5.0E-59	AV782898.1	EST_HUMAN	AV782898 MDS Homo sapiens cDNA clone MDSEIC12 5'
11146	24218	37845	4.54	5.0E-59	J1434908	NT	Homo sapiens hypothetical protein (LOC57143) mRNA
816	13995	27050	1.9	4.0E-59	D90006.1	NT	Human mRNA for KIA00784 gene, partial cds
1266	14423	27489	0.61	4.0E-59	4505818	NT	Homo sapiens phosphatidylinositol 4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products



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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1268	14423	27490	0.81	4.0E-59	4505918	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
4912	18042	31032	1.14	4.0E-59	4506758	NT	Homo sapiens ryandoline receptor 3 (RYR3) mRNA
4912	18042	31033	1.14	4.0E-59	4506758	NT	Homo sapiens ryandoline receptor 3 (RYR3) mRNA
5654	18848	32130	0.95	4.0E-59	11034810	NT	Homo sapiens actinin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
12498	25996		3.99	4.0E-59	AF05770.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
10	13248		6.74	3.0E-59	AW065524.1	EST_HUMAN	EST377582 MAGE resequences, MAGE Homo sapiens cDNA
234	13455	26481	3.89	3.0E-59	7682247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
1748	14897	27992	10.81	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLAT) mRNA
1748	14897	27993	10.81	3.0E-59	4505860	NT	Homo sapiens plasminogen activator, tissue (PLAT) mRNA
2198	15333	28459	8.54	3.0E-59	AB028035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2198	15333	28460	8.54	3.0E-59	AB028035.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3104	16280	29294	0.67	3.0E-59	T18865.1	EST_HUMAN	h020171 Testis 1 Homo sapiens cDNA clone h02017 5' end
3104	16280	29295	0.67	3.0E-59	T18865.1	EST_HUMAN	h020171 Testis 1 Homo sapiens cDNA clone h02017 5' end
3189	16374	28383	4.27	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3189	16374	28384	4.27	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3330	17089	30088	1.16	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sparm receptor) (ZP2) mRNA
4808	17942	30929	2.75	3.0E-59	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4865	18094	31071	2.12	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type T (PTPRT), mRNA
6162	18284		1.22	3.0E-59	MB95901.1	NT	Human probonema converging enzyme (NEC2) gene, exon 2
6350	18520	32877	2.4	3.0E-59	8924074	NT	Homo sapiens hypodermal protein PRO1741 (PRO1741), mRNA
7516	20589	34064	1.85	3.0E-59	5454137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA
8116	21198	34718	1.11	3.0E-59	X12566.1	NT	Human mRNA for dbi proto-oncogene
8116	21198	34719	1.11	3.0E-59	X12566.1	NT	Human mRNA for dbi proto-oncogene
10250	23285	36880	1.04	3.0E-59	X70281.3	NT	H. sapiens CKII-alpha gene
10250	23285	36881	1.04	3.0E-59	X70281.3	NT	H. sapiens CKII-alpha gene
12635	25428		11.11	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
6946	20259		0.59	2.0E-59	AA470073.1	EST_HUMAN	298405.51 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:730377 3'
7216	20081	33494	0.59	2.0E-59	AA135187.1	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
9837	22877		4.84	2.0E-59	AA309774.1	EST_HUMAN	EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end
10745	23778		1.34	2.0E-59	BF36554.1	EST_HUMAN	RCO-NT0036-100700-032-607 NT0036 Homo sapiens cDNA
11089	24144	37780	2.19	2.0E-59	AW410588.1	EST_HUMAN	h07704.X1 NIH MGCC 17 Homo sapiens cDNA clone IMAGE:2861654 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11089	24144	37781	2.19	2.0E-59	AW410688.1	EST_HUMAN	fl0704.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861854 5'
12373	26288	32118	4.28	2.0E-59	AI631809.1	EST_HUMAN	was6c72.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542
12863	28018	31668	3.87	2.0E-59	L11645.1	NT	Q86542 RTVL-H PROTEIN, contains LTR7.b1 LTR7 repetitive element;
167	13392		3.85	1.0E-59	BE286411.1	EST_HUMAN	Homo sapiens alpha-tubulin mRNA, complete cds
1589	14722	27803	1.04	1.0E-59	T82522.1	EST_HUMAN	ye25cd9.17 Stragene Lung (8937210) Homo sapiens cDNA clone IMAGE:3531927 5'
2683	15803		2.65	1.0E-59	AA748488.1	EST_HUMAN	ye25cd9.17 Stragene Lung (8937210) Homo sapiens cDNA clone IMAGE:118768 5' similar to SP:S21348
7735	20786	34285	1.14	1.0E-59	AI130894.1	NT	S21348 HYPOTHETICAL PROTEIN 4 - ;
7895	20947	34454	1.3	1.0E-59	BE258814.1	EST_HUMAN	oa56h11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309029 3' similar to TR:Q13637
7895	20947	34455	1.3	1.0E-59	BE258814.1	EST_HUMAN	Q13637 MIER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
8885	22727	38296	0.86	1.0E-59	11416630	NT	Homo sapiens mRNA for transcription factor
8804	22844	38421	0.58	1.0E-59	11428849	NT	Homo sapiens zinc finger protein 275 (ZNF275), mRNA
9804	22844	38422	0.58	1.0E-59	11428849	NT	Homo sapiens 3-hydroxyisovaleryl-Coenzyme A hydrolase (HIBCH), mRNA
11094	20786	34285	1.08	1.0E-59	AI130894.1	NT	Homo sapiens 3-hydroxyisovaleryl-Coenzyme A hydrolase (HIBCH), mRNA
783	13883	27013	1.45	8.0E-60	AW877845.1	EST_HUMAN	Homo sapiens mRNA for transcription factor
1499	14862	27734	3.21	8.0E-60	4759189	NT	EST388949 IMAGE resequences, IMAGE Homo sapiens cDNA
2241	15374	28502	4.76	8.0E-60	5174659	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18KD) (SNRPD3), mRNA
2241	15374	28503	4.76	8.0E-60	5174659	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP), mRNA
8103	19283	32816	1.18	8.0E-60	AB029004.1	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP), mRNA
8033	19792	33181	0.89	8.0E-60	S83182.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7874	20828	34434	0.89	8.0E-60	11420841	NT	hyaluronan-binding protein=heparocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
8152	21234	34765	3	8.0E-60	X17033.1	NT	Homo sapiens phosphatidylcholine transferase 1, choline, beta isoform (PCYT1B), mRNA
9139	22218	35762	2.83	8.0E-60	11428849	NT	Human mRNA for integrin alpha-2 subunit
9871	22833	36202	0.78	8.0E-60	11417118	NT	Homo sapiens S-antigen, retina and pineal gland (arrestin) (SAG), mRNA
8671	22833	36203	0.78	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10789	23832	37465	0.62	8.0E-60	5453897	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11071	24146	37783	4.17	8.0E-60	AL163204.2	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
11071	24146	37784	4.17	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
773	13854	27004	11.11	7.0E-60	AF059058.1	NT	Homo sapiens chromosome 21 segment HS21C004
774	13954	27004	25.11	7.0E-60	AF059058.1	NT	Homo sapiens MHC class 1 region
838	14016	27071	1.47	7.0E-60	4504634	NT	Homo sapiens MHC class 1 region
							Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2187	15332	28458	1.82	7.0E-60	AF077183.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2845	16969	28098	0.98	7.0E-60	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
4285	17438	30425	2.4	7.0E-60	AF05438	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
4638	17833	30818	0.81	7.0E-60	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
9807	22662	36235	4.21	7.0E-60	H58041.1	EST_HUMAN	Homo sapiens fetal liver spleen 1NFUS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element 1
11846	24725	38417	1.73	7.0E-60	H59041.1	EST_HUMAN	y12704.11 Scores fetal liver spleen 1NFUS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element 1
2248	15381	28509	1.16	8.0E-60	BE884974.2	EST_HUMAN	601658751R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886069 3'
8632	21712		8.04	6.0E-60	H52456.1	EST_HUMAN	y12704.11 Scores fetal liver spleen 1NFUS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element 1
86	13321	26348	1.06	5.0E-60	A1807817.1	EST_HUMAN	wf52c07.x1 Scores NFE_L_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
86	13321	26349	1.06	5.0E-60	A1807817.1	EST_HUMAN	wf52c07.x1 Scores NFE_L_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
2308	15440	28574	1.83	4.0E-60	AW 503208.1	EST_HUMAN	U1-HF-BNO-ak-g-07-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
2308	15440	28575	1.83	4.0E-60	AW 503208.1	EST_HUMAN	U1-HF-BNO-ak-g-07-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
3037	16213		1.45	4.0E-60	AA289037.1	EST_HUMAN	EST11499 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
7508	20592	34055	0.78	4.0E-60	BF198068.1	EST_HUMAN	tr8105.x1 NC_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
8328	22402		0.65	4.0E-60	AL163278.2	NT	Q61065 GTP-RHO BINDING PROTEIN 1
1907	15050	28161	4.93	3.0E-60	BE562611.1	EST_HUMAN	Homo sapiens chinosome 21 segment HS21C078
1907	15050	28162	4.98	3.0E-60	BE562611.1	EST_HUMAN	601338446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3880395 5'
1918	16061		2.81	3.0E-60	BC031190	NT	601338446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3880395 5'
4578	17716	30698	2.76	3.0E-60	AL271735.1	NT	Homo sapiens prohibitin (PHB) mRNA
5494	18693	31709	0.69	3.0E-60	BF365143.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
5787	18849	32251	2.21	3.0E-60	AW536196.1	EST_HUMAN	QV4-NN1149-250900-423-101 NT1149 Homo sapiens cDNA
7093	18520	31613	1.07	3.0E-60	AF28214.1	EST_HUMAN	RC3-LT0023-200100-012-401 LT0023 Homo sapiens cDNA
8597	21678	35215	4.69	3.0E-60	5174644	NT	606011.y5 NCL_CGAP_KR3 Homo sapiens cDNA clone IMAGE:1534053 5' similar to SW:UDP_MOUSE
8597	21678	35216	4.59	3.0E-60	5174644	NT	P52624 URIDINE PHOSPHORYLASE 1
8783	21862	35405	0.6	3.0E-60	AF04235.1	EST_HUMAN	Homo sapiens prolidase (proline oxidase) (PRODH) mRNA
8940	22019	35560	3.84	3.0E-60	5174644	NT	Homo sapiens prolidase (proline oxidase) (PRODH) mRNA
13053	25088		1.55	3.0E-60	AA48626.1	EST_HUMAN	ox56009.x1 Scores NIHMH2L.S1 Homo sapiens cDNA clone IMAGE:1660337 3' similar to SW:FORM_MOUSE
							ab07004.11 Stratiopoda lung (#637210) Homo sapiens cDNA clone IMAGE:840151 5' similar to contains LTR10.11 LTR10 repetitive element 1

Single Exon Probes Expressed In Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
31	13269	26273	1.7	2.0E-60	AY008285.1	NT	Homo sapiens soluble carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
1453	14608	27088	3.99	2.0E-60	Z11694.1	NT	H. sapiens 41kDa protein kinase related to rat ERK2
1756	14908	26001	2.2	2.0E-60	M24603.1	NT	Human bcr protein mRNA, 5' end
3669	16832	28943	0.78	2.0E-60	I4787807	NT	Homo sapiens v-rel murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
4025	17161	30180	0.73	2.0E-60	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
6430	19598	32984	0.85	2.0E-60	AF179185.1	EST_HUMAN	nm011212.96 NCL_CGAP_C09 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR11 THR repetitive element
6621	19781	33169	1.26	2.0E-60	AF004877.1	NT	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
6855	20008	33418	1.08	2.0E-60	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
6889	18508	31924	2.15	2.0E-60	I4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6889	18508	31625	2.15	2.0E-60	I4503044	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7259	20342	33793	8.18	2.0E-60	AA311169.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prollymucin, alpha
7259	20342	33794	8.18	2.0E-60	AA311169.1	EST_HUMAN	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to prollymucin, alpha
7810	20865		0.9	2.0E-60	BF512808.1	EST_HUMAN	UH-BV1-arnu-c02-0-UI.81 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071210 3'
8194	21276	34798	1.33	2.0E-60	X85597.1	EST_HUMAN	HS15BEST human adult testis Homo sapiens cDNA clone CAM.1EST15
8068	22147	36694	3.12	2.0E-60	L36033.1	NT	Human pre-B cell stimulating factor homolog (SDF1b) mRNA, complete cds
10183	23220	36913	1.83	2.0E-60	11891659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (sema4) 6A (SEMA4), mRNA
10183	23220	36914	1.83	2.0E-60	11891659	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (sema4) 6A (SEMA4), mRNA
11769	23945	37672	1.7	2.0E-60	11434729	NT	Homo sapiens ribosomal protein S6 kinase, 60kD, polypeptide 5 (RPS6KA5), mRNA (SEM6A), mRNA
12672	25448		2.36	2.0E-60	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae) like 1 (NHP2L1) mRNA
12829	25685		1.47	2.0E-60	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12848	25664		1.5	2.0E-60	AB011369.1	NT	Homo sapiens gene for A-F-6, complete cds
835	13728	26752	1.02	1.0E-60	BE178368.1	EST_HUMAN	PM2-HT0605-270200-001-c03 HT0605 Homo sapiens cDNA
4011	17168	30176	1.08	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5'
6070	18198	31172	2.57	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
8134	21216	34737	1.39	1.0E-60	BE006410.1	EST_HUMAN	RC4-B1T0311-141189-011-408 BT0311 Homo sapiens cDNA
8955	22034		2.84	1.0E-60	AA24404.1	EST_HUMAN	nc046122.1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1, L1 repetitive element
8982	22061	35601	1.35	1.0E-60	AV734057.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TPGAED06 5'
12606	26079		1.49	1.0E-60	AJ252313.1	NT	Homo sapiens genomic hybrid Rhesus box
1123	14288	27343	8.4	8.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8908	21987	35526	0.53	9.0E-61	4885548	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
8908	21987	35527	0.53	9.0E-61	4885548	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
2735	15852	28955	1.41	8.0E-61	AW006478.1	EST_HUMAN	w05b10.x1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:2506555 3'
2735	15852	28956	1.41	8.0E-61	AW006478.1	EST_HUMAN	w05b10.x1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:2506555 5'
3016	18192		2.63	8.0E-61	X57147.1	NT	Human endogenous retrovirus PHE.1 (ERV9)
8079	21161	34679	1.03	8.0E-61	AA58368.1	EST_HUMAN	nm59g08.s1 NCI_CGAP_Lat1 Homo sapiens cDNA clone IMAGE:1089218 3'
130	13357	28389	0.79	7.0E-61	7706970	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
130	13357	28390	0.79	7.0E-61	7706970	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
276	13494	28524	3.08	8.0E-61	BE409310.1	EST_HUMAN	601300935F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 6'
834	14012	27068	8.49	8.0E-61	BE409310.1	EST_HUMAN	601300935F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1352	14507	27578	12.72	8.0E-61	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1659	14811	27896	1.04	8.0E-61	BE287400.1	EST_HUMAN	601108235F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1679	14831	27916	2.91	8.0E-61	AA59893.1	EST_HUMAN	nm59f08.s1 NCI_CGAP_Lat1 Homo sapiens cDNA clone IMAGE:108897 3'
3391	16553	29687	8.16	8.0E-61	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
6155	19331	32977	2.86	8.0E-61	S72948.1	NT	ig-bet/b28=CD7b (alternatively spliced) [human, B cells, mRNA Partial, 375 nt]
7497	20572	34045	1.49	8.0E-61	AF035737.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
7785	20851	34343	1.85	8.0E-61	AF035737.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
12684	14012	27068	1.66	8.0E-61	BE409310.1	EST_HUMAN	Homo sapiens general transcription factor 2-1 (GTF2) mRNA, complete cds
13157	25752	31828	1.42	8.0E-61	U07000.1	NT	601300935F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
226	13448	26476	2.64	8.0E-61	8822890	NT	Human breakpoint cluster region (BCR) gene, complete cds
226	13448	26477	2.64	8.0E-61	8822890	NT	Human breakpoint cluster region (BCR) gene, complete cds
370	13579	26612	0.7	8.0E-61	4507500	NT	Homo sapiens hypophthal protein FLJ11316 (FLJ11316), mRNA
1713	14864	27953	2.84	8.0E-61	4606008	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3101	18277	29291	2.19	8.0E-61	AL163279.2	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3288	18442	29462	1.82	8.0E-61	4502168	NT	Homo sapiens chromosome 21 segment HS21C079
4090	17245		2.22	8.0E-61	AJ22804.1	NT	Homo sapiens amyloid beta (A4) precursor protein (protease notch-II, Alzheimer disease) (APP), mRNA
5118	13579	26612	0.76	8.0E-61	4507500	NT	Homo sapiens 655 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
1798	14947	28039	1.94	8.0E-61	AU140307.1	EST_HUMAN	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
5938	19122	32435	0.71	8.0E-61	7691637	NT	AU140307 PLAC2 Homo sapiens cDNA clone PLAC2000302 5'
12349	26252		8.47	8.0E-61	AV731140.1	EST_HUMAN	Homo sapiens DKFZP5668023 protein (DKFZP5668023), mRNA
8616	21698	35234	0.7	8.0E-61	AF150180.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFAR801 5'
611	13705	28733	1.8	8.0E-61	8922829	NT	AF150180 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAGB04
1239	14398	27480	6.33	8.0E-61	BE168410.1	EST_HUMAN	Human placental protein FLJ11026 (FLJ11026), mRNA
							QV3-H10513-060400-147-d01 HT0513 Homo sapiens cDNA

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1239	14398	27461	6.33	2.0E-61	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-401 HT0513 Homo sapiens cDNA
1899	14851	27938	1.38	2.0E-61	NC3039.1	EST_HUMAN	Y63d11.s1 Soares fetal liver spleen 1NFEL5 Homo sapiens cDNA clone IMAGE:248453 3' similar to gbL28444.605 RIBOSOMAL PROTEIN L35A (HUMAN)
2706	15824		1.72	2.0E-61	NC3397.1	EST_HUMAN	Y63f1.1T Soares melanocytes 2NBH4 Homo sapiens cDNA clone IMAGE:270189 5'
6556	19718	33094	0.88	2.0E-61	11426166	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110116KD) (ATP8N1A), mRNA
9217	22295	35839	1.67	2.0E-61	AV694317.1	EST_HUMAN	AV694317 GKC Homo sapiens cDNA clone GKCEL.G06 5'
9762	22700		0.98	2.0E-61	AB011108.1	NT	Homo sapiens mRNA for KIAA0539 protein, partial cds
10126	23164	36763	1.34	2.0E-61	AW500236.1	EST_HUMAN	U1HF-BN0-6164-120-U1.r NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076774 5'
10466	23491	37101	2.84	2.0E-61	11421778	NT	U1HF-BN0-6164-120-U1.r NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076774 5'
11123	24195		4	2.0E-61	11419729	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
13144	26744	31850	1.45	2.0E-61	AW69528.1	EST_HUMAN	QV0-BN0042-170300-162-110 BN0042 Homo sapiens cDNA
448	13644		1.37	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21.C003
794	13973	27026	1.29	1.0E-61	15459829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2), mRNA
1430	14584	27658	1.07	1.0E-61	AL163203.2	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2), mRNA
1809	14958		1.02	1.0E-61	U32857.1	NT	Homo sapiens chromosome 21 segment HS21.C003
1906	15049	28160	4.43	1.0E-61	16005883	NT	Homo sapiens zona pellucida glycoprotein 3A (spem receptor) (ZP3A), mRNA
2270	15403	28531	1.54	1.0E-61	AW827281.1	EST_HUMAN	MSR1 repetitive element
2896	16075	29093	0.88	1.0E-61	BE368353.1	EST_HUMAN	MSR1 repetitive element
3463	16630	28650	0.85	1.0E-61	7682319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3826	16886	29889	1.16	1.0E-61	BE174455.1	EST_HUMAN	QV2-HT0577-140300-077-506 HT0577 Homo sapiens cDNA
4374	17517	30497	1.05	1.0E-61	168840.1	NT	Human monomelic oxidase A (MAOA), mRNA, complete cds
4561	17699	30680	0.93	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK), mRNA
4561	17699	30681	0.95	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK), mRNA
4881	18110	31088	9.55	1.0E-61	AW283181.1	EST_HUMAN	Homo sapiens TRAF family member-associated NFKB activator (TANK), mRNA
4881	18110	31087	9.55	1.0E-61	AW283181.1	EST_HUMAN	U1-H-BW0-61b-08-Q-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
5076	18203	31176	0.62	1.0E-61	AL163210.2	NT	U1-H-BW0-61b-08-Q-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
5309	18708	31723	0.71	1.0E-61	167423.3	NT	Homo sapiens chromosome 21 segment HS21.C010
5908	18986	32301	1.07	1.0E-61	7662303	NT	H. sapiens carbonic anhydrase VII (CA VII) gene, exons 4,5,6, and 7, and complete cds
6004	19189	32508	1.32	1.0E-61	11416891	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
7041	20084	33510	8.82	1.0E-61	MS30135.1	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
7240	20324	33768	0.77	1.0E-61	4759171	NT	Homo sapiens survival of motor neuron 1, telomeric (SMN1), mRNA
7341	20421	33883	1.38	1.0E-61	8929130	NT	Human P40 T-cell and mast cell growth factor (P40) gene, complete cds
							Homo sapiens SC35-interacting protein 1 (SRIP129), mRNA
							Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7341	20421	33884	1.39	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8326	21408	34935	2.69	1.0E-61	11034840	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
8508	21569	35123	3.94	1.0E-61	AF224693.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D) genes, complete cds
8492	22639		2.78	1.0E-61	AW699726.1	EST_HUMAN	MRB-BN0070-040400-010-001 BN0070 Homo sapiens cDNA
9557	22822	36193	0.58	1.0E-61	11416230	NT	Homo sapiens cadherin 18 (CDH18), mRNA
10235	23270	36861	4.8	1.0E-61	11428892	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
10871	23956	37585	5.61	1.0E-61	11425578	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
11178	24247	37880	1.72	1.0E-61	AB044550.1	NT	Homo sapiens P10Kcl.19 mRNA for ubiquitin-conjugating enzyme E2, complete cds
11325	24398	38033	1.44	1.0E-61	AB007830.1	NT	Homo sapiens gene for CBR2, complete cds
12242	26043		21.57	1.0E-61	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
12286	26031	31677	4	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12286	26031	31678	4	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13026	25679	31859	10.94	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
10565	23600	37206	1.06	8.0E-62	BE064388.1	EST_HUMAN	RC4-BT0310-110300-015-410 BT0310 Homo sapiens cDNA
4673	17808	30786	0.85	8.0E-62	AA830420.1	EST_HUMAN	cc66h11.s1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVK
1131	14266	27351	1.12	7.0E-62	AV714334.1	EST_HUMAN	P31785 POL POLYPYRROLINE ;
3595	16759	29775	0.84	7.0E-62	P17480	SWISSPROT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1)
6038	19221	32544	0.97	7.0E-62	11427966	NT	(AUTANTIGEN NDR-90)
11632	24712	38403	4.05	7.0E-62	AI208681.1	EST_HUMAN	Homo sapiens hypothetical protein (FLJ20281), mRNA
3063	16238		1.55	6.0E-62	U09410.1	NT	gg58604.x1 Soares, testis, LNT Homo sapiens cDNA clone IMAGE:1839150 3' similar to TR:O18103
3471	16638		5.37	6.0E-62	11418255	NT	O15103 HYPOTHETICAL 27.3 KD PROTEIN ;
7603	20859	34351	3.47	6.0E-62	AI762801.1	EST_HUMAN	Human zinc finger protein ZNF131 mRNA, partial cds
7603	20859	34352	3.47	6.0E-62	AI762801.1	EST_HUMAN	Homo sapiens CGI-56 protein (CGI-56), mRNA
8277	21359		0.66	6.0E-62	AW501124.1	EST_HUMAN	w04d02.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
8462	21633	35063	1.52	6.0E-62	11431138	NT	w04d02.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
8554	22619	36189	3.87	6.0E-62	AW614393.1	EST_HUMAN	UHF-BPop-elt-d-08-0-UL11 NIH, MGC, 51 Homo sapiens cDNA clone IMAGE:3072833 5'
429	13624	26684	1.46	5.0E-62	AB950926.1	EST_HUMAN	Homo sapiens CGI-18 protein (LOC51008), mRNA
2478	15605	26729	5.16	6.0E-62	AJ271735.1	NT	MR3-ST0203-130100-025-403 ST0203 Homo sapiens cDNA
2478	15605	26730	5.16	5.0E-62	AJ271735.1	NT	w61601.x1 NCI CGAP L128 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:CG95_HUMAN
							C08379 GOLGIN-95, contains element MER22 repetitive element ;
							Homo sapiens Xq pseudautosomal region, segment 112
							Homo sapiens Xq pseudautosomal region, segment 112

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3506	16673	29693	2.55	5.0E-62	4506758	NT	Homo sapiensryanodine receptor 3 (RYR3) mRNA zw7669.s1 Scases_ntt Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT P47245 NARLD.YSIN:
4447	17567	30566	1.75	5.0E-62	AA431093.1	EST_HUMAN	Homo sapiensryanodine receptor 3 (RYR3) mRNA
8746	21825	35362	0.74	5.0E-62	4506758	NT	Homo sapiensryanodine receptor 3 (RYR3) mRNA
9717	22782	36363	12.91	5.0E-62	AW410697.1	EST_HUMAN	flm7609.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2951616 5'
11543	24599	38274	2.38	5.0E-62	1425574	NT	Homo sapiensmuscle specific gene (M9) mRNA
11543	24599	38275	2.38	5.0E-62	1425574	NT	Homo sapiensmuscle specific gene (M9) mRNA
863	14040	27102	2.17	4.0E-62	AW161479.1	EST_HUMAN	aw71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37100
863	14040	27103	2.17	4.0E-62	AW161479.1	EST_HUMAN	aw71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37100
864	14040	27102	1.32	4.0E-62	AW161479.1	EST_HUMAN	aw71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37100
864	14040	27103	1.32	4.0E-62	AW161479.1	EST_HUMAN	aw71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37100
864	14040	27103	1.32	4.0E-62	AW161479.1	EST_HUMAN	aw71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37100
2529	16654	28776	1.9	4.0E-62	A1827800.1	EST_HUMAN	wp12b08.x1 Scases_nfl_t GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to wp12b08.x1 Scases_nfl_t GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to wp12b08.x1 Scases_nfl_t GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
2529	16654	28776	1.9	4.0E-62	A1827800.1	EST_HUMAN	wp12b08.x1 Scases_nfl_t GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to wp12b08.x1 Scases_nfl_t GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to wp12b08.x1 Scases_nfl_t GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
2529	16654	28776	1.9	4.0E-62	A1827800.1	EST_HUMAN	wp12b08.x1 Scases_nfl_t GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to wp12b08.x1 Scases_nfl_t GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to wp12b08.x1 Scases_nfl_t GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
3486	16654	28776	1.9	4.0E-62	A1827800.1	EST_HUMAN	wp12b08.x1 Scases_nfl_t GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to wp12b08.x1 Scases_nfl_t GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to wp12b08.x1 Scases_nfl_t GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
6046	19229	32553	1.71	4.0E-62	4506758	NT	Homo sapienscolicin carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
6426	19594	32660	2.81	4.0E-62	11420654	NT	Homo sapiensubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USPBX) mRNA
7322	20404	33666	1.75	4.0E-62	11421041	NT	Homo sapiensphosphoribosyl pyrophosphate synthetase 2 (PPRS2) mRNA
7812	20867	34361	2.21	4.0E-62	7657057	NT	Homo sapienseukaryotic translation initiation factor 28, subunit 2 (beta, 39KD) (EIF2B2) mRNA
7812	20867	34362	2.21	4.0E-62	7657057	NT	Homo sapienseukaryotic translation initiation factor 28, subunit 2 (beta, 39KD) (EIF2B2) mRNA
864	21445	34988	1.12	4.0E-62	11429973	NT	Homo sapiens26S proteasome-associated pad1 homolog (POH1) mRNA
8047	22126	35670	6.42	4.0E-62	AB033089.1	NT	Homo sapiensmRNA for KIAA1263 protein, partial cds
11263	24332	37873	2.62	4.0E-62	Z18766.1	NT	H. sapiens flow-sorted chitosome 6 HincIII fragment, SC06pA16D3
11263	24332	37874	2.62	4.0E-62	Z18766.1	NT	H. sapiens flow-sorted chitosome 6 HincIII fragment, SC06pA16D3
11500	24558	38233	63.7	4.0E-62	ST0584.1	NT	thyroid-stimulating hormone alpha subunit [human, Genomic, 268 nt, segment 3 of 4]
12269	25202	38360	1.18	4.0E-62	11418086	NT	Homo sapiensputative nuclear protein (HRIHFB2122) mRNA
12497	25689		1.65	4.0E-62	11418192	NT	Homo sapiensputative nuclear protein (HRIHFB2122) mRNA



Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12946	25657	31855	1.68	4.0E-62	U418322	NT	Homo sapiens cadherin EGF LA6 seven-pass G-type receptor 1 (CELSR1), mRNA
13004	25653	31852	6.88	4.0E-62	U417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
13004	25653	31853	6.86	4.0E-62	U417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
13069	26683	31955	2.16	4.0E-62	U430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
76	13312	26338	0.69	3.0E-62	U457794	NT	Homo sapiens neurotrophin 2 (bilateral acoustic neuroma) (NF2) mRNA
3111	16287	29301	1.13	3.0E-62	AB040809.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3111	16287	29302	1.13	3.0E-62	AB040809.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3789	16950	29956	4.19	3.0E-62	X52856.1	NT	Human cyclophilin-related processed pseudogene
8737	21816	35351	3.74	3.0E-62	A1632738.1	EST_HUMAN	w83304.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2289903 3' similar to contains THR12 THR repetitive element;
1259	14417	27482	2.71	2.0E-62	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
8974	22053	35595	5.59	2.0E-62	BF329911.1	EST_HUMAN	RCO-BN0284-300500-031-605 BN0284 Homo sapiens cDNA
8974	22053	35596	5.59	2.0E-62	BF329911.1	EST_HUMAN	RCO-BN0284-300500-031-605 BN0284 Homo sapiens cDNA
10376	23411		3.71	2.0E-62	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
11988	24973		8.83	2.0E-62	BF330678.1	EST_HUMAN	QYA-BT0257-081199-017-603 BT0257 Homo sapiens cDNA
1069	14235	27294	1.14	1.0E-62	AF248540.1	NT	Homo sapiens Interactin 2 (SH3D1B) mRNA, complete cds
1579	14726	27809	18.41	1.0E-62	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
1842	14988	28088	1.64	1.0E-62	AA025207.1	EST_HUMAN	af70611.1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WPK01H12.1 CE03463;
2991	16167	29176	1.22	1.0E-62	AL038044.1	EST_HUMAN	DKFZp566F104_r1 568 (synonym: hnk42) Homo sapiens cDNA clone DKFZp566F104 5'
4648	17784	30797	1.84	1.0E-62	8923201	NT	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
6418	19587	32850	2.02	1.0E-62	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTT), CDM protein (CDM), adrenoleukodystrophy protein >
7284	20367	33820	1.07	1.0E-62	AA490060.1	EST_HUMAN	ab05602.1 Stratiagene fetal ratna 837202 Homo sapiens cDNA clone IMAGE:839806 3'
7295	20377	33834	2.69	1.0E-62	AA722878.1	EST_HUMAN	z88970.1 Soares_fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:408771 3'
7295	20377	33835	2.69	1.0E-62	AA722878.1	EST_HUMAN	z88970.1 Soares_fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:408771 3'
8937	22036	35577	0.54	1.0E-62	AA280060.1	EST_HUMAN	z893607.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:705080 5'
8258	22335	35885	1.65	1.0E-62		NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8258	22335	35886	1.65	1.0E-62		NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8302	22378	35928	1.92	1.0E-62	X15533.1	NT	H sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
8302	22378	35929	1.92	1.0E-62	X15533.1	NT	H sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
8757	22995	36263	3.03	1.0E-62	AA4691D.1	EST_HUMAN	aa33608.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 3'

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11848	24727	38419	2.28	1.0E-62	Z78688.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC8pA14D8
12808	25640		4.83	1.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
13042	25684	31862	3.16	1.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
348	13559	28587	2.27	8.0E-63	AW818405.1	EST_HUMAN	QV4-ST0234-101199-037-005 ST0234 Homo sapiens cDNA
2421	15550		2.17	9.0E-63	CT8159.1	EST_HUMAN	CT8159 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-598C10.5'
4152	17304	30287	8.77	8.0E-63	AB002848.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4152	17304	30288	8.77	8.0E-63	AB002848.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
6388	18484	38824	4.69	9.0E-63	11418186	NT	Homo sapiens acetylase 2, mitochondrial (AC02), mRNA
5582	18777	31822	1.44	9.0E-63	Y15056.1	NT	Homo sapiens mRNA for PKB kinase
7332	20413	33875	3.78	9.0E-63	11428985	NT	Homo sapiens nucleopoin 88KD (NUP88), mRNA
8008	21059	34571	1.77	9.0E-63	4885544	NT	Homo sapiens pyruvate dehydrogenase kinase, isoform 3 (PDK3), mRNA
8521	21602	35139	1.18	9.0E-63	11421160	NT	Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), mRNA
11286	24362	38003	1.3	8.0E-63	BF203408.1	EST_HUMAN	601865828F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4098487.5'
2420	16549	28677	3.05	8.0E-63	458734	NT	Homo sapiens monomelic oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2446	16574	28703	2.58	8.0E-63	5031870	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3550	16715	29727	4.26	8.0E-63	AF188349.1	NT	Gallus gallus Dact2 protein (Dact2), mRNA, complete cds
3650	16715	29728	4.26	8.0E-63	AF188349.1	NT	Gallus gallus Dact2 protein (Dact2), mRNA, complete cds
4381	17524	30505	4.36	8.0E-63	AL163238.2	NT	Homo sapiens chromosome 21 segment HS21C068
952	14125		3.38	7.0E-63	AB872137.1	EST_HUMAN	ym56g11.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2439808.3'
5455	18655		70.59	6.0E-63	AA420803.1	EST_HUMAN	nc6302.11 NCI CGAP_P11 Homo sapiens cDNA clone IMAGE:745947 similar to gb:Y00361.60S
6076	22154	35688	0.82	5.0E-63	114528464	NT	RIBOSOMAL PROTEIN (HUMAN);
3396	16668	29584	0.88	4.0E-63	AL183278.2	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
3910	17069	30066	1.06	4.0E-63	AB014607.1	NT	Homo sapiens chromosome 21 segment HS21C078
3810	17069	30067	1.08	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
8576	19737	33116	2.6	4.0E-63	AW750372.1	EST_HUMAN	Homo sapiens mRNA for KIAA0707 protein, partial cds
8576	19737	33117	2.6	4.0E-63	AW750372.1	EST_HUMAN	CMS-BT0595-190100-072-609 BT0595 Homo sapiens cDNA
11397	24458	38121	2.02	4.0E-63	AW134709.1	EST_HUMAN	CMS-BT0595-190100-072-609 BT0595 Homo sapiens cDNA
11397	24458	38122	2.02	4.0E-63	AW134709.1	EST_HUMAN	CMS-BT0595-190100-072-609 BT0595 Homo sapiens cDNA
1989	16131	28235	16.18	3.0E-63	AB018250.1	NT	U14-B11-abq-e-02-Q.U1.st NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482.3'
2840	15954	29061	1.49	3.0E-63	J00310.1	NT	U14-B11-abq-e-02-Q.U1.st NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482.3'
2892	14426	27493	11.84	3.0E-63	6005963	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
6603	18763	33151	33.63	3.0E-63	11545810	NT	Human Mel-RNA-1 gene 1
							Homo sapiens zinc finger protein 144 (Mat-18) (ZNF144), mRNA
							Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC68928), mRNA

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8907	22947	36533	0.83	3.0E-63	BE876136.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
8907	22947	36534	0.83	3.0E-63	BE876136.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
196	13419	26449	1.69	2.0E-63	U07804.1	NT	Human DNA topoisomerase I mRNA, partial cds
203	13423	26457	1.65	2.0E-63	4885226	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
510	13704		1.19	2.0E-63	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72 kDa) (GLCLC) mRNA
849	14027	27087	3.07	2.0E-63	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSOR1), mRNA
1697	14750	27634	1.54	2.0E-63	AB030388.1	NT	Homo sapiens RHGE mRNA for Rh blood CE group antigen polypeptide, complete cds
1597	14750	27635	1.54	2.0E-63	AB030388.1	NT	Homo sapiens RHGE mRNA for Rh blood CE group antigen polypeptide, complete cds
1806	14956	28049	2.02	2.0E-63	BE410738.1	EST_HUMAN	601301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3836103 5'
2146	15282	28407	1.05	2.0E-63	AB63691.1	EST_HUMAN	wfs4B02.X1 NCI CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406603 3' similar to gb:U57609 GLI3 PROTEIN (HUMAN);
3225	16399	29411	1.94	2.0E-63	4602166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant), Alzheimer disease (APP), mRNA
3357	16529	29544	2.4	2.0E-63	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
4014	17171	30179	3.19	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4998	18117	31096	1.28	2.0E-63	AF11167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene mRNA
5378	25802	31447	0.95	2.0E-63	14418429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
6005	18180	32509	2.41	2.0E-63	BF373541.1	EST_HUMAN	GV1-FT0170-040700-285-c05 FT0170 Homo sapiens cDNA
6005	18180	32510	2.41	2.0E-63	BF373541.1	EST_HUMAN	GV1-FT0170-040700-285-c05 FT0170 Homo sapiens cDNA
6315	19487	32842	1.07	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6315	19487	32843	1.07	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV7S1P, TCRBV22S1A2NT, TCRBV9S1A1T, TCRBV7S1A1NT, TCRBV9S1A1T, TCRBV13S3, TCRBV6S1P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2P1, TCRBV7S2A1N4T,
6841	19994	33403	1.43	2.0E-63	U86059.1	NT	Homo sapiens MIST mRNA, partial cds
6887	20039	33448	0.72	2.0E-63	AB032398.1	NT	Homo sapiens MIST mRNA, partial cds
6887	20039	33449	0.72	2.0E-63	AB032398.1	NT	Homo sapiens MIST mRNA, partial cds
7222	20086	33502	1.72	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56334), mRNA
7222	20086	33503	1.72	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56334), mRNA
7857	21007	34517	0.98	2.0E-63	AB046834.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
8730	21810	35346	4.29	2.0E-63	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8254	22331	35879	0.94	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
8254	22331	35880	0.94	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
10143	23181	38778	1.2	2.0E-63	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10985	24064	37689	10.73	2.0E-63	AF07945.1	EST_HUMAN	2018005.61 Soares, fetal lung, MbHL19W Homo sapiens cDNA clone IMAGE:302385 3' similar to gb:X17208.405 RIBOSOMAL PROTEIN S4 (HUMAN);
11012	24091	37728	2.89	2.0E-63	AF099810.1	NT	Homo sapiens neuridin III-alpha gene, partial cds
11012	24091	37729	2.89	2.0E-63	AF099810.1	NT	Homo sapiens neuridin III-alpha gene, partial cds
12360	25929	31769	3.64	2.0E-63	11418185	NT	Homo sapiens acetylase 2, mitochondrial (AC02), mRNA
13101	25717	31840	1.19	2.0E-63	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
13172	25760	31830	1.37	2.0E-63	AB011399.1	NT	Homo sapiens gene for AIF-6, complete cds
786	13965	27016	1.55	1.0E-63	7106446	NT	Mus musculus wingless-related MMTV integration site 3A (Wn13a), mRNA
786	13965	27017	1.66	1.0E-63	7106446	NT	Mus musculus wingless-related MMTV integration site 3A (Wn13a), mRNA
4461	17601	30579	3.31	1.0E-63	FO8485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zd11
4461	17601	30580	3.31	1.0E-63	FO8485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zd11
5468	18688	31647	1.73	1.0E-63	AL271738.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
6860	19078	32388	1.38	1.0E-63	AW582568.1	EST_HUMAN	QVO-ST0215-060100-083-b09 ST0215 Homo sapiens cDNA
6521	18688	33058	0.68	1.0E-63	AW451850.1	EST_HUMAN	UJ-H-B13-ali-h-02-0-UJ-st NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068763 3'
6521	18688	33059	0.68	1.0E-63	AW451850.1	EST_HUMAN	UJ-H-B13-ali-h-02-0-UJ-st NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068763 3'
8668	21748		2.97	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
13121	26047		8.88	1.0E-63	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6089	19270	32598	0.61	8.0E-64	AW401433.1	EST_HUMAN	UJ-H-BKO-head-b-09-0-UJ-1 NCI CGAP_38 Homo sapiens cDNA clone IMAGE:3053153 5'
8051	21134	34654	5.57	8.0E-64	AW478188.1	EST_HUMAN	Im50507.x1 NCI CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2161526 3'
1071	14237		3.46	8.0E-64	BE280793.1	EST_HUMAN	601156232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
6268	19442	32781	3.61	8.0E-64	BE885755.1	EST_HUMAN	601508968F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5'
12187	25146		2.79	8.0E-64	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12243	26185		3.68	8.0E-64	TF0651.1	EST_HUMAN	Y088802.11 Striatogene lung (#937210) Homo sapiens cDNA clone IMAGE:79179 5'
3618	16782		0.74	7.0E-64	BE394321.1	EST_HUMAN	801311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4854	17987	30874	6.34	7.0E-64	14507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1), mRNA
4854	17987	30876	6.34	7.0E-64	14507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1), mRNA
10239	23274	36865	2.92	7.0E-64	Y07648.1	NT	Homo sapiens EWS, gwi22, m22 and bami22 genes
1760	14809	28002	6.73	6.0E-64	AB51992.1	EST_HUMAN	wb51e07.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-
1760	14809	28003	5.73	6.0E-64	AB51992.1	EST_HUMAN	GLUCURONIDASE PRECURSOR (HUMAN);

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3182	16367	29372	3.91	6.0E-64	AW026445.1	EST_HUMAN	wf13603.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529438 3'
3182	16367	29373	3.91	6.0E-64	AW026445.1	EST_HUMAN	wf13603.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529438 3'
6739	18932	32230	2.85	6.0E-64	V18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6739	18932	32231	2.95	6.0E-64	V18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6758	18950	32252	6.32	6.0E-64	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
5767	18959	32260	0.66	6.0E-64	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
5851	19137	32452	0.74	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALCR), mRNA
5851	19137	32453	0.74	6.0E-64	11422189	NT	Homo sapiens calcitonin receptor (CALCR), mRNA
7384	20462	33929	2.54	6.0E-64	1182878	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
7384	20462	33928	2.54	6.0E-64	1182878	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
9528	22593	36164	7.39	6.0E-64	11923878	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
9709	22766	36326	1.75	6.0E-64	AF274733.1	NT	Homo sapiens acetyl-CoA synthetase (L0058902), mRNA
9919	22939	36548	2.16	6.0E-64	S76475.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
11008	24087	37724	4.88	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
11008	24087	37725	4.88	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
11269	18367	29372	1.73	6.0E-64	AW026445.1	EST_HUMAN	wf13603.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529438 3'
11269	18367	29373	1.73	6.0E-64	AW026445.1	EST_HUMAN	wf13603.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529438 3'
12400	25280	32081	2.98	6.0E-64	11628198	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
843	14021	27078	4.18	5.0E-64	AF231819.1	NT	Homo sapiens chromosome 21 unknown mRNA
843	14021	27079	4.18	5.0E-64	AF231819.1	NT	Homo sapiens chromosome 21 unknown mRNA
1369	14524	27698	1.02	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1453	14608	27695	1.16	5.0E-64	L40833.1	NT	Homo sapiens phospholipase-related protein (PLMRP) gene, complete cds
1453	14608	27696	1.15	5.0E-64	L40833.1	NT	Homo sapiens phospholipase-related protein (PLMRP) gene, complete cds
1749	14898	27694	1.54	5.0E-64	U89368.1	NT	Homo sapiens phospholipase-related protein (PLMRP) gene, complete cds
2887	14663	27746	4.43	5.0E-64	7882205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2887	14663	27747	4.43	5.0E-64	7882205	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
4068	17224	30231	7.25	5.0E-64	AF071433.1	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
8000	21050	34663	0.71	4.0E-64	BE794637.1	EST_HUMAN	Homo sapiens putative transcription factor CRE3 (CRE3) mRNA, partial cds
11051	24128	37763	2.34	4.0E-64	AW613783.1	EST_HUMAN	RC3-ST0197-120200-015-403 ST0197 Homo sapiens cDNA
11051	24128	37764	2.34	4.0E-64	AW613783.1	EST_HUMAN	RC3-ST0197-120200-015-403 ST0197 Homo sapiens cDNA
2271	15404	28532	8.77	3.0E-64	C18856	EST_HUMAN	RC3-ST0197-120200-015-403 ST0197 Homo sapiens cDNA
3327	18500	29618	0.82	3.0E-64	BE794637.1	EST_HUMAN	C18856 Human placenta cDNA (Tfubliet) Homo sapiens cDNA clone GEN:568602 5'
3529	18694	29704	1.83	3.0E-64	AV711714.1	EST_HUMAN	601589565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'

## Table 4

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10184	23221	36819	0.5	2.0E-64	T06397.1	EST_HUMAN	EST04286 Fetal brain, Striatum (cat#36206) Homo sapiens cDNA clone HFBDS88
10184	23221	36819	0.5	2.0E-64	T06397.1	EST_HUMAN	EST04286 Fetal brain, Striatum (cat#36206) Homo sapiens cDNA clone HFBDS88
11000	24079	37714	2.21	2.0E-64	BF528114.1	EST_HUMAN	602042882F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4180556 5'
11306	24371	38012	4.28	2.0E-64	A1922911.1	EST_HUMAN	W81B08.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2452211 3'
11306	24371	38013	4.28	2.0E-64	A1922911.1	EST_HUMAN	W81B08.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2452211 3'
11609	24667	38244	1.46	2.0E-64	AW894773.1	EST_HUMAN	PM2-SIN0018-220300-002-e12 SIN0018 Homo sapiens cDNA
12804	25537		3.59	2.0E-64	H55162.1	EST_HUMAN	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
268	13487	26517	1.39	1.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1820	14669	28091	24.22	1.0E-64	A1929419.1	EST_HUMAN	au80c01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519136 3' similar to gb:U21698 cde1 PROTHYMOSIN ALPMA (HUMAN);contains element MSR1 repetitive element;
3076	18232	28274	0.8	1.0E-64	4507334	NT	Homo sapiens synaptobrevin 1 (SYN1), mRNA
3601	16765	28781	5.47	1.0E-64	AF198179.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel alpha
3675	16838	28848	1.14	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3675	16838	28848	1.14	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
4008	17165	30173	0.88	1.0E-64	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
10269	23304	36901	1.17	1.0E-64	AA042675.1	EST_HUMAN	ZK5308.at Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:485667 3'
12291	25216		4.59	1.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2350	19481	28913	1.87	9.0E-65	X892111.1	NT	H. sapiens DNA for endogenous retroviral like element
2350	19481	28913	1.87	9.0E-65	X892111.1	NT	H. sapiens DNA for endogenous retroviral like element
2380	15481	28614	1.87	9.0E-65	X892111.1	NT	H. sapiens DNA for endogenous retroviral like element
11826	24815		19.08	8.0E-65	BF330876.1	EST_HUMAN	QV4-BT0257-081189-017-e03 BT0257 Homo sapiens cDNA
11799	24769	38486	7.24	8.0E-65	A1929244.1	EST_HUMAN	au58h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to SW:RL21_HUMAN P48778 60S RIBOSOMAL PROTEIN L21.;
10358	23383	37004	2.18	7.0E-65	BE081633.1	EST_HUMAN	QV2-BT0635-240400-182-c02 BT0635 Homo sapiens cDNA
12095	26075	38782	2.88	7.0E-65	ZZ13178.1	EST_HUMAN	HSAAEAWO TEST1, Human adult Testis tissue Homo sapiens cDNA clone test346 (b)
1081	14247	27304	0.81	6.0E-65	AV721896.1	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTBZC08 6'
1974	15117		20.04	6.0E-65	AA550929.1	EST_HUMAN	rib6d10.s1 NCI_CGAP_P111 Homo sapiens cDNA clone IMAGE:989379 similar to gb:K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN);
6889	18657	33247	0.8	6.0E-65	AA550882.1	EST_HUMAN	rib37007.s1 NCI_CGAP_P15 Homo sapiens cDNA clone IMAGE:954617
8946	22024	35564	2.45	6.0E-65	AW083582.1	EST_HUMAN	xc07509.x1 NCI_CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583545 3' similar to TR:Q83306 Q83306 LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORFS, contains L1.b2 L1 repetitive element.;
8213	22291	35933	4.63	6.0E-65	AA421878.1	EST_HUMAN	zw53b08.s1 Soares_totl_tetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:773747 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9213	22291	35834	4.63	6.0E-65	AA421878.1	EST_HUMAN	zms3p08.s1 Scores: total_fetus_Nb2HF8_gw Homo sapiens cDNA clone IMAGE:773747 3'
9276	22351	35902	0.62	6.0E-65	AJ08314.1	EST_HUMAN	pf18h05.x1 NCI CGAP_Bn25 Homo sapiens cDNA clone IMAGE:1750425 3'
9276	22351	35903	0.62	6.0E-65	AJ08314.1	EST_HUMAN	pf18h05.x1 NCI CGAP_Bn25 Homo sapiens cDNA clone IMAGE:1750425 3'
11113	24185	37817	3.58	6.0E-65	BE667818.1	EST_HUMAN	6013-0485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682677 6'
11284	24350	38001	4.18	6.0E-65	BF340825.1	EST_HUMAN	602037721F1 NCI CGAP_Bn84 Homo sapiens cDNA clone IMAGE:4165877 5'
11788	24778	38476	1.86	6.0E-65	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
648	13833	28859	1.89	5.0E-65	AF084504.1	NT	Homo sapiens KE03 protein mRNA, partial cds
1384	14539	27613	1.92	5.0E-65	7691851	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1384	14539	27614	1.92	5.0E-65	7691851	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2223	15357	28487	1.07	6.0E-65	AB033788.1	NT	Homo sapiens HPAD-cdony10 mRNA for peptidylarginine deiminase type I, complete cds
3328	16501	28518	1.79	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3328	16501	28520	1.79	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
7006	20144	33583	1.38	5.0E-65	4504608	NT	Homo sapiens interferon-related developmental regulator 1 (IFRD1), mRNA
10684	23718	37324	1.36	5.0E-65	AF009868.1	NT	Multiple sclerosis associated retrovirus polyprotein (p24) mRNA, partial cds
188	13421	28452	1.3	4.0E-65	AL120419.1	EST_HUMAN	DKFZp781G108.t1 759 (synonym: ham2) Homo sapiens cDNA clone DKFZp781G108 5'
764	13946	26991	1.23	4.0E-65	AI286493.1	EST_HUMAN	qnt46a01.x1 Scores: placenta_8to9weeks_2NbhHPctg9w Homo sapiens cDNA clone IMAGE:1891800 3'
764	13946	26992	1.23	4.0E-65	AI286493.1	EST_HUMAN	qnt46a01.x1 Scores: placenta_8to9weeks_2NbhHPctg9w Homo sapiens cDNA clone IMAGE:1891800 3'
1103	14268	27326	1.44	4.0E-65	4828735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1515	14668	27751	24.91	4.0E-65	4506659	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
2413	16543	28670	1.02	4.0E-65	BE221489.1	EST_HUMAN	nu25ed4.x1 NCI CGAP_Ma15 Homo sapiens cDNA clone IMAGE:3171102 3'
2413	16543	28671	1.02	4.0E-65	BE221489.1	EST_HUMAN	nu25ed4.x1 NCI CGAP_Ma15 Homo sapiens cDNA clone IMAGE:3171102 3'
6284	18457	32808	4.96	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6284	18457	32807	4.96	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
7233	20317	33760	0.66	4.0E-65	AY008372.1	NT	Homo sapiens oxygen binding protein-related protein 3 (ORP3) mRNA, complete cds
7268	20349	33801	6.04	4.0E-65	M19878.1	NT	Homo sapiens clathrin 27 gene, exons 10 and 11, and L1 and Alu repeats
7368	20447	33910	2.3	4.0E-65	11645780	NT	Homo sapiens hypodermal protein FLJ22087 (FLJ22087), mRNA
7721	20785	34273	0.65	4.0E-65	U403721	NT	Human 3'5' cyclic nucleotide phosphodiesterase (HSPDETC3A) mRNA, partial cds
7721	20785	34274	0.65	4.0E-65	U403721	NT	Human 3'5' cyclic nucleotide phosphodiesterase (HSPDETC3A) mRNA, partial cds
7883	21043	34565	0.67	4.0E-65	U886681	NT	Human MAP kinase kinase 6 (MKK6) mRNA, complete cds
8025	21108	34624	0.83	4.0E-65	5453765	NT	Homo sapiens nel (chicken)-like 2 (NEL2), mRNA
8025	21108	34625	0.83	4.0E-65	5453765	NT	Homo sapiens nel (chicken)-like 2 (NEL2), mRNA
8346	22422	35975	0.88	4.0E-65	11429127	NT	Homo sapiens janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA



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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10808	23841		2.12	4.0E-65	AL277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
11360	24422	38078	1.92	4.0E-65	AF118646.1	NT	Homo sapiens PR01474 mRNA, complete cds
12028	14288	27328	2.03	4.0E-65	4828735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
13201	13421	26452	1.26	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108.t1.761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108.5'
100	13336	28364	0.66	3.0E-65	5031676	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1260	15980		18.37	3.0E-65	X78932.1	NT	H. sapiens HZF9 mRNA for zinc finger protein
1689	14741	27822	4.52	3.0E-65	4504628	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1689	16014	28122	1.31	3.0E-65	AI000892.1	EST_HUMAN	0x2303.a1 Sources, tests, NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
3350	16522	28538	1.24	3.0E-65	4504850	NT	MSR1 repetitive element ;
3816	16975	28978	1.08	3.0E-65	AI000862.1	EST_HUMAN	0x2303.a1 Sources, tests, NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element
4773	17908	30891	1.38	3.0E-65	6912385	NT	MSR1 repetitive element ;
10274	23309	36905	1.61	3.0E-65	BE787386.1	EST_HUMAN	Homo sapiens rab8 GTPase activating protein (GAP and centrosome-associated) (GAPCEN), mRNA
11872	23900	37823	8.41	3.0E-65	AA430008.1	EST_HUMAN	601478686F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882405 5'
3490	16597	28670	7.53	2.0E-65	BF680294.1	EST_HUMAN	2w65406.t1 Sources, tests, NHT Homo sapiens cDNA clone IMAGE:781042 5'
6568	19825		3.73	2.0E-65	BE263373.1	EST_HUMAN	602156082F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295968 5'
7282	20365	33918	20.62	2.0E-65	BF576922.1	EST_HUMAN	601180883F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534741 5'
8046	22125	35668	1.2	2.0E-65	AK024433.1	NT	602134359F1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:4289295 5'
8046	22125	35669	1.2	2.0E-65	AK024433.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
10892	23976	37608	1.46	2.0E-65	11418247	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
12241	25184		6.27	2.0E-65	AA307804.1	EST_HUMAN	Homo sapiens SWISNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCD3), mRNA
12748	28906		3.99	2.0E-65	BT246038.1	EST_HUMAN	EST178755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus
93	13328		0.69	1.0E-65	BF126544.1	EST_HUMAN	601864033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073768 5'
582	13745	28770	1.43	1.0E-65	7857495	NT	601763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4028501 5'
1889	16033	28141	3.31	1.0E-65	AB026988.1	NT	Homo sapiens putative Rab5 GTP/GTP exchange factor homologue (RABEX6), mRNA
2088	15238	28360	1.48	1.0E-65	AB040548.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3458	16523	28645	0.8	1.0E-65	BE466681.1	EST_HUMAN	Homo sapiens mRNA for KIAA1513 protein, partial cds
4105	17259	30259	2.07	1.0E-65	4504082	NT	h224609.x1 NC1 CGAP_GCB Homo sapiens cDNA clone IMAGE:3208888 3'
							Homo sapiens glyceral 4 (GPC4) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4109	17256	30260	2.07	1.0E-65	4504082	NT	Homo sapiens glycylalanine 4 (GPC4) mRNA
4323	17466	30461	2.53	1.0E-65	AW028340.1	EST_HUMAN	w08a08.x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2543152.3'
4323	17466	30452	2.53	1.0E-65	AW028340.1	EST_HUMAN	w08a08.x1 NCI_CGAP_Ges4 Homo sapiens cDNA clone IMAGE:2543152.3'
5143	18266	31235	1.57	1.0E-65	AW238282.1	EST_HUMAN	x02c01.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2740896.3'
5143	18266	31236	1.57	1.0E-65	AW238282.1	EST_HUMAN	x02c01.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2740896.3'
5400	18602	31572	0.86	1.0E-65	BE089509.1	EST_HUMAN	QV0-BT0702-170400-184-109 BT0702 Homo sapiens cDNA
5400	18602	31573	0.86	1.0E-65	BE089509.1	EST_HUMAN	QV0-BT0702-170400-184-109 BT0702 Homo sapiens cDNA
5594	18789	31837	0.58	1.0E-65	AI243738.1	EST_HUMAN	qb88h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854109.3' similar to TRC07823
8448	21528	35057	1.5	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-112 ST0298 Homo sapiens cDNA
8448	21528	35058	1.5	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-112 ST0298 Homo sapiens cDNA
8475	21556	35088	0.60	1.0E-65	BE732116.1	EST_HUMAN	601566124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012.5'
8475	21556	35089	0.60	1.0E-65	BE732116.1	EST_HUMAN	601566124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012.5'
8514	21585	35129	2.04	1.0E-65	AU141295.1	EST_HUMAN	AU141295 THYR01 Homo sapiens cDNA clone THYR01000356.5'
8514	21585	35130	2.04	1.0E-65	AU141295.1	EST_HUMAN	AU141295 THYR01 Homo sapiens cDNA clone THYR01000356.5'
9041	22120	35862	1.01	1.0E-65	BF698707.1	EST_HUMAN	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313.5'
9222	22300	35843	1.33	1.0E-65	AU128040.1	EST_HUMAN	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714.5'
9222	22300	35844	1.33	1.0E-65	AU128040.1	EST_HUMAN	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714.5'
9231	22309		2.78	1.0E-65	11431884	NT	Homo sapiens Insulin1,4,5-triphosphatase receptor, type 1 (TTPR1) mRNA
9309	22365	35837	0.55	1.0E-65	7662227	NT	Homo sapiens KIAA0656 gene product (KIAA0656), mRNA
9678	22840	36210	5.5	1.0E-65	AI191716.1	EST_HUMAN	q056a02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1739450.3' similar to gb:M29581 ZINC
10089	23127	36730	1.32	1.0E-65	AU153793.1	EST_HUMAN	FINGER PROTEIN 8 (HUMAN), contains MIER18, MIER19 repetitive element;
10509	23544	37155	0.65	1.0E-65	AA089593.1	EST_HUMAN	275604.1 Soares_pituitary_gland_N3HPG Homo sapiens cDNA clone NT2RP3004016.3'
10786	23829	37453	1.23	1.0E-65	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
10886	23869	37598	1.91	1.0E-65	MA261671	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11016	24095	37734	9.39	1.0E-65	4508860	NT	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
11395	24456	38118	1.9	1.0E-65	BF698707.1	EST_HUMAN	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313.5'
11486	24545	38217	2.58	1.0E-65	AB210471.1	EST_HUMAN	ts78a08.x1 NCI_CGAP_GOS Homo sapiens cDNA clone IMAGE:2231710.3' similar to gb:L15533_mai
12892	25217		2.38	1.0E-65	11418041	NT	PANCRAEATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
12891	25276	32078	3.77	1.0E-66	11418322	NT	Homo sapiens TNF-inducible protein CG12.1 (CG12.1), mRNA
73	13310	28334	0.9	8.0E-66	AL160311.1	NT	Homo sapiens cadherin EGF_LAG seven-pass G-type receptor 1 (CELSR1), mRNA
73	13310	28335	0.9	8.0E-66	AL160311.1	NT	Novel human gene mapping to chromosome 22

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1385	14540	27615	1.53	9.0E-08	5031980	NT	Homo sapiens 28S proteasome-associated pad1 homolog (POH1) mRNA
1385	14540	27618	1.53	9.0E-08	5031980	NT	Homo sapiens 28S proteasome-associated pad1 homolog (POH1) mRNA
1813	14656		6.83	9.0E-08	M87289.1	NT	Human transposon-like element, partial
4007	17184	30171	0.06	9.0E-08	MT2393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4007	17184	30172	0.66	9.0E-08	MT2393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
11628	24708		1.6	7.0E-08	BE064410.1	EST_HUMAN	RC4-BT031-141198-014-H06 BT0311 Homo sapiens cDNA
4485	17625	30605	1.16	6.0E-08	AB224653.1	EST_HUMAN	wn57n07.x1 NC1_CGAP_Lut18 Homo sapiens cDNA clone IMAGE:2449597.3 similar to WIP:F15G9.4A
4485	17625	30606	1.16	6.0E-08	AB224653.1	EST_HUMAN	wn57n07.x1 NC1_CGAP_Lut18 Homo sapiens cDNA clone IMAGE:2449597.3 similar to WIP:F15G9.4A
4485	17625	30607	1.16	6.0E-08	AB224653.1	EST_HUMAN	wn57n07.x1 NC1_CGAP_Lut18 Homo sapiens cDNA clone IMAGE:2449597.3 similar to WIP:F15G9.4A
8628	21708	38162	0.46	6.0E-08	BE178683.1	EST_HUMAN	PM2-HT0604-030300-001-b06 HT0604 Homo sapiens cDNA
11427	24498	38162	3.22	6.0E-08	X69181.1	NT	H sapiens mRNA for ribosomal protein L31
1398	14552	27627	2.45	6.0E-08	BE064410.1	EST_HUMAN	RC4-BT031-141198-014-H06 BT0311 Homo sapiens cDNA
8484	22551	38113	8.4	6.0E-08	11420557	NT	Homo sapiens thyroid hormone receptor binding protein (AIB3) mRNA
813	13992	27046	1.8	4.0E-08	6878816	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1) mRNA
1775	14824	28018	0.87	4.0E-08	AW697798.1	EST_HUMAN	RC1-NN0063-100500-022-802 NN0063 Homo sapiens cDNA
2355	15488	28818	5.3	4.0E-08	X69211.1	NT	H sapiens DNA for endogenous retroviral like element
2543	15698		3.15	4.0E-08	AJ223394.1	NT	Homo sapiens germ-line DNA upstream of dkkappa locus
4905	18035		5.02	4.0E-08	8835487	NT	Human endogenous retrovirus, complete genome
5668	18882	32147	3.57	4.0E-08	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent) methyltetrahydrofolate
6861	19051	32368	0.87	4.0E-08	AW639116.1	EST_HUMAN	QV1-DT0069-110200-057-g10 DT0069 Homo sapiens cDNA
6995	18514	31506	4.81	4.0E-08	AW665473.1	EST_HUMAN	EST377548 MAGE repeat sequences, MAGI Homo sapiens cDNA
7281	20364	33817	7.88	4.0E-08	U78188.1	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
7807	18882	32147	0.83	4.0E-08	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent) methyltetrahydrofolate
8269	21361	34887	6.14	4.0E-08	11421638	NT	cyclohydrolase (MTHFD2) mRNA
8327	21409	34938	0.7	4.0E-08	X67147.1	NT	Homo sapiens hypoxanthine phosphoribosyl transferase 1 (HGPRT) mRNA
10886	23980	37612	1.49	4.0E-08	BE507453.1	EST_HUMAN	UI-H-BW1-arr1-a-10-Q-UJ.61 NC1_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070747.3
11650	24739	38430	1.63	4.0E-08	AB2023216.1	NT	Homo sapiens mRNA for KIAA0898 protein, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1458	14611	27692	14.03	3.0E-66	4502098	NT	Homo sapiens soluble carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1458	14611	27693	14.83	3.0E-66	4502098	NT	Homo sapiens soluble carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
2039	15180	28290	1.04	3.0E-66	N55323.1	EST_HUMAN	Y27012.1 Soares, multiple, sclerosis, 2NBHMSIP Homo sapiens cDNA clone IMAGE:284328 5' similar to SW:H2B1, TIGCA P35069 HISTONE H2B.1/H2B.2, [2] PIR:B56812;
2039	15180	28291	1.04	3.0E-66	N55323.1	EST_HUMAN	Y27012.1 Soares, multiple, sclerosis, 2NBHMSIP Homo sapiens cDNA clone IMAGE:284328 5' similar to SW:H2B1, TIGCA P35069 HISTONE H2B.1/H2B.2, [2] PIR:B56812;
2039	15180	28292	1.04	3.0E-66	N55323.1	EST_HUMAN	Y27012.1 Soares, multiple, sclerosis, 2NBHMSIP Homo sapiens cDNA clone IMAGE:284328 5' similar to SW:H2B1, TIGCA P35069 HISTONE H2B.1/H2B.2, [2] PIR:B56812;
2772	15867	28997	3.44	3.0E-66	11141980	NT	Homo sapiens TGF-beta1-induced transcription factor 2 (TGIF2), mRNA
3168	16361	29367	7.29	3.0E-66	7662223	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
5583	18778	31823	0.85	3.0E-66	AB020699.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
5583	18889	32180	0.65	3.0E-66	M13976.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
6893	18081	32391	1.72	3.0E-66	11417948	NT	Homo sapiens NIPSNAP, C, elegans, homolog 1 (NIPSNAP1), mRNA
6893	18081	32392	1.72	3.0E-66	11417948	NT	Homo sapiens NIPSNAP, C, elegans, homolog 1 (NIPSNAP1), mRNA
7585	20657	34134	1.74	3.0E-66	X92211.1	NT	H. sapiens germline immunoglobulin heavy chain, variable region, (15-1)
8726	22780	36361	0.59	3.0E-66	AK024433.1	NT	Homo sapiens mRNA for FLJ00046 protein, partial cds
9920	22960	36547	0.52	3.0E-66	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10278	23313	36911	0.86	3.0E-66	7019480	NT	Homo sapiens proteoglycan beta 1 (PCDH-beta1), mRNA
10741	23774	37386	0.95	3.0E-66	AF155859.1	NT	Homo sapiens myocardin cofactor biosynthesis protein E (MCBP-E) mRNA, complete cds
11800	24780	38487	4.55	3.0E-66	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
52	13291	26304	1.48	2.0E-66	7657334	NT	Homo sapiens Mtschapanin1-related kinase (MINK), mRNA
52	13291	26305	1.48	2.0E-66	7657334	NT	Homo sapiens Mtschapanin1-related kinase (MINK), mRNA
435	13235	26235	0.87	2.0E-66	4505624	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog) like (ORCSL) mRNA, and translated products
435	13235	26236	0.87	2.0E-66	4505624	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog) like (ORCSL) mRNA, and translated products
1873	15017	28128	2.02	2.0E-66	AL169301.2	NT	Homo sapiens chromosome 21 segment HS21C101
3039	16216	29236	1.07	2.0E-66	X65659.1	NT	H. sapiens pseudogene for the low affinity IL-6 receptor
3609	16773	29768	0.85	2.0E-66	8923280	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3881	17021	30019	0.78	2.0E-66	AL117233.1	NT	Novel human gene mapping to chromosome 1
4176	17328	30317	0.69	2.0E-66	AF108359.1	NT	Homo sapiens sodium/calcium exchanger isoform Ncaex3 (NCX1) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4778	17813	30888	13.88	2.0E-68	AJ133287.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
4778	17813	30889	13.88	2.0E-68	AJ133287.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
5637	18123	32436	0.82	2.0E-68	AW988854.1	EST_HUMAN	EST1380330 MAGE resequences, MAGE-Homo sapiens cDNA
5637	18123	32437	0.82	2.0E-68	AW988854.1	EST_HUMAN	EST1380330 MAGE resequences, MAGE-Homo sapiens cDNA
6048	22127	35671	3.57	2.0E-68	N45480.1	EST_HUMAN	Y56062.1 Soares, multiple sclerosis, 2NblMSP Homo sapiens cDNA clone IMAGE:277826 5'
12637	26147		2.84	2.0E-68		NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
1717	14867		1.14	1.0E-68	BE887173.1	EST_HUMAN	60150376F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:380931 5'
2859	16136	28153	1.47	1.0E-68	AV1717817.1	EST_HUMAN	AV1717817 DC8 Homo sapiens cDNA clone DCBADC07 5'
2859	16136	28154	1.47	1.0E-68	AV1717817.1	EST_HUMAN	AV1717817 DC8 Homo sapiens cDNA clone DCBADC07 5'
4504	16136	28153	4.18	1.0E-68	AV1717817.1	EST_HUMAN	AV1717817 DC8 Homo sapiens cDNA clone DCBADC07 5'
4504	16136	28154	4.18	1.0E-68	AV1717817.1	EST_HUMAN	AV1717817 DC8 Homo sapiens cDNA clone DCBADC07 5'
5497	18698	31712	5.97	1.0E-68	BE767308.1	EST_HUMAN	60215289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294151 5'
5900	19059	32402	0.67	1.0E-68	BE765332.1	EST_HUMAN	IL2N10701-280700-118-E04 NT0101 Homo sapiens cDNA
5900	19059	32403	0.67	1.0E-68	BE765332.1	EST_HUMAN	IL2N10701-280700-118-E04 NT0101 Homo sapiens cDNA
7076	20131	33548	1.53	1.0E-68	BF328623.1	EST_HUMAN	RC6-BN0193-010800-034-G08 BN0193 Homo sapiens cDNA
8662	21732	35271	1.2	1.0E-68	AA68858.1	EST_HUMAN	aa60904.s1 NCI_CGAP_G081 Homo sapiens cDNA clone IMAGE:827262 3'
9826	22861	38250	0.64	1.0E-68	AA018826.1	EST_HUMAN	z657e12.1 Soares refina N2b4HR Homo sapiens cDNA clone IMAGE:363118 5'
10582	23617	37223	0.83	1.0E-68	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
10582	23617	37224	0.83	1.0E-68	AV748749.1	EST_HUMAN	AV748749 NPC Homo sapiens cDNA clone NPCBVA05 5'
11185	24254	37889	2.24	1.0E-68	AF111497.2	NT	Homo sapiens Jun dimerization protein gene, partial cds, cfos gene, complete cds, and unknown gene
12398	25278		1.02	8.0E-67		NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
6034	18162		0.81	8.0E-67	M78158.1	EST_HUMAN	EST101750 Subtracted Hippocampus, Striatum (cell. #536205) Homo sapiens cDNA clone HHQPN31 similar to L1 repetitive element
391	13628	28665	1.53	7.0E-67	AW162232.1	EST_HUMAN	6u76d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:U63710.4 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1413	14567	27841	2.86	7.0E-67	AA383416.1	EST_HUMAN	EST196812 Testis 1 Homo sapiens cDNA 5' and similar to C. elegans hypothetical protein, cosmid ZK353
1585	14737	27817	1.39	7.0E-67	W85947.1	EST_HUMAN	Z156b05.1 Soares, fetal liver, spleen, 1NF.LS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
1585	14737	27818	1.39	7.0E-67	W85947.1	EST_HUMAN	Z156b05.1 Soares, fetal liver, spleen, 1NF.LS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
2089	15228	28350	1.94	7.0E-67		NT	Homo sapiens Inositol 1,3,4-trisphosphate 5/6 kinase (ITPK1), mRNA
2089	15228	28351	1.94	7.0E-67		NT	Homo sapiens Inositol 1,3,4-trisphosphate 5/6 kinase (ITPK1), mRNA
2871	13628	28665	1.36	7.0E-67	AW162232.1	EST_HUMAN	6u76d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:U63710.4 ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6205	19380	32730	0.88	7.0E-67	10190696	NT	Homo sapiens zinc finger protein 304 (ZNF304), mRNA
6400	19569	32830	1.67	7.0E-67	11426572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6400	19569	32831	1.67	7.0E-67	11426572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
6863	20015	33425	1.12	7.0E-67	4886084	NT	Homo sapiens ATPase, H <sup>+</sup> transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116D) (ATP6N1A), mRNA
7809	20864	34358	0.89	7.0E-67	11418212	NT	Homo sapiens mitochondrial carrier family protein (LOC56872), mRNA
7809	20864	34359	0.89	7.0E-67	11418212	NT	Homo sapiens mitochondrial carrier family protein (LOC56872), mRNA
8266	21340	34857	0.52	7.0E-67	4826889	NT	Homo sapiens mitochondrial carrier family protein (LOC56872), mRNA
8518	21699	35134	0.7	7.0E-67	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2), mRNA
9132	22211	35758	0.66	7.0E-67	10835044	NT	Homo sapiens retinaldehyde dehydrogenase 2 (RALDH2), mRNA
11565	24620	38650	2.42	7.0E-67	11434678	NT	Homo sapiens fucosyltransferase 8 (alpha (1,6) fucosyltransferase) (FUT8), mRNA
11973	24938	38629	2.02	7.0E-67	11430460	NT	Human cytochrome oxidase subunit VIa (COX6A1P) pseudogene, complete cds
12168	25131	38630	4.05	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12168	25131	38630	4.05	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12684	25441	32053	1.92	7.0E-67	AB011388.1	NT	Homo sapiens gene for AIF-6, complete cds
13106	25721		1.74	7.0E-67	11421527	NT	Homo sapiens calcium channel, voltage-dependent, alpha 2/delta subunit 1 (CACNA2D1), mRNA
573	13765	26788	1.09	6.0E-67	X69868.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
818	13997	27051	2.4	6.0E-67	Z17227.1	NT	Homo sapiens PMP89 gene, exons 3, 4, 5, 6 & 7
1302	14458	27524	1.07	6.0E-67	Y14320.1	NT	Homo sapiens retinoblastoma 1 (including osteosarcoma) (RB1), mRNA
3237	16411	28426	1.39	6.0E-67		NT	Homo sapiens Synapsin III (SYN3), mRNA, and translated products
3524	16889	28698	1.32	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3), mRNA, and translated products
3524	16889	28699	1.32	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3), mRNA, and translated products
4243	17389	30375	0.92	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4243	17389	30376	0.92	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4827	17860	30947	2.22	6.0E-67	7657020	NT	Homo sapiens DKFZ434P211 protein (DKFZ434P211), mRNA
4827	17860	30948	2.22	6.0E-67	7657020	NT	Homo sapiens DKFZ434P211 protein (DKFZ434P211), mRNA
13224	13765	28788	2.74	6.0E-67	X69868.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
3238	16467	28483	2.28	5.0E-67	AF000690.1	NT	Homo sapiens T cell receptor beta locus, TCRCBV3S42 to TCRCBV12S2 region
11230	24239		2.17	5.0E-67	BE010036.1	EST_HUMAN	PM3-BN0176-100400-001-004 BN0176 Homo sapiens cDNA
1359	14514	27593	1.13	4.0E-67	RC081819.1	EST_HUMAN	pm2d11.11 Soares adult brain N2641B55V Homo sapiens cDNA clone IMAGE:167253.5
8211	21293	34813	0.8	4.0E-67	A1733032.1	EST_HUMAN	Q06730 ZINC FINGER PROTEIN 334.1
8576	21657		1.48	4.0E-67	BF357321.1	EST_HUMAN	RC0-HT0934-150900-028-c03 HT0934 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11318	24381		1.76	4.0E-67	AA714294.1	EST_HUMAN	nm06a01.s1 NCL CGAP SS1 Homo sapiens cDNA clone IMAGE:1238472.3 similar to TR:O10385 O10385
2874	13835	26862	2.03	3.0E-67	AA333788.1	EST_HUMAN	PRO-POL-DUTPASE POLYPROTEIN;
3542	16707	29716	2.05	3.0E-67	BE06410.1	EST_HUMAN	EST37953 Embryo, 8 week Homo sapiens cDNA 5' end
4816	17949	30934	2.98	3.0E-67	AW869159.1	EST_HUMAN	RC4-BT0371-147189-011-h08 BT0371 Homo sapiens cDNA
4846	17978		1.38	3.0E-67	AL163279.2	NT	MIR3-SND066-040500-008-401 SND066 Homo sapiens cDNA
8376	21458	34980	1.37	3.0E-67	BF198088.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
11537	24583		15.42	3.0E-67	AA927874.1	EST_HUMAN	h81105.x1 NCL CGAP_Kid1 Homo sapiens cDNA clone IMAGE:3134913.3 similar to SW:RHOP_MOUSE
183	13416	26445	0.59	2.0E-67	BE348354.1	EST_HUMAN	Q61085 GTP-RHO BINDING PROTEIN 1;
888	14044	27109	6.29	2.0E-67	AW816405.1	EST_HUMAN	Q61807.s1 Scars_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541365.3
1129	14284		2.48	2.0E-67	AF187480.1	NT	nm18b07.s1 Scars_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3183136.3 similar to WP:F23H11.9
1833	15076	28179	1.23	2.0E-67	BE303037.1	EST_HUMAN	h81105.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183136.3 similar to WP:F23H11.9
1933	15076	28180	1.23	2.0E-67	BE303037.1	EST_HUMAN	CE08617;
2458	16885	28713	1.18	2.0E-67	AF308561.1	NT	QV4-ST0234-187189-037-105 ST0234 Homo sapiens cDNA
2502	15629	28749	1.37	2.0E-67	AF187480.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4
3557	16722	29737	3.76	2.0E-67	AA625755.1	EST_HUMAN	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4
4109	17283	30263	3.13	2.0E-67	AL163300.2	NT	ba72905.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976.5 similar to TR:O84892 O84892
6187	18372	32723	0.83	2.0E-67	AL049784.1	NT	KIAA0798 PROTEIN;
6252	18428	32722	4.85	2.0E-67	BF240738.1	EST_HUMAN	ba72905.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2905976.5 similar to TR:O84892 O84892
6425	18593	32858	1.74	2.0E-67	AB051783.1	NT	KIAA0798 PROTEIN;
6425	18593	32859	1.74	2.0E-67	AB051783.1	NT	KIAA0798 PROTEIN;
6779	18834	33330	0.64	2.0E-67	AL120542.1	EST_HUMAN	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
8755	21834	35374	1.09	2.0E-67	AA334608.1	EST_HUMAN	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
8755	21834	35375	1.09	2.0E-67	AA334608.1	EST_HUMAN	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
9187	22275	35812	1.31	2.0E-67	AW602635.1	EST_HUMAN	DKFZp781A229.1 781 (synonym: hairy2) Homo sapiens cDNA clone DKFZp781A229.5
9187	22275	35813	1.31	2.0E-67	AW602635.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin
9766	22763	36332	0.95	2.0E-67	AV731333.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
9910	22890	36536	0.89	2.0E-67	AW283624.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
10848	23881	37501	0.53	2.0E-67	AA828629.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
11141	24213	37840	1.75	2.0E-67	BF685788.1	EST_HUMAN	AV731333 HTF Homo sapiens cDNA clone HTFARD03.5
							U1-H-BI2-ahn-e-10-04U1.s1 NCL CGAP_Suba Homo sapiens cDNA clone IMAGE:2727283.3
							on6607.s1 Scars_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1563541.3
							602140470F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301705.5

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11310	26230		2.66	2.0E-67	11438448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
11604	24662	38240	2.05	2.0E-67	BE285714.1	EST_HUMAN	601176762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
11743	23928	37655	2.44	2.0E-67	BF377169.1	EST_HUMAN	PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA
12527	25988	31770	2.47	2.0E-67	11418169	NT	Homo sapiens thyroid autoantigen T0KD (Ku antigen) (G22P1), mRNA
263	13482	26514	2.37	1.0E-67	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
728	13908	26948	0.86	1.0E-67	AA702794.1	EST_HUMAN	290B04.s1 Soares [total liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:448016 3'
4833	17896	30934	0.73	1.0E-67	BF439247.1	EST_HUMAN	mb6108.xt Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3'
11298	24337		1.47	1.0E-67	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
12105	25085		3.44	9.0E-68	4506090	NT	Homo sapiens mitogen-activated protein kinase 6 (MAPK6), mRNA
2245	15378	28506	8.3	8.0E-68	BE870732.1	EST_HUMAN	60144858F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3973	17130	30133	6.73	8.0E-68	AA209436.1	EST_HUMAN	zq82h10.t1 Striatogeno hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648163 5' similar to
3973	17130	30133	6.73	8.0E-68	AA209436.1	EST_HUMAN	SW_SAV_SULAC_Q07690 SAV PROTEIN.1
3973	17130	30134	6.76	8.0E-68	AA209436.1	EST_HUMAN	zq82h10.t1 Striatogeno hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648163 5' similar to
8253	21375	34895	0.56	7.0E-68	AA10505.1	EST_HUMAN	SW_SAV_SULAC_Q07690 SAV PROTEIN.1
10668	23700	37310	6.43	6.0E-68	11422086	NT	mb89603.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2312860 3'
11417	24478	38143	1.31	6.0E-68	AF133901.1	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
12868	26579		2.84	6.0E-68	BE612564.1	EST_HUMAN	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
13165	25756	31927	1.45	6.0E-68	BF310676.1	EST_HUMAN	601452067F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3855761 5'
825	15688	27069	2	5.0E-68	AF231619.1	NT	601894635F2 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4124144 5'
825	15688	27069	2	5.0E-68	AF231619.1	NT	Homo sapiens chromosome 21 unknown mRNA
842	14020	27076	4.83	5.0E-68	AF231619.1	NT	Homo sapiens chromosome 21 unknown mRNA
842	14020	27077	4.93	5.0E-68	AF231619.1	NT	Homo sapiens chromosome 21 unknown mRNA
3216	16380	29401	2.88	5.0E-68	AB037862.1	NT	Homo sapiens chromosome 21 unknown mRNA
4287	17440		0.64	5.0E-68	4826967	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
2594	15719	28836	1	4.0E-68	11421388	NT	Homo sapiens ribitolbiosynthesis-binding protein 2 (RIBBP2), mRNA
2594	15719	28837	1	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
5090	18216		7.11	4.0E-68	P04406	SWISSPROT	Homo sapiens transcription factor NRF (NRF), mRNA
6085	19267	32696	0.69	4.0E-68	AF157063.1	NT	GLYERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
6912	20227	33658	6.03	4.0E-68	11055891	NT	Homo sapiens seryl carboxypeptidase 1 precursor protein (HSCP1), mRNA
6912	20227	33659	6.03	4.0E-68	11055891	NT	Homo sapiens seryl carboxypeptidase 1 precursor protein (HSCP1), mRNA
7859	20913	34418	0.84	4.0E-68	7661683	NT	Homo sapiens DKFZP586L0724 protein (DKFZP586L0724), mRNA



Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8240	22317	35859	5.59	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
8240	22317	35860	5.59	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
8380	22453	36018	3.17	4.0E-68	AB040918.1	NT	Homo sapiens mRNA for KIAA1483 protein, partial cds
11251	24320	37860	1.64	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11251	24320	37861	1.64	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
11434	24495	38161	1.72	4.0E-68	AB040944.1	NT	Homo sapiens mRNA for KIAA1616 protein, partial cds
12728	25485	32028	1.17	4.0E-68	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2) mRNA
3751	16912	28916	3.54	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
9656	21089		3.5	3.0E-68	A1342322.1	EST_HUMAN	q38n02.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1850291 3' similar to contains THR_L2 THR repetitive element:
10720	23733	37339	1.35	3.0E-68	F28184.1	EST_HUMAN	HSPD18178 HM3 Homo sapiens cDNA clone s3000023D09
13111	26902		2.83	3.0E-68	AW639485.1	EST_HUMAN	QV1-DT0072-310200-036-108 DT0072 Homo sapiens cDNA
2925	18474		29.7	2.0E-68	D00622.1	NT	Citriculcus longicaudatus mRNA for EF-1 alpha, complete cds
4135	17288	30283	0.79	2.0E-68	BE875768.1	EST_HUMAN	7F16R2.x1 NC1 CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3294747 3' similar to TR:080828 O80828
4803	17938	30929	2.33	2.0E-68	AB008631.1	NT	HYPOTHETICAL 88.8 KD PROTEIN:
7016	20161		9.21	2.0E-68	R45088.1	EST_HUMAN	Homo sapiens gene for actin receptor type IIb, complete cds
7209	20074	33486	3.81	2.0E-68	BF036316.1	EST_HUMAN	y38g04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34898 3'
7527	20800	34074	0.88	2.0E-68	BF036316.1	EST_HUMAN	601488614F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862034 5'
9150	22228	35772	0.56	2.0E-68	CO5859	SWISSPROT	IL3-CT0534-180800-273-A01 CT0534 Homo sapiens cDNA
11521	24577	38255	1.49	2.0E-68	BF330594.1	EST_HUMAN	FORMIN 4 (LIMB DEFORMITY PROTEIN)
12285	26170		1.59	2.0E-68	BE897376.1	EST_HUMAN	QV0-BT0074-130999-014-g04 BT0074 Homo sapiens cDNA
13182	28778		1.32	2.0E-68	AW016803.1	EST_HUMAN	60143736F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922192 5'
81	13316	28344	0.53	1.0E-68	4506222	NT	U1-H-B10-aam-b-05-0-U1.s1 NC1 CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709824 3'
307	13523	28557	18.49	1.0E-68	AW816405.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1) mRNA
2326	15458	28590	1.24	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2326	15458	28591	1.24	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
4117	17271	30273	0.93	1.0E-68	BE286932.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
5140	18283	31231	0.71	1.0E-68	AA897343.1	EST_HUMAN	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:1460618 3'
5437	18637	31616	1.92	1.0E-68	7682349	NT	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:1460618 3'
7653	20808	34412	0.75	1.0E-68	11436716	NT	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:1460618 3'
10385	23420	37027	0.45	1.0E-68		NT	Homo sapiens cell recognition molecule Casp2 (KIA0869) mRNA
11089	24163	37799	2.16	1.0E-68	11419429	NT	Homo sapiens centrin/SMO-specific protease (SENP1) mRNA
					11418869	NT	Homo sapiens similar to actin nucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
						NT	Homo sapiens phosphodiesterase 7B (PDE7B) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11089	24163	37800	2.16	1.0E-68	U50318.1	NT	Homo sapiens phospholipase 7B (PDE7B), mRNA
11142	24214	37841	2.81	1.0E-68	U76416.1	NT	Homo sapiens MIF2 suppressor (HSMIT3), mRNA, complete cds
11468	24527	38200	1.7	1.0E-68	U143327.7	NT	Homo sapiens myosin IC (MYOTC), mRNA
11580	24534	38313	2.83	1.0E-68	U50318.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11580	24534	38314	2.83	1.0E-68	U50318.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11683	24848	38653	1.81	1.0E-68	U141843.1	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
11683	24848	38654	1.81	1.0E-68	U141843.1	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
12849	13316	28344	2.53	1.0E-68	U50318.1	NT	Homo sapiens meninoma (disrupted in balanced translocation) 1 (MNI), mRNA
13100	26082	31661	3.05	1.0E-68	U143048.0	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13164	25755	28260	1.88	1.0E-68	U141821.3	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARF-GAP1), mRNA
22	13260	28260	2.42	8.0E-68	U50318.1	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF), mRNA
22	13260	28261	2.42	8.0E-68	U50318.1	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF), mRNA
1063	14218	27275	0.89	8.0E-68	U50318.1	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
1053	14218	27276	0.89	8.0E-68	U50318.1	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1), mRNA
4246	17392	30380	0.6	8.0E-68	U50318.1	NT	Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF), mRNA
4266	17411	30397	0.89	8.0E-68	U50318.1	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kd) (GLCLR), mRNA
11128	24200		7.86	8.0E-68	U117241.1	EST_HUMAN	U117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000968 5'
3473	18640		1.28	8.0E-68	U1237744.1	NT	Homo sapiens RIBBIK gene (partial), exon 12
6482	18648	33011	4.44	7.0E-69	U86812	NT	Homo sapiens actin-related protein 3-beta (ARPB3BETA), mRNA
8047	21130	34849	1.85	8.0E-69	U192764.1	EST_HUMAN	q652h01.x1 Soares, fetal lung, NBHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to
8047	21130	34850	1.85	8.0E-69	U192764.1	EST_HUMAN	q652h01.x1 Soares, fetal lung, NBHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to
9174	22252	35785	1.05	5.0E-69	U625033.1	EST_HUMAN	cd60a03.s1 NCJ CGAP CGBT Homo sapiens cDNA clone IMAGE:2437125 3'
633	13728		1.18	4.0E-69	U187360.1	EST_HUMAN	wn28h11.x1 NCJ CGAP U14 Homo sapiens cDNA clone IMAGE:2437125 3'
6861	25612	32378	1.33	4.0E-69	U6681033.1	EST_HUMAN	601344705F NIH MGCC 8 Homo sapiens cDNA clone IMAGE:3677641 5'
6866	19162	32467	4.82	4.0E-69	U764979.1	EST_HUMAN	wn57b08.x1 NCJ CGAP Kdt1 Homo sapiens cDNA clone IMAGE:2384819 3' similar to TR:O55137
6784	18920	33315	3.17	4.0E-69	U557732	NT	O55137 ACYL-CoA THIOESTERASE, .
6764	18920	33316	3.17	4.0E-69	U557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2), mRNA
9115	22184	35739	0.55	4.0E-69	U118634.1	EST_HUMAN	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2), mRNA
397	13634	26672	5.24	3.0E-69	U625033.1	EST_HUMAN	U118634 HEMBA1 Homo sapiens cDNA clone HEMBA1006283 5'
627	13612	26634	2.78	3.0E-69	U7221712.1	NT	601110371F1 NIH MGCC 16 Homo sapiens cDNA clone IMAGE:3351352 5'
							Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1586	14738		1.12	3.0E-69	T80514.1	EST_HUMAN	y08a02.1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:24880 5' similar to SP-A48936
2449	15677		2.18	3.0E-69	57289210	NT	A48936 SPECIFIC ILL-EGF REPEAT-CONTAINING FIBROPELIN-LIKE PROTEIN - SEA URCHIN :
5357	16483	38823	1.37	3.0E-69	11478185	NT	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA
7629	20602	34076	0.76	3.0E-69	AF095103.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7578	20650	34128	1.74	3.0E-69	U52351.1	NT	Homo sapiens arm-repeat protein NRPAP1/pneurogranin (CTNND2) mRNA, partial cds
7724	20788	34277	8.4	3.0E-69	AF268073.1	NT	Homo sapiens TRA-F6-binding protein T6BP mRNA, complete cds
8667	21848	35180	1.33	3.0E-69	AW138848.1	EST_HUMAN	U1-H-B1-ecw-9-01-0-U1.ct NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2715840 3'
8997	22048		0.74	3.0E-69	AA376399.1	EST_HUMAN	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
9613	22686	36236	1.74	3.0E-69	X13223.1	NT	H. sapiens mRNA for N-acetylglucosaminide-(beta 1-4)-galactosyltransferase
							Human mRNA for calcium-binding protein in macrophages (MCP-14) macrophage migration inhibitory factor (MIF)-related protein
9733	22798	36372	3.15	3.0E-69	X06233.1	NT	Homo sapiens SEC10 (S. cerevisiae)-like 1 (SEC10L1) mRNA
10034	23072	36672	0.56	3.0E-69	57300361	NT	Homo sapiens ribosomal protein S15a (RPS15A) mRNA
10877	23662	37590	2.74	3.0E-69	11432120	NT	Homo sapiens ribosomal protein S18
11080	24155		7.68	3.0E-69	AA376399.1	EST_HUMAN	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
12112	25082	38785	1.77	3.0E-69	AB011541.1	NT	Homo sapiens mRNA for NIEGF8, partial cds
12112	25092	38786	1.77	3.0E-69	AB011541.1	NT	Homo sapiens mRNA for NIEGF8, partial cds
12305	25223		3.1	3.0E-69	11418157	NT	Homo sapiens HGC6.2 protein (HGC6.2) mRNA
131	13612	26851	1.09	2.0E-69	AF160232.1	NT	Homo sapiens KIAA0653 protein gene, complete cds, and alpha1b protein gene, partial cds
131	13612	26852	1.09	2.0E-69	AF160232.1	NT	Homo sapiens KIAA0653 protein gene, complete cds, and alpha1b protein gene, partial cds
417	13612	26851	4.42	2.0E-69	AF160232.1	NT	Homo sapiens KIAA0653 protein gene, complete cds, and alpha1b protein gene, partial cds
417	13612	26852	4.42	2.0E-69	AF160232.1	NT	Homo sapiens KIAA0653 protein gene, complete cds, and alpha1b protein gene, partial cds
1834	15077	28181	1.79	2.0E-69	BE257857.1	EST_HUMAN	Homo sapiens KIAA0553 protein gene, complete cds, and alpha1b protein gene, partial cds
2806	16084		4.14	2.0E-69	AA431167.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'
8761	21830	35368	0.55	2.0E-69	AA114270.1	EST_HUMAN	zw77g02.1 Scores_tadla_NH-TT Homo sapiens cDNA clone IMAGE:781662 5'
1080	14832		2.4	1.0E-69	BF330124.1	EST_HUMAN	zmi29g01.1 Stralagene parvovirus (#837203) Homo sapiens cDNA clone IMAGE:527088 5'
1739	14888	27880	0.83	1.0E-69	AF036768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
5137	18260		0.83	1.0E-69	BE409094.1	EST_HUMAN	601301284F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635781 5'
6176	18351	32697	0.83	1.0E-69	BE802501.1	EST_HUMAN	601675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3858532 5'
6175	18351	32698	0.83	1.0E-69	BE802501.1	EST_HUMAN	601675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3858532 5'
6738	18994	33285	4.36	1.0E-69	AW393989.1	EST_HUMAN	QVO-TT0010-031199-045-07 TT0010 Homo sapiens cDNA
6858	20271	33709	1.22	1.0E-69	7682263	NT	Homo sapiens KIAA0716 gene product (KIAA0716) mRNA

### Single Exon Probes Expressed in Placenta

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9857	22897	36480	0.53	7.0E-70	4857624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.BHD) (GLCLC) mRNA
10505	23540	37149	0.85	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
10505	23540	37150	0.85	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylase/N-sulfotransferase 4, complete cds
11329	24392	38039	1.77	7.0E-70	11429865	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant, spastin) (SPG4), mRNA
11329	24392	38040	1.77	7.0E-70	11429865	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant, spastin) (SPG4), mRNA
11897	24885	38683	2.37	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
11897	24885	38684	2.37	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
894	14070	27135	2.51	6.0E-70	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant, Alzheimer disease) (APP), mRNA
2205	15339	28486	2.29	6.0E-70	M30933.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4629	17765	30747	0.7	6.0E-70	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity deacetylase transporter (NADC3) mRNA, complete cds
2818	15066	28854	1.78	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2618	15066	28855	1.78	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
12247	25188		5	5.0E-70	BE166034.1	EST_HUMAN	MR3-1T0487-15-608 H1T0487 Homo sapiens cDNA
6894	20045	33454	1.03	4.0E-70	T06603.1	EST_HUMAN	EST05928 Fetal brain, Striatum (cat336206) Homo sapiens cDNA
6933	20248	33682	1.84	4.0E-70	AW793226.1	EST_HUMAN	CM4-UM0003-010300-105-608 UM0003 Homo sapiens cDNA
6933	20248	33683	1.84	4.0E-70	AW793226.1	EST_HUMAN	CM4-UM0003-010300-105-608 UM0003 Homo sapiens cDNA
1819	14771	27853	1.71	3.0E-70	BE071798.1	EST_HUMAN	RCB-BT0522-071299-011-612 BT0522 Homo sapiens cDNA
1819	14771	27854	1.71	3.0E-70	BE071798.1	EST_HUMAN	RCB-BT0522-071299-011-612 BT0522 Homo sapiens cDNA
6270	18389	31367	1.11	3.0E-70	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
5737	18930	32227	0.58	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
6737	18930	32228	0.59	3.0E-70	11430988	NT	Homo sapiens plakophilin 4 (PKP4), mRNA
6068	19248	32575	1	3.0E-70	AI831975.1	EST_HUMAN	WM80403.x1 NC1_CGAP_QL1 Homo sapiens cDNA clone IMAGE:238805 3'
6603	19669	33033	1.69	3.0E-70	BF68533.1	EST_HUMAN	602141681F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
6503	19669	33034	1.69	3.0E-70	BF68533.1	EST_HUMAN	602141681F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302806 5'
10314	23349	36956	0.82	3.0E-70	BE502373.1	EST_HUMAN	h281h02.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214419 3'
39	13277	28283	1.03	2.0E-70	AF012972.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
707	13890	28923	15.24	2.0E-70	N42161.1	EST_HUMAN	h07a10.1 Soares melanocyte 2bH-H1 Homo sapiens cDNA clone IMAGE:270522 5' similar to SW-620L RAT P29266 3'-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							W07a10.1 Scores melanocyte 2HbHM Homo sapiens cDNA clone IMAGE:270525 5' similar to SW:IDH1_RAT P29268 5-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
707	13680	26924	15.24	2.0E-70	N42161.1	EST_HUMAN	q55h101.x1 NC1_OGAP
723	13305	26947	1.85	2.0E-70	A1246893.1	EST_HUMAN	Homo sapiens hypophthalic protein FLJ20758 (FLJ20758). mRNA
1048	14212	27269	1.36	2.0E-70	3923369	NT	Homo sapiens KIAA0183 gene product (KIAA0183). mRNA
1211	14372	27432	2.16	2.0E-70	7691983	NT	Homo sapiens KIAA0183 gene product (KIAA0183). mRNA
1211	14372	27433	2.16	2.0E-70	7691983	NT	Homo sapiens KIAA0183 gene product (KIAA0183). mRNA
1441	14594	27693	1.23	2.0E-70	BE467311.1	EST_HUMAN	h264c12.x1 NC1_OGAP_L124 Homo sapiens cDNA clone IMAGE:3212788.3'
1686	14840	27924	1.07	2.0E-70	AA180063.1	EST_HUMAN	zpd5105.1 Stragene HeLa cell c3 837216 Homo sapiens cDNA clone IMAGE:512441 5' similar to TR:G1041293 G1041293 D2085.5 ;
1688	14840	27925	1.07	2.0E-70	AA180063.1	EST_HUMAN	TR:G1041293 G1041293 D2085.5 ;
1781	14830	28023	4.92	2.0E-70	AL163202.2	NT	TR:G1041293 G1041293 D2085.5 ;
2294	15525		9.42	2.0E-70	AA054010.1	EST_HUMAN	TR:G1041293 G1041293 D2085.5 ;
3923	17082	30078	0.71	2.0E-70	AL133207.2	NT	TR:G1041293 G1041293 D2085.5 ;
4160	17311	30307	6.88	2.0E-70	M69181.1	NT	TR:G1041293 G1041293 D2085.5 ;
5632	18826	31801	8.42	2.0E-70	X72662.1	NT	TR:G1041293 G1041293 D2085.5 ;
5632	18826	31802	8.42	2.0E-70	X72662.1	NT	TR:G1041293 G1041293 D2085.5 ;
6333	19504	32882	1.23	2.0E-70	AF310105.1	NT	TR:G1041293 G1041293 D2085.5 ;
6771	19926	33321	2.65	2.0E-70	D12625.1	NT	TR:G1041293 G1041293 D2085.5 ;
6806	19980	33362	10.35	2.0E-70	AF123074.1	NT	TR:G1041293 G1041293 D2085.5 ;
6806	19980	33363	10.35	2.0E-70	AF123074.1	NT	TR:G1041293 G1041293 D2085.5 ;
7136	18582	31477	1.5	2.0E-70		NT	TR:G1041293 G1041293 D2085.5 ;
8103	21185	34704	2.81	2.0E-70	M21741.1	NT	TR:G1041293 G1041293 D2085.5 ;
8417	21498	35030	0.66	2.0E-70		NT	TR:G1041293 G1041293 D2085.5 ;
8860	21639	36007	1.34	2.0E-70	H47659.1	EST_HUMAN	TR:G1041293 G1041293 D2085.5 ;
9370	22445	36007	1.14	2.0E-70		NT	TR:G1041293 G1041293 D2085.5 ;
10342	23377	36888	1.26	2.0E-70	AF123303.1	NT	TR:G1041293 G1041293 D2085.5 ;
11324	24387	38031	3.39	2.0E-70	8923420	NT	TR:G1041293 G1041293 D2085.5 ;
11324	24387	38032	3.39	2.0E-70	8923420	NT	TR:G1041293 G1041293 D2085.5 ;
11940	24628	38628	7.78	2.0E-70		NT	TR:G1041293 G1041293 D2085.5 ;
12602	25439	32060	2.42	2.0E-70	11430460	NT	TR:G1041293 G1041293 D2085.5 ;

### Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12682	25439	32051	2.42	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2) mRNA
3480	16647		3.72	1.0E-70	4507476	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutaminase-gamma-glutamyltransferase) (TGMS3) mRNA
9480	22637		0.84	1.0E-70	W65795.1	EST_HUMAN	ZB5605.1 Soares, fetal liver, spleen, TNF.LS, S1 Homo sapiens cDNA clone IMAGE:416024 5'
10003	23041		0.88	1.0E-70	AA44282.1	EST_HUMAN	ZB5603.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:757444 5'
11175	24244	37877	7.61	1.0E-70	AV73858.1	EST_HUMAN	AV38838 CB Homo sapiens cDNA clone CBLB6810 5'
6065	19247	32573	6.03	8.0E-71	AI143870.1	EST_HUMAN	q60401.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
6065	19247	32573	6.03	8.0E-71	AI143870.1	EST_HUMAN	O14045 PHOSPHOTRANSFERASE ;
6065	19247	32573	6.03	8.0E-71	AI143870.1	EST_HUMAN	q60401.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
6065	19247	32573	6.03	8.0E-71	AI143870.1	EST_HUMAN	O14045 PHOSPHOTRANSFERASE ;
7175	20308	33751	2.05	9.0E-71	AI654903.1	EST_HUMAN	wb52c05.x1 NCI, CGAP, G68 Homo sapiens cDNA clone IMAGE:2308288 3' similar to TR:P97213 P97213
11813	20308	33751	3.47	9.0E-71	AI654903.1	EST_HUMAN	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
9270	22346		2.88	8.0E-71	AA117451.1	EST_HUMAN	wb52c05.x1 NCI, CGAP, G68 Homo sapiens cDNA clone IMAGE:2308288 3' similar to TR:P97213 P97213
10828	23661	37484	0.63	8.0E-71	AW273920.1	EST_HUMAN	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
7633	20606	34081	7.86	7.0E-71	AA442230.1	EST_HUMAN	wb52c05.x1 NCI, CGAP, G68 Homo sapiens cDNA clone IMAGE:2308288 3' similar to TR:P97213 P97213
8877	21666	35491	1.34	7.0E-71	AA703457.1	EST_HUMAN	CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES. ;
11614	24065	38363	2.2	7.0E-71	AI163210.2	NT	z621d11.1 Stada gene neurophilin (H83723) Homo sapiens cDNA clone IMAGE:610101 5' similar to
2284	16416	28848	7.11	6.0E-71	AF056322.1	NT	TR:G1143061 G1143061 STRAIN XA34 POL. ;
4235	17382	30371	1.18	6.0E-71	AF056322.1	EST_HUMAN	KX24401.x1 Soares, NFI, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2814049 3' similar to TR:O54730
6002	18187	32666	1.59	5.0E-71	4502740	NT	O64730 TRANSPLANTABILITY ASSOCIATED PROTEIN 1 ;
6801	18986	33356	1.4	6.0E-71	11641408	NT	z601008.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:758076 5'
7060	20113	33828	0.94	5.0E-71	7662209	NT	z601008.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:758076 5'
7266	20378	33836	0.82	5.0E-71	11431590	NT	z601008.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:758076 5'
7678	20344	34225	1.79	5.0E-71	M38106.1	NT	z601008.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:758076 5'
7884	20336	34442	0.8	5.0E-71	11628445	NT	z601008.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:758076 5'
7912	20983	34471	20.85	5.0E-71	AF072810.1	NT	z601008.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:758076 5'
8720	21800	35335	0.66	5.0E-71	5453777	NT	z601008.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:758076 5'
8720	21800	35336	0.66	5.0E-71	5453777	NT	z601008.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:758076 5'
10116	23163		2.06	5.0E-71	X13497.1	NT	z601008.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:758076 5'
10476	23511		0.48	5.0E-71	U70969.1	NT	z601008.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:758076 5'

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10870	23955	37584	1.45	5.0E-71	5729900	NT	Homo sapiens IGF-II mRNA-binding protein 3 (KOC1), mRNA
10843	24025	37660	1.63	5.0E-71	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
10843	24025	37691	1.53	5.0E-71	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
11226	24295	37836	3.85	5.0E-71	11436614	NT	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide II, neutrophil-activating peptide-2) (PPBP), mRNA
11467	24528	38189	2.1	5.0E-71	11438069	NT	Homo sapiens similar to hypothetical protein FLJ20163 (H. sapiens) (LOC63325), mRNA
12558	25380		1.75	5.0E-71	11418039	NT	Homo sapiens RNA binding motif protein 9 (RBM9), mRNA
106	19342	26370	1.84	4.0E-71	4507692	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
360	13571	26601	31.91	4.0E-71	AF157826.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
360	13571	26602	31.91	4.0E-71	AF157826.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2951	16128	29141	1.67	4.0E-71	4508880	NT	Homo sapiens plasminogen (PLG) mRNA
4548	17686	30687	1.67	4.0E-71	AF058322.1	NT	Homo sapiens SP-100-HMG nuclear autoantigen (SP-100) mRNA, complete cds
5101	18229	31200	4.59	4.0E-71	7637602	NT	Homo sapiens putative heme-binding protein (SOL), mRNA
8223	21305		1.13	3.0E-71	AU135734.1	EST_HUMAN	AU135734 PLACE1 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5 repetitive element;
10931	24013	37646	3.92	3.0E-71	AA557683.1	EST_HUMAN	HLA510.1 NCI_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5 repetitive element;
1258	14416	27481	4.54	2.0E-71	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5435	18635	31614	7.23	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
5435	18635	31615	7.23	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
7107	18334	31489	0.71	2.0E-71	AL042438.1	EST_HUMAN	DKFZP434D1721.1 434 (synonym: hla3) Homo sapiens cDNA clone DKFZP434D1721 5'
8207	22285	35828	0.5	2.0E-71	BF195588.1	EST_HUMAN	7n85c11.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3571221 3' similar to TRQ82165 Q82165 PUTATIVE FOUR REPEAT ION CHANNEL ;
10813	23846	37467	2.12	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10813	23846	37468	2.12	2.0E-71	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10833	24015	37847	4.37	2.0E-71	BE018472.1	EST_HUMAN	bb81a06.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW-R23B_HUMAN PB472Z LUV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG B ;
11860	24848	38545	1.46	2.0E-71	BF149173.1	EST_HUMAN	Tm1022 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA similar to gi 6598861
11860	24848	38546	1.46	2.0E-71	BF149173.1	EST_HUMAN	Tm1022 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA similar to gi 6598861
11882	24670	38567	2.05	2.0E-71	R55628.1	EST_HUMAN	y77c11.t1 Soares breast 2NB1Bst1 Homo sapiens cDNA clone IMAGE:154772 5'
12318	26231		4.88	2.0E-71	T85488.1	EST_HUMAN	y643609.1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:120520 5'



### Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
665	13941	28868	1.55	1.0E-71	AF077927.1	EST_HUMAN	cy15603.s1 Scars, senescent, fibroblasts, NBHSF Homo sapiens cDNA clone IMAGE:1665916 3 similar to contains LOR1, b2 LOR1 repetitive element;
684	14137	27198	1.38	1.0E-71	U70628.1	NT	Homo sapiens neuronal cell death-related protein (LOC51616), mRNA
1124	14289	27344	13.07	1.0E-71	AF28860.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1371	14626	27600	11.13	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230), mRNA, complete cds
2147	15283	28408	1.52	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2147	15283	28409	1.52	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2757	16814	28982	6.09	1.0E-71	U763753.1	NT	Homo sapiens hairyenhancer-of-epil related with YRPV motif-like (HEVL), mRNA
3550	16764	29769	1.66	1.0E-71	AF119855.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3685	16848	28855	6.57	1.0E-71	AF246218.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3685	16848	28856	6.57	1.0E-71	AF246218.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3685	16848	28856	6.57	1.0E-71	AF246218.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3736	16899	28902	0.9	1.0E-71	BE122850.1	EST_HUMAN	clone 02_15 5' similar to Homo sapiens chromosome 19
3736	16899	28902	0.9	1.0E-71	BE122850.1	EST_HUMAN	clone 02_15 5' similar to Homo sapiens chromosome 19
3736	16899	28902	0.9	1.0E-71	BE122850.1	EST_HUMAN	clone 02_15 5' similar to Homo sapiens chromosome 19
3835	16895	28987	2.2	1.0E-71	AF218904.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 19
4593	17730	30712	2.13	1.0E-71	D28476.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 19
6881	20033	33443	1.46	1.0E-71	U1428182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homodog)-like 2 (GCNEL2), mRNA
7235	20319	33762	1.49	1.0E-71	AB011331.1	NT	Homo sapiens mRNA for KIAA0359 protein, partial cds
7464	20539	34013	12.52	1.0E-71	U80753.1	NT	Homo sapiens CAGL70 mRNA, partial cds
8340	21421	34946	0.82	1.0E-71	AF105267.1	NT	Homo sapiens glycyl-6 (GPC6) mRNA, complete cds
8382	21443	34965	2.21	1.0E-71	U14283430	NT	Homo sapiens myomesin (M-protein) 2 (16SHD) (MYOM2), mRNA
8841	21721	35257	4.23	1.0E-71	8822811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10988), mRNA
8841	21721	35258	4.23	1.0E-71	8822811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10988), mRNA
9429	22503	38069	0.88	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10988), mRNA
10211	23247	38637	6.22	1.0E-71	AV007643.1	NT	CSNK2A1 (casein kinase II (CKII)) subunit alpha flumatin, Genomic, 18862 nt
10211	23247	38637	6.22	1.0E-71	AV007643.1	NT	CSNK2A1 (casein kinase II (CKII)) subunit alpha flumatin, Genomic, 18862 nt
10273	23308	37411	0.97	1.0E-71	U1453142	NT	Homo sapiens cytochrome c oxidase subunit VII-related protein gene, complete cds
10759	23792	37411	0.97	1.0E-71	U1453142	NT	Homo sapiens cytochrome c oxidase subunit VII-related protein gene, complete cds
11024	24103	37824	2.49	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSJAC3 5'
11121	24183	37824	3.31	1.0E-71	U1418903	NT	AV761217 MDS Homo sapiens cDNA clone MDSJAC3 5'
11413	24474	38138	3.2	1.0E-71	U1417191	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
11413	24474	38139	3.2	1.0E-71	U1417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
12709	25471	38139	10.17	1.0E-71	AB011399.1	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
12709	25471	38139	10.17	1.0E-71	AB011399.1	NT	Homo sapiens gene for Af-3, complete cds

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
420	13615	26654	0.77	9.0E-72	A1857635.1	EST_HUMAN	W65903.x1 NCL CGAP. Lutr8 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705
420	13615	26655	0.77	9.0E-72	A1857635.1	EST_HUMAN	HYPOTHETICAL 38.6 KD PROTEIN. ; contains Alu repetitive element:
6237	19412	32760	0.86	8.0E-72	BF033732.1	EST_HUMAN	W65903.x1 NCL CGAP. Lutr8 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705
4228	17375	30361	1.75	7.0E-72	4501866	NT	HYPOTHETICAL 38.6 KD PROTEIN. ; contains Alu repetitive element:
4228	17375	30362	1.75	7.0E-72	4501866	NT	601459747F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862431 3'
4228	17375	30363	1.75	7.0E-72	4501866	NT	Homo sapiens acolinase 2, mitochondrial (ACQ2), nuclear gene encoding mitochondrial protein, mRNA
4228	17375	30363	1.75	7.0E-72	4501866	NT	Homo sapiens acolinase 2, mitochondrial (ACQ2), nuclear gene encoding mitochondrial protein, mRNA
7274	20357	33811	3	7.0E-72	S41694.1	NT	Homo sapiens acolinase 2, mitochondrial (ACQ2), nuclear gene encoding mitochondrial protein, mRNA
12857	25659		1.53	7.0E-72	F26286.1	EST_HUMAN	(pseudogene) PTMAP2-prothymosin alpha [human, Genomic, 1192 nt, segment 2 of 3]
8578	21659		6.7	6.0E-72	AL163246.2	NT	HSPD13670 Hm3 Homo sapiens cDNA clone 3400051G02
64	13302	26324	1.19	5.0E-72	BF333707.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
64	13302	26324	1.19	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-611 CS0010 Homo sapiens cDNA
65	13302	26324	3.1	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-611 CS0010 Homo sapiens cDNA
65	13302	26324	3.1	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-611 CS0010 Homo sapiens cDNA
1162	14326		2.31	5.0E-72	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
7089	20183	33607	1.62	5.0E-72	AU128584.1	EST_HUMAN	AU128584 NTZRP2 Homo sapiens cDNA clone NTZRP2003751 5'
8976	22055	36598	4.16	5.0E-72	AW161274.1	EST_HUMAN	bu8003.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782564 5' similar to
10166	23203	36797	0.71	5.0E-72	AV724832.1	EST_HUMAN	TR:O86785 O86785 HYPOTHETICAL 32.4 KD PROTEIN ; contains element MSR1 repetitive element ;
11519	24575	38252	2.96	5.0E-72	BF331571.1	EST_HUMAN	AV724832 HTB Homo sapiens cDNA clone HTBAKB01 5'
11519	24575	38253	2.96	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-005 BT0598 Homo sapiens cDNA
11945	24831	38633	1.55	5.0E-72	BE208545.1	EST_HUMAN	MR4-BT0598-010600-005-005 BT0598 Homo sapiens cDNA
11945	24831	38634	1.55	5.0E-72	BE208545.1	EST_HUMAN	MR4-BT0598-010600-005-005 BT0598 Homo sapiens cDNA
12390	25136		2.46	5.0E-72	BE826845.1	EST_HUMAN	bu0808.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823808 5'
4943	18073		0.91	4.0E-72	11034844	NT	bu0808.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823808 5'
5361	18776	31821	0.68	4.0E-72	AF170025.1	NT	QV1-BT0632-280800-342-a10 BT0632 Homo sapiens cDNA
6887	18945	33236	0.86	4.0E-72	T87947.1	EST_HUMAN	QV1-BT0632-280800-342-a10 BT0632 Homo sapiens cDNA
7567	20639	34115	3.26	4.0E-72	5728867	NT	Homo sapiens hypothetical protein clj1057820.2 (J1057820.2), mRNA
							Homo sapiens zinc finger protein ZFP-93 (ZFP93) mRNA, alternatively spliced, complete cds
							Y93601.r1 Soares fetal liver spleen 1NF5 Homo sapiens cDNA clone IMAGE:115752 5' similar to
							SP.A44282 A44282 RETROVIRUS-RELATED POL POLYPROTEIN - HUMAN ;
							Homo sapiens hcd domain and RLD 2 (HERC2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9887	23026	36818	0.87	4.0E-72	8923069	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20759), mRNA
10312	23347	36853	0.57	4.0E-72	11434344	NT	Homo sapiens SEC10 (S. cerevisiae)-like 1 (SEC10L), mRNA
10604	23638	37245	0.64	4.0E-72	AW839230.1	EST_HUMAN	Homo sapiens CDNA
10604	23638	37245	0.54	4.0E-72	AW839230.1	EST_HUMAN	RC3-LT0023-200100-012-d11 LT0023 Homo sapiens CDNA
							q167c02.x1 Soares_fetal_liver_spleen_TNFRSF_5r Homo sapiens cDNA IMAGE:1849730.3 similar to TRC14498 Q14498 SPLICING FACTOR; [1], contains Ali repetitive element;contains element L1 repetitive element;
10634	23688	37278	1.04	4.0E-72	AU248793.1	EST_HUMAN	paz3309.s1 NCI CGAP GCBB Homo sapiens cDNA clone IMAGE:814121.3 similar to SW:CPTR_FLAPR
11963	24618	38288	1.57	4.0E-72	AA465388.1	EST_HUMAN	P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR.; paz3309.s1 NCI CGAP GCBB Homo sapiens cDNA clone IMAGE:814121.3 similar to SW:CPTR_FLAPR
11963	24618	38299	1.57	4.0E-72	AA465388.1	EST_HUMAN	P49131 CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR.; paz3309.s1 NCI CGAP GCBB Homo sapiens cDNA clone IMAGE:814121.3 similar to SW:CPTR_FLAPR
11818	24807	38503	6.28	4.0E-72	HT942.1	EST_HUMAN	yv28ad3.r1 Soares fetal liver spleen TNFRSF5 Homo sapiens cDNA clone IMAGE:235084.5
11938	24824	38824	2.19	4.0E-72	T657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
11938	24824	38825	2.19	4.0E-72	T657057	NT	Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
11978	24961	38863	1.87	4.0E-72	T61910.1	EST_HUMAN	yv28ad09.s1 Soares fetal liver spleen TNFRSF5 Homo sapiens cDNA clone IMAGE:109949.3
12778	26521	32003	11.86	4.0E-72	AJ277548.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
21	13269	28259	0.7	3.0E-72	6031876	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF), mRNA
926	14101		1.48	3.0E-72	AA228823.1	EST_HUMAN	ab39406.at Soares_testis_NK1T Homo sapiens cDNA clone U310290.3
1180	14343	27398	6.32	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1180	14343	27398	6.32	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1220	14381	27440	3.88	3.0E-72	U80223.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1220	14381	27441	3.88	3.0E-72	U80223.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1548	14700	27778	1.16	3.0E-72	BE24261.1	EST_HUMAN	TCAAP1E1252 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project TCAA Homo sapiens cDNA clone TCAAP1252
3143	16319	28331	12.72	3.0E-72	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3362	16624	28539	2.7	3.0E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20586), mRNA
3927	17086	30082	2.51	3.0E-72	S7589.1	NT	TCR V delta 2-C alpha epsilon T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4687	17802	30789	3.17	3.0E-72	AF16782.1	NT	[human, precursor B-cell line REH, mRNA Partial, 21 nt]
4689	18019	31003	1.25	3.0E-72	AF16782.1	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
4689	18019	31004	1.25	3.0E-72	AF16782.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds
4689	18019	31004	1.25	3.0E-72	AF16782.1	NT	Homo sapiens protein methyltransferase (JBP1) mRNA, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5837	18831		1.12	3.0E-72	4759083	NT	Homo sapiens semaphorin W (SEMAW) mRNA
6101	19281	32613	1.84	3.0E-72	AF073387.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6101	19281	32814	1.94	3.0E-72	AF073387.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6295	19468	32822	4.53	3.0E-72	AB023004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6295	19468	32823	4.53	3.0E-72	AB023004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6747	19903	33286	4.1	3.0E-72	4826987	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
7768	20817	34307	2.01	3.0E-72	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8369	21450	34873	5.42	3.0E-72	6031882	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3) mRNA
10646	23680	37280	1.09	3.0E-72	X88289.1	NT	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds
12678	25453	32018	2.18	3.0E-72	AB011398.1	NT	Homo sapiens gene for AIF-6, complete cds
6078	10261	32560	1.38	2.0E-72	11428071	NT	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA
9297	22373	35923	0.84	2.0E-72	BF308580.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
9297	22373	35924	0.84	2.0E-72	BF308580.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
10978	24057	37691	5.46	2.0E-72	AA789277.1	EST_HUMAN	aj28609, at Soares, teste, NHT Homo sapiens cDNA clone 1391609 3' similar to gtxX02067 H. sapiens mRNA for TSL RNA pseudogene (HUMAN);
12772	26515	31989	3.39	2.0E-72	AF182714.1	NT	Rattus norvegicus putative phosphatidylcholine transferase translocator mRNA, complete cds
2137	15273	28394	8.14	1.0E-72	AA849236.1	EST_HUMAN	ai83402.at Soares, parathyroid tumor, NIH/PA Homo sapiens cDNA clone IMAGE:1387395 3'
6887	18075	32384	3.54	1.0E-72	7657676	NT	Homo sapiens vacuolar protein sorting 41 (yeast homolog) (VPS41), mRNA
6659	18947	33237	1.22	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6889	18947	33238	1.22	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6769	26832	33319	1.28	1.0E-72	AA761818.1	EST_HUMAN	Homo sapiens cDNA clone NPDAIE11 5'
7816	20870	34366	3.5	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
7816	20870	34367	3.5	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
9760	22830	36408	7.37	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SCG2 (SC2) mRNA, complete cds
8760	22830	36409	7.37	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SCG2 (SC2) mRNA, complete cds
1488	14641	27723	1.17	8.0E-73	AA737488.1	EST_HUMAN	MRO-CT0083-071099-002-h11 CT0083 Homo sapiens cDNA
6164	16940	32687	0.92	9.0E-73	11525983	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
11183	24262		24.49	8.0E-73	11424089	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
1063	14228	27285	0.73	8.0E-73	AA071755.1	EST_HUMAN	wa55c08.x1 NCI_CGAP_Bln25 Homo sapiens cDNA clone IMAGE:2601096 3' similar to TR:Q59050
5698	18892	32184	0.98	8.0E-73	4805798	NT	Q59050 HYPOTHETICAL PROTEIN MA1659, ; Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6702	19860	33250	6.26	8.0E-73	11428469	NT	Homo sapiens lyszyme homolog (LOC57151), mRNA
8287	21369	34890	2.1	8.0E-73	AF113129.1	NT	Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds
8953	22618	36188	4.35	8.0E-73	BE019300.1	EST_HUMAN	bb62a6.yt NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb-X04098, cdc1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb-M21495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOUSE).
8941	22980	36570	1.76	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
9941	22980	36571	1.76	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
10134	23172	36770	0.57	8.0E-73	X91940.1	NT	H. sapiens mRNA for WNT-85 protein
10834	23867	37490	0.47	8.0E-73	4607628	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNPT1) mRNA
12001	24986	38630	1.49	8.0E-73	AF084320.1	NT	Homo sapiens breifeldin A-inhibited guanine nucleotide-exchange protein 1 mRNA, complete cds
12698	25403	32044	1.2	8.0E-73	AB002359.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12842	25550	31938	4.65	8.0E-73	11418159	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (Q22P1), mRNA
1157	14321	27376	1.61	7.0E-73	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3373	16545	28559	0.7	7.0E-73	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5059	18187		1.29	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C008
162	13387		3.04	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
7323	20405	33887	3.42	6.0E-73	BE166374.1	EST_HUMAN	QV04HT0494-020300-137-403 HT0494 Homo sapiens cDNA
5368	18571	31439	2.05	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM4A1), mRNA
1811	16054	28165	1.34	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
1811	19054	28166	1.34	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
6837	19990	33398	0.73	3.0E-73	AA138403.1	EST_HUMAN	zn55e04.e1 Stratagene fetal retina 687202 Homo sapiens cDNA clone IMAGE:565950 3' similar to gb-Z23084_cdc1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HUMAN);
8958	22037	35578	0.73	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTG Homo sapiens cDNA clone HTCAAF071 5'
8958	22037	35579	0.73	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTG Homo sapiens cDNA clone HTCAAF071 5'
10927	24010		1.45	3.0E-73	X99650.1	NT	H. sapiens SH3GLP2 pseudogene, 5' end
11261	24330	37870	1.41	3.0E-73	BE111238.1	EST_HUMAN	RC6-H1T0878-280600-013-H10 HT0878 Homo sapiens cDNA
11261	24330	37871	1.41	3.0E-73	BE111238.1	EST_HUMAN	RC6-H1T0878-280600-013-H10 HT0878 Homo sapiens cDNA
11910	24897		1.82	3.0E-73	AB004040.1	EST_HUMAN	cu11d02.x1 Scierex_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1025555 5'
13118	26790		3.04	3.0E-73	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
13122	25732		2.05	3.0E-73	AW88081.1	EST_HUMAN	RC3-AN0006-270400-011-c04 NN0066 Homo sapiens cDNA
874	14030	27115	1.57	2.0E-73	AF139893.1	NT	Homo sapiens BAS31 (BAS31) mRNA, partial cds
2000	15141		0.67	2.0E-73	AW88081.1	EST_HUMAN	RC3-AN0006-270400-011-c04 NN0066 Homo sapiens cDNA
2371	15502		1.49	2.0E-73	U01317.1	NT	Human beta globin region on chromosome 11
3299	16423	28440	2.03	2.0E-73	4502592	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3640	16904	29816	0.68	2.0E-73	7669339	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3640	16904	29817	0.68	2.0E-73	7669339	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
4656	17693		1.31	2.0E-73	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
6667	16729	33106	0.58	2.0E-73	AF086824.1	NT	Mus musculus thylac-interacting citron kinase (Ctik) mRNA, complete cds
6567	19729	33107	0.59	2.0E-73	AF086824.1	NT	Mus musculus thylac-interacting citron kinase (Ctik) mRNA, complete cds
6610	16770	33160	5.48	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6839	16992	33400	1.87	2.0E-73	U1431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6839	16992	33401	1.87	2.0E-73	U1431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7884	21033	34546	1.01	2.0E-73	M94046.1	NT	Human peripheral myelin protein 22 mRNA, complete cds
8732	22767	36370	0.54	2.0E-73	AF198349.1	NT	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
8732	22767	36371	0.54	2.0E-73	AF198349.1	NT	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
10637	23671	37281	1.31	2.0E-73	U1431471	NT	Homo sapiens glutathione synthetase (GSS) mRNA
10716	23748	37365	1.38	2.0E-73	U1431471	NT	Homo sapiens superinilin (SVIL), transcript variant 1, mRNA
10716	23748	37366	1.38	2.0E-73	U1431471	NT	Homo sapiens superinilin (SVIL), transcript variant 1, mRNA
11309	24374	38017	2.91	2.0E-73	U1431471	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11309	24374	38018	2.91	2.0E-73	U1431471	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
11339	24402	38051	1.44	2.0E-73	AB029882.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
12599	15141		4.32	2.0E-73	AW898081.1	EST_HUMAN	Homo sapiens mRNA for KIAA1059 protein, partial cds
1824	14673	28068	3.52	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA, clone MAMMA1000490 5'
6490	19656	33018	1.19	1.0E-73	BE151283.1	EST_HUMAN	CM14HT0282-111189-042410 HT0282 Homo sapiens cDNA
6699	22748	36316	1.22	1.0E-73	AI147427.1	EST_HUMAN	qg61b07.r1 Soares, testis NHT Homo sapiens cDNA, clone IMAGE:1839837 5' similar to contains element
11736	28922	37647	3.74	1.0E-73	BE36577.1	EST_HUMAN	MER22 repetitive element
12045	26026	38731	1.34	8.0E-74	X77226.1	NT	80127607.F1 NIH_MGC_20 Homo sapiens cDNA, clone IMAGE:3617105 5'
12045	26026	38732	1.34	8.0E-74	X77226.1	NT	H. sapiens mRNA for TTRIA
769	19840	26985	4.83	8.0E-74		NT	H. sapiens mRNA for TTRIA
6036	19219	32641	1.73	8.0E-74	S83194.1	NT	Homo sapiens CDB9-like 4 (CDB9L4) mRNA
6036	19219	32642	1.73	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rat, brain, mRNA, 3429 nt]
2004	15144	28249	4.86	7.0E-74	AJ001689.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rat, brain, mRNA, 3429 nt]
3407	16577	29592	1.83	7.0E-74	AL163283.2	NT	Homo sapiens NKG2D gene, exon 10
6444	22560	36123	1.48	7.0E-74	BE967432.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
12841	25559	31895	4.73	7.0E-74	BE266305.1	EST_HUMAN	60164928.F1 NIH_MGC_73 Homo sapiens cDNA, clone IMAGE:3932997 5'
							60118182.F1 NIH_MGC_7 Homo sapiens cDNA, clone IMAGE:3535855 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1146	14311	27368	3.66	6.0E-74	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
1656	14809	27893	1.03	6.0E-74	AW293177.1	EST_HUMAN	h78g07.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2700838 3'
2380	15621	28849	15.52	6.0E-74	BE388280.1	EST_HUMAN	60128352.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3805453 5'
2390	15521	28650	16.52	6.0E-74	BE388280.1	EST_HUMAN	60128352.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3805453 5'
2927	16104	28118	0.87	6.0E-74	AW014039.1	EST_HUMAN	UH-B10-aah-h-03-0-J1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
2927	16104	28120	0.97	6.0E-74	AW014039.1	EST_HUMAN	UH-B10-aah-h-03-0-J1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
3805	16865	28968	1.22	6.0E-74	BE048846.1	EST_HUMAN	h54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
3805	16865	28969	1.22	6.0E-74	BE048846.1	EST_HUMAN	h54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
6481	16860	31695	3.48	6.0E-74	11056073	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
828	14103	27186	1.93	5.0E-74	AW020986.1	EST_HUMAN	dt17c09.y1 Morton Fetal Coclea Homo sapiens cDNA clone IMAGE:2483704 5'
2767	15882	31736	4.86	5.0E-74	AW362766.1	EST_HUMAN	PMO-CT0289-271099-001407 CT0289 Homo sapiens cDNA
6623	18720	31736	1.92	5.0E-74	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
5910	19099	32413	12.5	5.0E-74	X89070.1	NT	H. sapiens mRNA for TP-CR16 protein
5961	19147	32462	8.1	5.0E-74	4507866	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33ND) (VAPA) mRNA, and translated products
6030	19213	32533	2.94	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6030	19213	32534	2.94	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
7035	20171	33593	3.58	6.0E-74	7862263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
8226	21306	34828	2.33	5.0E-74	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
10973	24053	37698	1.67	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
10873	24053	37697	1.67	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
11090	24184	37801	1.36	5.0E-74	5729786	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
280	13507	28542	3.31	4.0E-74	DB7876.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
876	14031	27116	10.3	4.0E-74	AB028042.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
2018	15158	28282	3.07	4.0E-74	AB028198.1	NT	Homo sapiens DNA, DIEC1 to ORCTL4 gene region, section 1/2 (DIEC1, ORCTL3, ORCTL4 genes, complete cds)
2018	15158	28283	3.07	4.0E-74	AB028198.1	NT	Homo sapiens DNA, DIEC1 to ORCTL4 gene region, section 1/2 (DIEC1, ORCTL3, ORCTL4 genes, complete cds)
2134	15270	28380	8.96	4.0E-74	4506182	NT	Homo sapiens profilin (profilin, macropain) subunit, beta type, 1 (PSMB1) mRNA
2134	15270	28397	9.96	4.0E-74	4506182	NT	Homo sapiens profilin (profilin, macropain) subunit, beta type, 1 (PSMB1) mRNA
2201	15338	28463	1.32	4.0E-74	AB032994.1	NT	Homo sapiens mRNA for KIAA1169 protein, partial cds
2488	15625	28745	1.16	4.0E-74	AJ008976.1	NT	Homo sapiens PLP gene

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3160	16335	26346	6.22	4.0E-74	AL008976.1	NT	Homo sapiens PLP gene
3616	16780	26795	1.1	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4174	17324	30315	1.26	4.0E-74	AL163217.2	NT	Homo sapiens chromosome 21 segment HS21C047
4679	17814	30802	1.86	4.0E-74	7662183	NT	Homo sapiens KIA0569 gene product (KIA0569), mRNA
4735	17870	30854	1.07	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
5133	18256	31224	1.03	4.0E-74	AB040938.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
5185	18307	31271	1.12	4.0E-74	4504326	NT	Homo sapiens hydroxyethyl-Coenzyme A dehydrogenase(3-ketacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB), mRNA
6185	18307	31272	1.12	4.0E-74	4504326	NT	Homo sapiens hydroxyethyl-Coenzyme A dehydrogenase(3-ketacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB), mRNA
6747	21628		3.53	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Tyrosinase (tyrosinase) gene, similar to similar to ribosomal protein L37
8773	21652	36394	0.62	3.0E-74	5908912	NT	Homo sapiens actin-related protein 3-beta (ARPP3BETA), mRNA
9572	22714	36282	2.32	3.0E-74	M78984.1	EST_HUMAN	EST01132 Subtracted Hippocampus, Striatum (cat. #836205) Homo sapiens cDNA clone HICP91
10548	23681	37191	2.16	3.0E-74	AA601493.1	EST_HUMAN	nc017605.st1 NC1 CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100934.3
880	14153	27213	28.83	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
880	14153	27214	28.83	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1202	14364	27424	1.63	2.0E-74	AF02092.1	NT	Human endogenous retrovirus HERV-K-147D
1273	14430	27901	1.44	2.0E-74	AI050538.1	EST_HUMAN	w61e07.st1 NC1 CGAP_Luz8 Homo sapiens cDNA clone IMAGE:2647204.3 similar to SW:G366_HUMAN
1625	14777	27861	10.45	2.0E-74	4885198	NT	Q08379 GOLGIN-95, contains element MER22 repetitive element
1625	14777	27861	10.45	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblast leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1625	14777	27862	10.45	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblast leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
2668	15769	28905	2.18	2.0E-74	AI557230.1	EST_HUMAN	PT2.1_15_G11.1 Homo sapiens cDNA 3'
5118	18245	31210	2.52	2.0E-74	AL356592.1	NT	Novel human gene mapping to chromosome 22
5119	18245	31211	2.62	2.0E-74	AL356592.1	NT	Novel human gene mapping to chromosome 22
6619	25813	32419	1.86	2.0E-74	BE11134.1	EST_HUMAN	ROCHT0678-220500-011-C03 HT0678 Homo sapiens cDNA
6017	25816	32518	1.77	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6017	25816	32519	1.77	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6087	25816	32518	2.78	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
6087	25816	32519	2.78	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
7252	20335	33784	2.5	2.0E-74	BF030789.1	EST_HUMAN	B01657524F1 NIH MGC_58 Homo sapiens cDNA clone IMAGE:3827549.5
8126	21208	34728	1.8	2.0E-74	AB037316.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds



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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit: Accession No.	Top Hit: Database Source	Top Hit Descriptor
8582	22724	36294	5.27	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C04
12526	25369		2.87	2.0E-74	AA108181.1	EST_HUMAN	zpb8a06. s1 Striatogene muscle 837209 Homo sapiens cDNA clone IMAGE:628018 3'
13169	26176		1.16	2.0E-74	BF002855.1	EST_HUMAN	7g5a08.x1 NC1_CGAP_P128 Homo sapiens cDNA clone IMAGE:3309878 3'
54	13293	26308	1.5	1.0E-74	7657334	NT	Homo sapiens Mismatch/NIK-related kinase (MINK) mRNA
347	13598	26586	3.71	1.0E-74	AW816405.1	EST_HUMAN	QV4-ST0234-181199-Q37-05 ST0234 Homo sapiens cDNA
512	13708	26734	1.8	1.0E-74	8922828	NT	Homo sapiens hypodermal protein FLJ11026 (FLJ11026), mRNA
519	13712	26739	2.59	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
614	13803	26823	1.28	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
804	13984	27036	0.89	1.0E-74	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cde
1024	14195	27253	2.26	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2301	15433	28566	6.03	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XX4, complete cds
3209	16393	29394	2.82	1.0E-74	4768697	NT	Homo sapiens marrocidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3460	16627	29646	1.29	1.0E-74	AA256549.1	EST_HUMAN	z60d01.r1 Sceres_NHMP_2.S1 Homo sapiens cDNA clone IMAGE:687776 5'
3460	16627	29647	1.29	1.0E-74	AA238549.1	EST_HUMAN	z60d01.r1 Sceres_NHMP_2.S1 Homo sapiens cDNA clone IMAGE:687776 5'
4031	17187	30197	0.84	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4031	17187	30198	0.84	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4075	17231	30237	6.41	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
4175	17325	30316	0.85	1.0E-74	BE083030.1	EST_HUMAN	RC2-BT0642-270300-019-106 BT0642 Homo sapiens cDNA
4382	17525	30506	0.87	1.0E-74	BE467739.1	EST_HUMAN	h23n08.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213863 3' similar to WIP.B0511.12
6844	19997	33404	1.29	1.0E-74	MB991411	NT	CE17351
7804	20860	34353	1.05	1.0E-74	11417977	NT	Human neurotrophin (NFI) gene, complete cds
8246	21328	34844	1.27	1.0E-74	BE549105.1	EST_HUMAN	Homo sapiens KIA0852 protein (KIA0852), mRNA
8246	21328	34845	1.27	1.0E-74	BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
8005	22084	35627	7.81	1.0E-74	AE214562.1	NT	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
8034	22113	35656	0.87	1.0E-74	BE351651.1	EST_HUMAN	Homo sapiens tracheal epithelium enriched protein (PULNC) gene, complete cds
10445	23480	37086	0.65	1.0E-74	AA251550.1	NT	WFO-HT0569-230500-021-803 HT0569 Homo sapiens cDNA
10445	23480	37087	0.65	1.0E-74	AA251550.1	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
10699	23732	37337	1.77	1.0E-74	11420549	NT	Homo sapiens partial AK155 gene for AK155 protein, exons 1-3 and joined CDS
12154	25124	38826	1.84	1.0E-74	11417856	NT	Homo sapiens hypodermal protein FLJ10763 (FLJ10763), mRNA
12238	25182		4.87	1.0E-74	11417856	NT	Homo sapiens hypodermal protein FLJ10763 (FLJ10763), mRNA
12386	15433	28566	1.61	1.0E-74	AB002059.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12923	25610		1.38	1.0E-74	AE240766.1	NT	Homo sapiens DNA for Human P2XX4, complete cds
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2708	15827		5.1	8.0E-75	AF176228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
12652	26375		3.07	8.0E-76	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2395	15326	28654	1.25	6.0E-76	AI817415.1	EST_HUMAN	W638a08.x1 NC1 CGAP_P122 Homo sapiens cDNA clone IMAGE:2417654 3' similar to gb:U14123_cds4
11780	24770	38468	1.39	6.0E-75	BE701831.1	EST_HUMAN	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN);
9109	22189	35731	1.09	5.0E-75	BE272826.1	EST_HUMAN	601128086f1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:289985 5'
9317	22363	36944	0.77	5.0E-75	AA132611.1	EST_HUMAN	2017608.t1 Stragena cdon (8937204) Homo sapiens cDNA clone IMAGE:897174 5'
9395	22470	36034	0.47	5.0E-75	BE61635.1	EST_HUMAN	601346908f1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687458 5'
9395	22470	36035	0.47	5.0E-75	BE61635.1	EST_HUMAN	601346908f1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687458 5'
8973	22715	36283	1.1	5.0E-75	BF690294.1	EST_HUMAN	602186016f1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3'
10439	23474	37078	2.64	5.0E-75	AI698623.1	EST_HUMAN	H31c12.x1 NC1 OGAP_G08 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TRP97361 P97361
115	13346	28373	2.1	4.0E-75	BE01333.1	EST_HUMAN	HYPOTHETICAL 20.1 KD PROTEIN;
471	13666		1.68	4.0E-75	NS6737.1	EST_HUMAN	QY1-BT0632-210200-079-e02 BT0632 Homo sapiens cDNA
1805	14954	28048	1.08	4.0E-75	AW897230.1	EST_HUMAN	Y607008.t1 Scores melanocyte 2NDHM Homo sapiens cDNA clone IMAGE:268055 5'
2910	18088	29101	5.84	4.0E-75	BE408464.1	EST_HUMAN	GM0-NIN0057-160400-335-e11 NIN0057 Homo sapiens cDNA
6646	18840	32120	0.68	4.0E-75	11417946	NT	601303866f1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638344 5'
6646	18840	32121	0.68	4.0E-75	11417946	NT	Homo sapiens NIPSNAF, C. elegans, homolog 1 (NIPSNAF1) mRNA
6688	18668	32829	5.18	4.0E-75	5579457	NT	Homo sapiens NIPSNAF, C. elegans, homolog 1 (NIPSNAF1) mRNA
6898	20048	33458	1.4	4.0E-75	11417946	NT	Homo sapiens NIPSNAF, C. elegans, homolog 1 (NIPSNAF1) mRNA
6898	20048	33459	1.4	4.0E-75	11417946	NT	Homo sapiens NIPSNAF, C. elegans, homolog 1 (NIPSNAF1) mRNA
10924	24007	37642	10.52	4.0E-76	7669505	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1) mRNA
1027	14198	27256	3.6	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1028	14198	27256	3.59	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1883	15027	28134	2.23	3.0E-76	AB011183.1	NT	Homo sapiens mRNA for KIA0581 protein, partial cds
2180	16315	28444	1.44	3.0E-75	4507334	NT	Homo sapiens synaptojanin 1 (SYNJ1) mRNA
2494	16621	28740	4.39	3.0E-76	4759163	NT	Homo sapiens synaptojanin-associated protein, 29kD (SNAP29) mRNA
3086	16262	29279	0.86	3.0E-75	AL169201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3259	16432	29449	1.09	3.0E-75	AB011183.1	NT	Homo sapiens mRNA for KIA0581 protein, partial cds
3431	16399	28616	0.83	3.0E-75	MM2393.1	NT	Homo sapiens calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3431	16399	28617	0.83	3.0E-75	MM2393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3833	16693	28985	0.6	3.0E-75	MM2393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4283	17428	30418	2.82	3.0E-75	DB76751	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
5365	18598	31434	1.15	3.0E-75	11420356	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2) mRNA

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Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5365	18558	31435	1.16	3.0E-76	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
6637	19798	33185	0.59	3.0E-76	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6637	19798	33186	0.59	3.0E-75	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6609	20224	33654	1.57	3.0E-76	11626318	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6609	20224	33655	1.57	3.0E-76	11626318	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7285	20368	33821	4.12	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7285	20368	33822	4.12	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7800	20856	34346	2.66	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
7800	20856	34347	2.66	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
9185	22263	35905	1.33	3.0E-75	11420804	NT	Homo sapiens snail 1 (Drosophila homolog), zinc finger protein (SNAIL1), mRNA
9880	22820	36504	0.83	3.0E-75	11420222	NT	Homo sapiens Drosophila Kctd10 like protein (DKELCHL), mRNA
5780	18982		1.34	2.0E-76	AV34690.1	EST_HUMAN	q6b1602.x1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69386
8950	22029	35570	1.36	2.0E-75	AI31783.1	EST_HUMAN	POLENV GENE; q6b1602.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2692707 3' similar to contains PTR7.11
2377	15508	28635	10.98	1.0E-76	AW168135.1	EST_HUMAN	PTR7 repetitive element; H sapiens ERCC2 gene, exons 1 & 2 (partial)
3012	16188	29213	2.95	1.0E-75	X62221.1	NT	H sapiens ERCC2 gene, exons 1 & 2 (partial)
7762	20821	34311	0.64	1.0E-75	BE082628.1	EST_HUMAN	RC5-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA
7762	20821	34312	0.64	1.0E-75	BE082628.1	EST_HUMAN	RC5-BT0640-020300-031-H03 BT0640 Homo sapiens cDNA
8609	21689		3.12	1.0E-75	AA399270.1	EST_HUMAN	z157h03.s1 Soares_testes_NHT Homo sapiens cDNA clone IMAGE:728485 3' similar to gb:U13932 40S
8626	22683	36263	3.95	1.0E-75	BF313645.1	EST_HUMAN	RIBOSOMAL PROTEIN S17 (HUMAN); B01800294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128678 5'
8626	22683	36264	3.95	1.0E-75	BF313645.1	EST_HUMAN	B01800294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128678 5'
11122	24194		8.88	1.0E-75	AA66477.1	EST_HUMAN	ac77b08.s1 Straligene lung (H837210) Homo sapiens cDNA clone IMAGE:688599 3'
11351	24413	38067	2.22	1.0E-75	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12440	18502	31538	1.97	1.0E-75	BE894192.1	EST_HUMAN	B01437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3923303 5'
45	13284	26292	0.89	9.0E-76	AI652648.1	EST_HUMAN	WB30b10.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O76235 O76235
45	13284	26293	0.89	9.0E-76	AI652648.1	EST_HUMAN	WB30b10.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O76235 O76235
2486	15613		0.94	9.0E-76	AA702415.1	EST_HUMAN	TRAP1; WB30b10.x1 NCI CGAP_G08 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O76235 O76235
							TRAP1; z157h03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:447541 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10105	23143	36741	5.44	8.0E-76	M12937.1	NT	Human ferritin Heavy subunit mRNA, complete cds
961	14134	27194	1.18	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
961	14134	27195	1.18	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2876	16152	29173	0.95	8.0E-76	7708724	NT	Homo sapiens mediator (Sur2), mRNA
6300	19473	32828	5.84	8.0E-76	11421442	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
7668	20725	34200	1.17	8.0E-76	11433215	NT	Homo sapiens serine/threonine kinase 2 (STK2), mRNA
7739	20800	34288	1.05	8.0E-76	11418212	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
8482	21573	35110	0.69	8.0E-76	11416961	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
10589	23624	37231	1.26	8.0E-76	M13782.1	NT	Human adenovirus deaminase (ADA) gene, complete cds
10803	23987	37619	4.29	8.0E-76	10442821	NT	Homo sapiens baculoviral IAP repeat-containing 9 (BIRC9), mRNA
12824	25550		2.51	8.0E-76	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0350), mRNA
797	13976	27029	1.69	7.0E-76	5016092	NT	Homo sapiens dihydropyrimidin dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3366	16638	29531	3.84	7.0E-76	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3372	16544	29558	9.08	7.0E-76	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
4481	17631	30612	5.52	7.0E-76	14507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4491	17631	30613	5.52	7.0E-76	14507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1282	14419		37.29	6.0E-76	BE398233.1	EST_HUMAN	801312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658767 5'
11753	28339	37565	2.52	6.0E-76	BE273201.1	EST_HUMAN	601142235F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3508029 5'
1987	15138	28243	9.61	5.0E-76	DE3874.1	NT	Human mRNA for HMG-1, complete cds
1987	15138	28244	9.61	5.0E-76	DE3874.1	NT	Human mRNA for HMG-1, complete cds
1997	15138	28245	9.61	5.0E-76	DE3874.1	NT	Human mRNA for HMG-1, complete cds
3278	18452	29473	0.64	4.0E-76	BE814098.1	EST_HUMAN	GV3-BND047-270700-283-908 BND047 Homo sapiens cDNA
5384	18588	31455	1.13	4.0E-76	BE783412.1	EST_HUMAN	801471725F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874470 5'
10230	22265	36954	5.48	4.0E-76	DB18261	EST_HUMAN	HUM178G01B Human fetal brain (TFujwara) Homo sapiens cDNA clone GEN-178G01 5'
10230	22265	36955	5.48	4.0E-76	DB18261	EST_HUMAN	HUM178G01B Human fetal brain (TFujwara) Homo sapiens cDNA clone GEN-178G01 5'
646	13631	26856	2.01	3.0E-76	BE16282.1	EST_HUMAN	U1-H-BW1-anz-b-04-0-UL1 st NC1 CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
646	13631	26857	2.01	3.0E-76	BE16282.1	EST_HUMAN	U1-H-BW1-anz-b-04-0-UL1 st NC1 CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1629	14781	27865	8.04	3.0E-76	4503478	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1629	14781	27867	8.04	3.0E-76	4503478	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3515	16681	28691	6.75	3.0E-76	BF376939.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3515	16681	28692	6.75	3.0E-76	BF376939.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
5352	18490	39822	1.82	3.0E-76	Z413141	EST_HUMAN	HSC2QD0042 normalized infant brain cDNA Homo sapiens cDNA clone c-zd004 3'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5851	18041	32347	0.92	3.0E-76	AA160611.1	EST_HUMAN	2073c07.11 Stratiogene pancreas (8937208) Homo sapiens cDNA clone IMAGE:592524 5' similar to
6110	18220	32825	0.61	3.0E-76	AW027705.1	EST_HUMAN	gb L32978 MIXED LINEAGE KINASE 1 (HUMAN);
6498	18384	33027	8.19	3.0E-76	AF280598.1	NT	WV75c05.x1 Soeres thymus Nt-Fth Homo sapiens cDNA clone IMAGE:2565368 3'
8344	21429	34951	1.27	3.0E-76	NA2671.1	EST_HUMAN	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
9817	22867	36544	3.03	3.0E-76	AA286333.1	EST_HUMAN	W20670.11 Soeres melanocyte 2NtHm Homo sapiens cDNA clone IMAGE:271842 5'
9842	22881	36572	1.08	3.0E-76	AA442308.1	EST_HUMAN	Xc48f01.x1 NCJ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773008 3'
9842	22881	36573	1.08	3.0E-76	AA442309.1	EST_HUMAN	Xc48f01.x1 NCJ CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773008 3'
12144	26943	31763	2.1	3.0E-76	AW867894.1	EST_HUMAN	Zv54d11.11 Soeres testis NHT Homo sapiens cDNA clone IMAGE:757461 5'
12251	26184	31642	6.95	3.0E-76	AW950456.1	EST_HUMAN	EST380069 MAGE resequences, MAGD Homo sapiens cDNA
282	13509	26544	1.11	2.0E-76	D84285.1	NT	EST388525 MAGE resequences, MAGD Homo sapiens cDNA
352	13563	26580	3.21	2.0E-76	D84285.1	NT	Human mRNA for possible protein TPRDII, complete cds
352	13563	26591	3.21	2.0E-76	D84285.1	NT	Human mRNA for possible protein TPRDII, complete cds
473	13688	26612	0.98	2.0E-76	1457662	NT	Human mRNA for possible protein TPRDII, complete cds
603	13792	26812	1.07	2.0E-76	4303944	NT	Human mRNA for possible protein TPRDII, complete cds
1088	14222	27281	1.68	2.0E-76	4758053	NT	Human mRNA for possible protein TPRDII, complete cds
1568	14719	27789	11.31	2.0E-76	4504028	NT	Human mRNA for possible protein TPRDII, complete cds
1568	14719	27800	11.31	2.0E-76	4504028	NT	Human mRNA for possible protein TPRDII, complete cds
1882	15125	28227	0.99	2.0E-76	AA23394.1	EST_HUMAN	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
2804	18082	28097	2.13	2.0E-76	P23208	SWISSPROT	z560h1.11 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:701925 3'
3369	18541	29555	2.21	2.0E-76	AA445892.1	EST_HUMAN	OLFATORY RECEPTOR LIKE PROTEIN F5
3369	18541	29556	2.21	2.0E-76	AA445892.1	EST_HUMAN	z464c02.11 Soeres testis NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN
3369	18541	29556	2.21	2.0E-76	AA445892.1	EST_HUMAN	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;
3665	18730	29746	0.93	2.0E-76	AA821149.1	EST_HUMAN	z464c02.11 Soeres testis NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN
4254	13509	26544	1.01	2.0E-76	D84285.1	NT	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR ;
4633	17769	30773	0.91	2.0E-76	AL163283.2	NT	ac83b02.16 Stratiogene lung (8937210) Homo sapiens cDNA clone IMAGE:869163 5' similar to TR:O14591
5062	18150	31165	11.15	2.0E-76	AW879318.1	EST_HUMAN	O14591 SIMILARITY TO P22059 ;
5163	18285	31249	3.13	2.0E-76	AF127845.1	NT	Human mRNA for possible protein TPRDII, complete cds
5424	18626	32226	2.88	2.0E-76	AB029004.1	NT	ac83b02.16 Stratiogene lung (8937210) Homo sapiens cDNA clone IMAGE:869163 5' similar to TR:O14591
5736	18928	34119	4.83	2.0E-76	11421326	NT	Human mRNA for possible protein TPRDII, complete cds
7570	20842	34119	0.86	2.0E-76	11421326	NT	Human mRNA for possible protein TPRDII, complete cds
7592	20883	34139	0.69	2.0E-76	11420908	NT	Human mRNA for possible protein TPRDII, complete cds

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7940	20695	34397	1.82	2.0E-76	U427410	NT	Homo sapiens TPOR88 protein (HSTPOR88P), mRNA
10489	23524	37134	1.42	2.0E-76	U437211	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC83150), mRNA
11161	24232	37862	2.44	2.0E-76	U49807	NT	Homo sapiens HIRA interacting protein 4 (dnal-like) (HIRIP4), mRNA
4412	17554	30539	2.49	1.0E-76	U63874.1	NT	Human mRNA for HMG-1, complete cds
4412	17554	30540	2.49	1.0E-76	U63874.1	NT	Human mRNA for HMG-1, complete cds
5364	18761	31801	5.83	1.0E-76	U6798507.1	EST_HUMAN	601589886F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
6374	19543		0.7	1.0E-76	U633207.1	EST_HUMAN	ESTJ37301 Embryo, 8 week I Homo sapiens cDNA 5' end
7063	20116	33530	4.66	9.0E-77	U6889525.1	EST_HUMAN	601302335F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636753 5'
13003	26652		1.98	9.0E-77	U6410314.1	EST_HUMAN	6011102.1 Scores breast SNB1Bst Homo sapiens cDNA clone IMAGE:187155 5' similar to SP-ANKB_HUMAN Q01484 ANKYRIN, BRAIN VARIANT 1;
192	13414	26443	0.77	8.0E-77	U63144.1	EST_HUMAN	801869926F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5'
4644	17780	30792	1.41	8.0E-77	U6205181.1	EST_HUMAN	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mbn34 homolog) (PSMD7) mRNA
5569	18766	31807	1.37	8.0E-77	U606230	NT	z662502.1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
11668	24746	38438	1.78	8.0E-77	U619770.1	EST_HUMAN	z662502.1 Scores retina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
11669	24746	38439	1.78	8.0E-77	U619770.1	EST_HUMAN	y663704.81 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains MER10 repetitive element;
12978	25637	31982	32.6	8.0E-77	U60245.1	EST_HUMAN	z661901.81 Scores testis, NIH Homo sapiens cDNA clone IMAGE:745392 3'
1983	15126	28228	2.2	7.0E-77	U602755.1	EST_HUMAN	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2482	15609	28733	2.78	7.0E-77	U605944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2482	15609	28734	2.78	7.0E-77	U605944	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
273	13491	28522	4	6.0E-77	U604800	NT	Homo sapiens interleukin 1 (CCL1) mRNA
1155	14329	27394	1.05	6.0E-77	U603753.1	EST_HUMAN	EST368823 MAGE resequences, MAGE Homo sapiens cDNA
1574	14727	27808	3.29	6.0E-77	U6120408.1	EST_HUMAN	q677h12.x1 Scores fetal lung NBHL19V Homo sapiens cDNA clone IMAGE:1745093 3'
1284	14421	27489	2.89	5.0E-77	U6041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1391	14545	27821	3.46	5.0E-77	U657250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2749	16866	28977	1.76	6.0E-77	U6162635.1	NT	Homo sapiens localized-like kinase 1 (TLK1) mRNA, complete cds
2822	15938	29046	1.68	6.0E-77	U603160	NT	Homo sapiens cullin 1 (CUL1) mRNA
3811	16775	29791	0.95	6.0E-77	U609416	NT	Homo sapiens ubiquitin specific protease 18 (USP18), mRNA
4825	17958	30944	0.97	6.0E-77	U603160	NT	Homo sapiens EGF-like repeats and discoidin like domains 3 (EDIL3), mRNA
4825	17958	30945	0.97	6.0E-77	U603160	NT	Homo sapiens EGF-like repeats and discoidin like domains 3 (EDIL3), mRNA
5062	18160	31156	3.67	5.0E-77	U6043933.1	EST_HUMAN	DKFZ454G1728 J1 434 (synonym: hcs3) Homo sapiens cDNA clone DKFZ454G1728 5'
6922	20237	33671	0.65	5.0E-77	U613976.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
7460	20565	34027	0.59	5.0E-77	U608296.1	NT	H. sapiens mRNA for ubiquitin hydrolase

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7767	20555	34027	0.72	5.0E-77	X99286.1	NT	H. sapiens mRNA for ubiquitin hydrolase
8663	21644	35163	1.21	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH) mRNA
8663	21644	35184	1.21	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH) mRNA
8769	22765	36335	2.61	5.0E-77	11421928	NT	Homo sapiens sorting nexin 6 (SNX6) mRNA
8769	22765	36336	2.61	5.0E-77	11421928	NT	Homo sapiens sorting nexin 6 (SNX6) mRNA
10708	23741	37346	0.97	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
10708	23741	37347	0.97	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
2029	16170	28277	1.39	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
2029	16170	28278	1.39	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10486	23531	37139	0.9	3.0E-77	H65187.1	EST_HUMAN	Y64901.1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 6' similar to SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 -1
10486	23531	37140	0.9	3.0E-77	H65187.1	EST_HUMAN	Y64901.1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238608 6' similar to SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 -1
11115	24187	37819	2.83	3.0E-77	BF36917.1	EST_HUMAN	PM3-MT0078-060800-005-003 MT0078 Homo sapiens cDNA
1383	14538	27612	1.74	2.0E-77	AV764617.1	EST_HUMAN	AV764617 MDS Homo sapiens cDNA clone MDSBTF10.5
1464	14618	27702	9.74	2.0E-77	AW697712.1	EST_HUMAN	RC3-BN0053-170200-011-011 BN0053 Homo sapiens cDNA
2157	15283	28419	1.1	2.0E-77	L41826.1	NT	Homo sapiens CYP17 gene, 5' end
2170	15305	28432	2.75	2.0E-77	7706316	NT	Homo sapiens CG1-79 protein (LOC51634) mRNA
2658	18067	28895	1.69	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2658	18067	28896	1.69	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4143	17285	30287	1.98	2.0E-77	BE044316.1	EST_HUMAN	h64503.x1 Soares NF1_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAQ2_HUMAN P10284 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4534	17672	30856	0.67	2.0E-77	AB13519.1	EST_HUMAN	h64503.x1 Soares NF1_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2280486 3' similar to TR:065245
4534	17672	30857	0.67	2.0E-77	AB13519.1	EST_HUMAN	h64503.x1 Soares NF1_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2280486 3' similar to TR:065245
4891	18021	31006	2.34	2.0E-77	AA65026.1	EST_HUMAN	ns68912.s1 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:1198938 similar to SW:RL29_HUMAN P47814 60S RIBOSOMAL PROTEIN L28. [1] ; contains element MSRI repetitive element ;
6075	19257	32566	2.08	2.0E-77	BE288940.1	EST_HUMAN	601119852.F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
6301	19474	32829	1.86	2.0E-77	BE187143.1	EST_HUMAN	601476802.F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3879505 5'
7325	20407	33869	16.02	2.0E-77	AB33003.1	EST_HUMAN	a674609.x1 Barstead codon HPLRB7 Homo sapiens cDNA clone IMAGE:2277720 3' similar to TR:Q13311 Q13311 TAX1-BINDING PROTEIN TXBP151. [1] ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8726	21806	35343	0.88	2.0E-77	AB02707.1	EST_HUMAN	qy70c09.x1 NC1_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2017380 3' similar to WP.F29D11.1
8728	22793	36366	6.68	2.0E-77	U50324.1	NT	CE05765 LOW DENSITY LIPID RECEPTOR-RELATED PROTEIN ;
8728	22793	36367	5.68	2.0E-77	U50324.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7
10199	23236	36826	0.47	2.0E-77	BF310349.1	EST_HUMAN	601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
10199	23236	36826	0.47	2.0E-77	BF310349.1	EST_HUMAN	601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
44	13282	26289	2.82	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
44	13282	26289	2.62	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
283	13501	26533	1.68	1.0E-77	4502169	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
283	13501	26534	1.68	1.0E-77	4502169	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
898	16025	27140	3.4	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
898	16025	27141	3.4	1.0E-77	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1989	15112	28213	1.36	1.0E-77	AW058118.1	EST_HUMAN	W63605.x1 Soares, thymus, NHFTb Homo sapiens cDNA clone IMAGE:2536160 3'
2516	15641	28763	1.17	1.0E-77	AB029024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3110	16289	29300	2.28	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1), mRNA
4473	17613	30592	4.24	1.0E-77	17706299	NT	Homo sapiens OGI-60 protein (LOC51826), mRNA
4848	17782	30704	22.17	1.0E-77	AJ22804.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22 segment 1/3
4774	17909	30882	2.05	1.0E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
4816	17948	30833	0.61	1.0E-77	AJ273014.1	EST_HUMAN	qy06g04.x1 NC1_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1981110 3'
6051	18233	32357	1.48	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6051	18233	32558	1.48	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6172	18348	32694	1.72	1.0E-77	M25844.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exon 20
6577	18739	33120	1.1	1.0E-77	4885182	NT	Human von Willebrand factor gene, exon 20
7198	20063	33473	15.87	1.0E-77	6881412	NT	Homo sapiens elastin (supraaortic aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA
7844	20869	34402	0.82	1.0E-77	1420169	NT	Homo sapiens cullin 1 (CUL1), mRNA
7940	20890	34600	0.71	1.0E-77	X04571.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
8465	22522	36085	0.83	1.0E-77	X04364.1	NT	Human mRNA for keratin 16 (K16), PDE gene
8465	22522	36086	0.83	1.0E-77	X04364.1	NT	Human mRNA for keratin 16 (K16), PDE gene
10742	23776	37387	1.05	1.0E-77	AB028396.1	NT	Homo sapiens hnu-GlcAT-2 mRNA for glucuronyltransferase, complete cds
10742	23776	37388	1.05	1.0E-77	AB028396.1	NT	Homo sapiens hnu-GlcAT-2 mRNA for glucuronyltransferase, complete cds



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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10773	23806	37429	2.76	9.0E-78	AW753302.1	EST_HUMAN	RC3-CT0254-280999-011-b05 CT0254 Homo sapiens cDNA
6576	19738	33118	2.29	8.0E-78	AW647061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
6576	19738	33119	2.29	8.0E-78	AW647061.1	EST_HUMAN	RC2-ET0023-080500-012-e09 ET0023 Homo sapiens cDNA
89	13323	28351	1.66	9.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354.5'
89	13323	28352	1.66	9.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354.5'
3389	16399	28574	0.9	8.0E-78	BF344101.1	EST_HUMAN	602016926F1 NC1 CGAP_Bris4 Homo sapiens cDNA clone IMAGE:4152511.5'
6680	19848		2.54	6.0E-78	11432710	NT	Homo sapiens GDNF family receptor alpha 1 (GFRAL1) mRNA
224	13446	28474	6.13	5.0E-78	11422486	NT	Homo sapiens hypodermal protein FLJ11318 (FLJ11318) mRNA
2629	15752	28867	6.71	5.0E-78	AW673424.1	EST_HUMAN	ba54h03.y9 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800405.5' similar to WIP-Y48B6A.6
3472	16638	29659	5.09	5.0E-78	M5556.1	NT	CE22121
5528	18725	31741	2.73	5.0E-78	AF038536.1	NT	Human collagenase type IV (C1G4) gene, exon 8
5693	18887	32177	18.13	6.0E-78	11416565	NT	Homo sapiens Beaf1 muscular dystrophy-related protein mRNA, partial cds
7304	20386	33946	2.18	5.0E-78	AW653120.1	EST_HUMAN	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1) mRNA
9284	22360	35910	7.02	5.0E-78	UB0989.1	NT	Human lysosomal alpha-mannosidase (manb) gene, exon 7
9285	22361	35911	2.94	5.0E-78	BE60836.1	EST_HUMAN	601648081F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3931887.5'
1160	14324	27378	1.29	4.0E-78	AL043314.2	EST_HUMAN	DKFZp434N0323_J1 434 (synonym: hba3) Homo sapiens cDNA clone DKFZp434N0323.5'
1547	14889	27778	1.81	4.0E-78	AL355941.1	NT	Novel human gene mapping to chromosome 22
2392	15523	28552	5.1	4.0E-78	AF107405.1	NT	Homo sapiens pre-miRNA splicing factor (SFRS3) mRNA, complete cds
4442	17582	30560	6.17	4.0E-78	7866876	NT	Homo sapiens syncytin (LOC30816) mRNA
4896	18026	31012	1.2	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
4898	18026	31013	1.2	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
5888	18076	32385	1.25	4.0E-78	11420732	NT	Homo sapiens SFRS3 protein kinase 2 (SFRS3) mRNA
6302	19475	32830	0.71	4.0E-78	7862109	NT	Homo sapiens KIAA0428 gene product (KIAA0428) mRNA
6302	19475	32831	0.71	4.0E-78	7862109	NT	Homo sapiens KIAA0428 gene product (KIAA0428) mRNA
6703	19861	33261	0.74	4.0E-78	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
7690	20727	34203	0.69	4.0E-78	4506736	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
9054	22133	35677	1.15	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pik4230) mRNA, complete cds
9054	22133	35678	1.16	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pik4230) mRNA, complete cds
9598	22710	36278	0.61	4.0E-78	11417251	NT	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4) mRNA
10660	23694	37303	1.95	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504) mRNA
10660	23694	37304	1.95	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504) mRNA
11705	24702	38394	1.84	4.0E-78	AF16918.1	NT	Homo sapiens s-CaBP1 (CaBP1) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11854	24842	38538	6.72	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
12855	25568	31981	3.83	4.0E-78	A3011380.1	NT	Homo sapiens gene for AF-5, complete cds
165	13390	28417	1.69	3.0E-78	AF095601.1	NT	Homo sapiens eRF1 gene, complete cds
165	13390	28418	1.69	3.0E-78	AF095601.1	NT	Homo sapiens eRF1 gene, complete cds
2485	15615	28736	1.01	3.0E-78	7706705	NT	Homo sapiens SH3 and PX domain-containing protein SH3PX1 (SH3PX1), mRNA
3860	17020	30074	0.81	3.0E-78	AU140504.1	EST_HUMAN	AU140504 PLAGE3 Homo sapiens cDNA clone PLAGE3000373 5'
3916	17077	30074	0.78	3.0E-78	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
4221	17077	30074	0.82	3.0E-78	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
10493	23528		5.44	3.0E-78	BE144758.1	EST_HUMAN	CMO-H10180-041099-065-07 HT0180 Homo sapiens cDNA
11227	24296	37897	2.5	3.0E-78	BE156316.1	EST_HUMAN	QV0-H10367-150200-114-909 HT0367 Homo sapiens cDNA
3191	16366		2.49	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
4122	17276		1.69	2.0E-78	AA311872.1	EST_HUMAN	EST182383 Juncat T-cells VI Homo sapiens cDNA 5' and
7631	20700	34177	1.09	2.0E-78	AW402306.1	EST_HUMAN	UHF-B10-af-g-10-Q-UJ.1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3064139 5'
7631	20700	34178	1.09	2.0E-78	AW402306.1	EST_HUMAN	UHF-B10-af-g-10-Q-UJ.1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3064139 5'
7908	20860	34466	3.36	2.0E-78	BF689800.1	EST_HUMAN	602186528F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:429559 5'
8230	21312	34832	2.49	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBAWF09 5'
8948	21728	35262	1.72	2.0E-78	AI657508.1	EST_HUMAN	P2.1_16_B07.r tumor2 Homo sapiens cDNA 3'
8646	21726	35263	1.72	2.0E-78	AI657509.1	EST_HUMAN	P2.1_16_B07.r tumor2 Homo sapiens cDNA 3'
11336	24399	38048	9.59	2.0E-78	AI197837.1	EST_HUMAN	q60005.x1 NC1_CGAP_Brn26 Homo sapiens cDNA clone IMAGE:186991 3' similar to WP.R60.1
11338	24420		1.47	2.0E-78	BE439408.1	EST_HUMAN	CE03925 PROTEIN KINASE :
11386	24447	38108	3.01	2.0E-78	N859511.1	EST_HUMAN	HTM1-028F1 HTM1 Homo sapiens cDNA
5420	18521	31697	3.16	1.0E-78	11417304	NT	z48112.s1 Soares fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:263823 3'
7094	18521	31614	0.82	1.0E-78	AV648698.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC51306), mRNA
8363	21434		1.81	1.0E-78	U52373.1	NT	AV648699 G1C Homo sapiens cDNA clone Q1CBM01 3'
12324	26234	32107	1.83	1.0E-78	11430460	NT	Human serine/threonine kinase MNB (mnb) mRNA, complete cds
12422	26236	32086	2.44	1.0E-78	11435903	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4820	17853	30938	4.04	9.0E-79	11525891	NT	Homo sapiens similar to lymphocyte activation-associated protein (L- sapiens) (LOC63140), mRNA
4986	18115	31093	1.6	8.0E-79	BE000837.1	EST_HUMAN	Homo sapiens peptide YY (PYY), mRNA
5349	18740	31781	16.98	8.0E-79	AB028070.1	NT	RC2-BN0074-090300-014-012 BN0074 Homo sapiens cDNA
6470	19837	32896	2.52	9.0E-79		NT	Homo sapiens mRNA for activator of S phase kinase, complete cds
6752	18908	33301	0.98	8.0E-78	11430822	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5) (UBE2E3) mRNA
							Homo sapiens hypothetical protein FLJ11294 (FLJ11294), mRNA

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7505	25846		0.99	9.0E-79	11424427	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7748	20808	34298	0.63	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
7748	20808	34298	0.63	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
8541	21622	35158	0.52	9.0E-79	11417260	NT	Homo sapiens threonine-RNA synthetase (TARS), mRNA
8541	21622	35158	0.52	9.0E-79	11417260	NT	Homo sapiens threonine-RNA synthetase (TARS), mRNA
8263	22340	35890	4.78	9.0E-79	102853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
8263	22340	35891	4.78	9.0E-79	102853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
8580	22722	36282	0.66	9.0E-79	087674.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10574	23809	37214	0.82	9.0E-79	11438643	NT	Homo sapiens hypothetical protein FLJ20535 (FLJ20535), mRNA
10632	23866	37274	1.05	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10632	23866	37275	1.05	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
11322	24385	36029	1.61	9.0E-79	AY003673.1	NT	Homo sapiens TRAF6-regulated IKK activator 1 Delta Uev1a mRNA, complete cds
11802	24782	38489	2.84	9.0E-79	11423827	NT	Homo sapiens suppressor of white apicotic homolog 2 (SWAP2), mRNA
11802	24782	38490	2.94	9.0E-79	11423827	NT	Homo sapiens suppressor of white apicotic homolog 2 (SWAP2), mRNA
13088	25711	31867	1.4	9.0E-79	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3636	16696	28998	1.18	8.0E-79	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3325	16498	29516	6.38	7.0E-79	BE618948.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657.3'
8844	21823		0.62	8.0E-79	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
12169	25132		5.44	8.0E-79	AA698629.1	EST_HUMAN	294604.S1 Soares_fetal_liver_spleen_1NFLS.S1 Homo sapiens cDNA clone IMAGE:452558.3' similar to
11785	24776	38473	3.63	5.0E-79	AL163282.2	NT	TR:Q15408 Q15408 NEUTRAL_PROTEASE LARGE SUBUNIT :
323	13537	28569	1.74	3.0E-79	AF114488.1	NT	Homo sapiens chromosome 21 segment HS21C082
1001	14172	27233	1.22	3.0E-79	AF232708.1	NT	Homo sapiens intronless short isoform (ITSN) mRNA, complete cds
3168	16343	28351	1.74	3.0E-79	U08410.1	NT	Homo sapiens cell-line tsA201 a chloride ion current inducer protein (Cin) gene, complete cds
5477	18076	31089	7.05	3.0E-79	AF110322.1	NT	Homo sapiens zinc finger protein ZNF131 mRNA, partial cds
5847	18037	32337	1.69	3.0E-79	AB020699.1	NT	Homo sapiens MST1P018 (MST018) mRNA, complete cds
5866	18036	32363	0.93	3.0E-79	BE789470.1	EST_HUMAN	Homo sapiens mRNA for KIAA0892 protein, partial cds
5866	18036	32364	0.93	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3894554.5'
5889	19077	32386	3.87	3.0E-79	11428770	NT	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3894554.5'
5889	19077	32387	3.87	3.0E-79	11428770	NT	Homo sapiens neitin 1 (NTN1), mRNA
6884	20036	33445	0.84	3.0E-79	BE256693.1	EST_HUMAN	Homo sapiens neitin 1 (NTN1), mRNA
7206	20071	33481	2.58	3.0E-79	AB014520.1	NT	601112055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352885.5'
7206	20071	33482	2.58	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
8012	21062	34574	0.87	3.0E-79	6912455	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
							Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8358	21439	34961	0.78	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
8603	22656	38230	0.59	3.0E-79	10835036	NT	Homo sapiens tetrapeptide repeat domain 3 (TTC3), mRNA
10555	23590		0.62	3.0E-79	AV089115.1	EST_HUMAN	AV089115 GKX Homo sapiens cDNA clone GKCAHE11.5
288	13518		1.4	2.0E-79	H03128.1	EST_HUMAN	y4803.s1 Soares fetal liver spleen 11NF15 Homo sapiens cDNA clone IMAGE:208541.3
951	13837	28834	1.05	2.0E-79	BE379823.1	EST_HUMAN	601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107.6
951	14124	27186	1.14	2.0E-79	475784.1	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
1007	14178	27239	4.87	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
1007	14178	27240	4.87	2.0E-79	4886234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
1080	14226		2.15	2.0E-79	AI523747.1	EST_HUMAN	h18107.x1 NC1_CGAP_P28 Homo sapiens cDNA clone IMAGE:2118685.3
2215	15349	28478	6.17	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2215	15349	28479	6.17	2.0E-79	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2268	15399	28527	1.35	2.0E-79	ALJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
2387	15516	28648	1.1	2.0E-79	AF244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
2780	15898	29008	1.2	2.0E-79	AE023134.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
4023	17179	30188	0.69	2.0E-79	AF170422.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
4280	17425	30414	1.25	2.0E-79	ALJ271408.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
4813	17846	30831	0.83	2.0E-79	AL163206.2	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
6788	18990		1.06	2.0E-79	AA312223.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C006
5844	19334	32340	0.9	2.0E-79	11181789	NT	EST182928 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to C. elegans hypothetical protein, cosmid B0303.15
6373	19542	32901	1.18	2.0E-79	AB020637.1	NT	Homo sapiens X transporter protein 3 (XT3), mRNA
7100	19527	31519	0.89	2.0E-79	AF283613.1	NT	Homo sapiens X transporter protein 3 (XT3), mRNA
7317	20399	33861	2.09	2.0E-79	7382479	NT	Homo sapiens X transporter protein 3 (XT3), mRNA
7317	20399	33862	2.09	2.0E-79	7382479	NT	Homo sapiens X transporter protein 3 (XT3), mRNA
8282	21374	34894	1.1	2.0E-79	4506442	NT	Homo sapiens Rho GTPase activating protein 6 (ARRGAP6), transcript variant 4, mRNA
8714	21784	35331	2.13	2.0E-79	11427428	NT	Homo sapiens Rho GTPase activating protein 6 (ARRGAP6), transcript variant 4, mRNA
8865	22044	35587	0.55	2.0E-79	8923248	NT	Homo sapiens retinoblastoma-like 1 (p107) (RBL1) mRNA
8905	22044	35588	0.65	2.0E-79	8923248	NT	Homo sapiens retinoblastoma-like 1 (p107) (RBL1) mRNA
9205	22283	35823	0.69	2.0E-79	11432164	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
10287	23332	36935	1.98	2.0E-79	S72869.1	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
10287	23332	36936	1.88	2.0E-79	S72869.1	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
11284	24350	37987	2.94	2.0E-79	BE064386.1	EST_HUMAN	Homo sapiens similar to A1Pase, H+ transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-9 (H+ sepiens) (LOC33961), mRNA
							H4(10S170)-putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
							H4(10S170)-putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
							RC4B10310-110300-015-f10 B10310 Homo sapiens cDNA

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11284	24350	37888	2.94	2.0E-79	BE064386.1	EST_HUMAN	RC4.BT0310-110300-015-410 BT0310 Homo sapiens cDNA
12208	18498	31634	4.27	2.0E-79	7662357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
12298	25218	32100	2.3	2.0E-79	AB020640.1	NT	Homo sapiens KIAA0833 protein, partial cds
12531	25362	32067	3.08	2.0E-79	11416322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6718	25830		3.28	1.0E-79	BF363071.1	EST_HUMAN	MRO-NN0087-280600-017-b10 NN0087 Homo sapiens cDNA
6633	18986	33364	0.65	1.0E-79	A1613480.1	EST_HUMAN	h37e08.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2281286 3' similar to TR:Q26623 Q26623
6633	18986	33364	0.65	1.0E-79	A1613480.1	EST_HUMAN	TEKTIN C1.1
6633	18986	33364	0.65	1.0E-79	A1613480.1	EST_HUMAN	TEKTIN C1.1
8439	21520	35049	0.9	1.0E-79	BE394211.1	EST_HUMAN	601311517F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632909 5'
11822	24008	38609	1.9	1.0E-79	BF087405.1	EST_HUMAN	QV2.HT0540-120900-358-c05 HT0540 Homo sapiens cDNA
12328	29107	29389	1.44	1.0E-79	A1460115.1	EST_HUMAN	a7p8a04.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151438 3'
3215	16389	28400	6.95	9.0E-80	AA728848.1	EST_HUMAN	a23a05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
3215	16389	28400	6.95	9.0E-80	AA728848.1	EST_HUMAN	a23a05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
10217	23253	36842	1.3	9.0E-80	BE788605.1	EST_HUMAN	601581652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3836061 5'
11564	24609	38288	7.63	9.0E-80		NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y <sup>+</sup> system) member 8 (SLC7A8), mRNA
11564	24609	38288	7.63	9.0E-80		NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y <sup>+</sup> system) member 8 (SLC7A8), mRNA
11564	24609	38288	7.63	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y <sup>+</sup> system) member 8 (SLC7A8), mRNA
3691	16853		1.01	8.0E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
7780	20836	34328	2.82	8.0E-80	11422647	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
7780	20836	34328	2.82	8.0E-80	11422647	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
8602	22657	36228	2.2	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
8602	22657	36228	2.2	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
7114	18540	31497	0.61	7.0E-80	AF127852.1	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
923	14098	27162	0.74	6.0E-80	A1422197.1	EST_HUMAN	h5g402.x1 NCL CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2103458 3' similar to SW:NUEM_HUMAN
1878	14827	27910	2.41	6.0E-80	U94888.1	NT	Q16786 NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR
2372	16503	28628	1.14	6.0E-80	6631094	NT	Homo sapiens NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR
2372	16503	28628	1.14	6.0E-80	6631094	NT	Homo sapiens NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR
5922	18108	32422	1.48	8.0E-80	11421482	NT	Homo sapiens NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR
6200	18375	32726	3.35	6.0E-80	A1404438.1	NT	Homo sapiens NADH-UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6368	19528	32886	4.07	8.0E-80	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
6402	19671		1.08	6.0E-80	7862393	NT	Homo sapiens KIAA0941 protein (KIAA0941), mRNA
6452	19619	32982	0.82	6.0E-80	M18533.1	NT	Homo sapiens dystrophin (DMD) mRNA, complete cds
6024	22103	35843	3.4	6.0E-80	11526464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
9024	22103	35644	3.4	6.0E-80	11526464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
9221	22299	35842	1.57	6.0E-80	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21G101
8959	22624	36198	0.65	6.0E-80	AF161453.1	NT	Homo sapiens HSPC148 mRNA, complete cds
10065	23103	36706	1.83	6.0E-80	U20211.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exon 21
11183	24252	37897	2	6.0E-80	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11498	24566	38231	20.86	6.0E-80	AF226733.1	NT	Homo sapiens Oq19 mRNA, complete cds
12053	25034	38740	1.48	6.0E-80	AF102263.1	NT	Homo sapiens N-acetylglucosaminyl-phosphatase mRNA, complete cds
12176	14088	27162	1.75	6.0E-80	A1422197.1	EST_HUMAN	tt58d02x1 NCL CGAP. Bin23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN Q16795 NACH-LIBICULINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR.
12309	25972		2	6.0E-80	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12512	26351		3.32	6.0E-80	AB028900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
13081	26115		2.69	6.0E-80	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
801	13790	26811	1.7	6.0E-80	14506228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
858	14035	27097	1.89	5.0E-80	AF108330.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
858	14035	27098	1.89	5.0E-80	AF108330.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1210	14377		1.49	5.0E-80	X91647.1	NT	H. sapiens nocl gene (exon 12)
1485	14638		2.89	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2501	15628	28748	3.51	6.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2855	15969	29078	1.78	5.0E-80	14504292	NT	Homo sapiens H3 histone family, member J (H3FJ) mRNA
4150	17302	30285	0.8	5.0E-80	AB018038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4088	17302	30286	0.8	5.0E-80	AB018038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
6089	18195	31170	1.23	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C068
8562	21633	35170	1.28	5.0E-80	19910283	NT	Mus musculus keratin complex 2, gene 6g (Kt2-6g), mRNA
9458	22574	36140	5.03	4.0E-80	F26916.1	EST_HUMAN	HSPD13155 HM3 Homo sapiens cDNA clone e4000045f03
223	13445		6.03	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5026	18167		2.3	3.0E-80	BE817455.1	EST_HUMAN	QV4-BN0263-040600-241-g10 BN0263 Homo sapiens cDNA
5941	18127	32440	1.78	3.0E-80	A1091675.1	EST_HUMAN	0023e12x1 Soar66 NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1567054 3' similar to TR:035790 Q35790 PIG-L.

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1841	14987	28087	4.85	2.0E-80	R35321.1	EST_HUMAN	y865a08.r1 Scores infant brain 11B Homo sapiens cDNA clone IMAGE:38060 5'
1008	15051	28163	1.57	2.0E-80	AI444821.1	EST_HUMAN	RET487 subcloned retina cDNA library Homo sapiens cDNA clone RET487
2116	16263	28372	7.03	2.0E-80	AI04316.2	EST_HUMAN	DKFZp434D1323.r1 494 (synonym: hlec3) Homo sapiens cDNA clone DKFZp434D1323 5'
6844	20257	33696	0.95	2.0E-80	AA582832.1	EST_HUMAN	nr8001.s1 NC1_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1090177 3'
7053	20108	33622	1.89	2.0E-80	11421830	NT	Homo sapiens Golgi transport complex protein (90 kDa) (GTC80). mRNA
7401	20479	33947	0.89	2.0E-80	T75215.1	EST_HUMAN	y088f12.r1 Scores infant brain 11B Homo sapiens cDNA clone IMAGE:22851 5' similar to SPK1CR_XENLA P08802 KERATIN, TYPE I CYTOSKELETAL ENDO B :
8360	22435	35994	1.21	2.0E-80	AW684270.1	EST_HUMAN	EST376343 MAGC resequences, MAGH Homo sapiens cDNA
8970	23009	36503	0.99	2.0E-80	AI007378.1	NT	Homo sapiens GGT gene, exon 6
11109	24181	37816	6.84	2.0E-80	AA393332.1	EST_HUMAN	z70f12.r1 Scores testis 11H Homo sapiens cDNA clone IMAGE:72727 5' similar to TR:G191315
350	13561		1.52	1.0E-80	AL163303.2	NT	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN :
822	14001	27055	1.3	1.0E-80	AF231820.1	NT	Homo sapiens chromosome 21 unknown mRNA
2009	15149		2.42	1.0E-80	AI732656.1	EST_HUMAN	nm0114235 NC1_CGAP_Co9 Homo sapiens cDNA clone IMAGE:1076495 3' similar to OFR.11 OFR
4583	17720	30703	0.85	1.0E-80	AF077188.1	NT	Homo sapiens chromosome 21 unknown mRNA
5343	18458		3.32	1.0E-80	Y13932.1	NT	repetitive element :
5442	18642		5.25	1.0E-80	BE386615.1	EST_HUMAN	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
6083	19274	32603	6.12	1.0E-80	L103471	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA). mRNA
6627	19787	33176	1.17	1.0E-80	5174540	NT	protein, mRNA
7356	20435	33897	1.18	1.0E-80	AI224172.1	NT	Homo sapiens mRNA for lipophilin B
7747	20807	34296	8.03	1.0E-80	AI848731.1	EST_HUMAN	wq25605.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
7747	20807	34297	8.03	1.0E-80	AI848731.1	EST_HUMAN	wq25605.x1 NC1_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
8428	21807	35039	0.67	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA). mRNA
8897	21876	35514	0.76	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA). mRNA
8897	21876	35514	0.76	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA). mRNA
9485	22942	36104	1.17	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
9485	22942	36104	1.17	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
9485	22942	36104	1.17	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
10640	22674	37284	0.7	1.0E-80	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10887	23971	37601	4.9	1.0E-80	11641276	NT	Homo sapiens similar to rat myomesin (LOC64182). mRNA
10887	23971	37602	4.9	1.0E-80	11641276	NT	Homo sapiens similar to rat myomesin (LOC64182). mRNA
12953	25398	32042	1.32	1.0E-80	11417901	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MNT1) mRNA
12953	25398	32042	1.32	1.0E-80	11417901	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MNT1) mRNA
12953	25398	32042	1.32	1.0E-80	11417901	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MNT1) mRNA
12953	25398	32042	1.32	1.0E-80	11417901	NT	Homo sapiens gene for A-F-6, complete cds
12953	25398	32042	1.32	1.0E-80	11417901	NT	Homo sapiens gene for A-F-6, complete cds
12953	25398	32042	1.32	1.0E-80	11417901	NT	Homo sapiens gene for A-F-6, complete cds

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10823	24006	37840	1.93	8.0E-81	AI251752.1	EST_HUMAN	qth00g05.x1 Soares_NFL_T_C8C_S1 Homo sapiens cDNA clone IMAGE:1854298 3'
10823	24006	37841	1.93	8.0E-81	AI251752.1	EST_HUMAN	qth00g05.x1 Soares_NFL_T_C8C_S1 Homo sapiens cDNA clone IMAGE:1854298 3'
11422	24483	38147	5.89	8.0E-81	BE256829.1	EST_HUMAN	601310531F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632070 5'
							z621d10.r1 Soares_Jeiel_Heart_NbH-19W Homo sapiens cDNA clone IMAGE:359535 5' similar to SW:KRIA_RABIT_Q02937 KERATIN, GLYCINETYROSINE-RICH OF HAIR, [1] contains element MER22 repetitive element:
2280	16412	28543	0.94	7.0E-81	AA011080.1	EST_HUMAN	z601c08.x5 Soares_fetal_Lung_NbH-19W Homo sapiens cDNA clone IMAGE:289918 3'
7402	20480	33948	3.89	7.0E-81	AI822115.1	EST_HUMAN	601111870F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4506	17645	30632	3.73	6.0E-81	BE256829.1	EST_HUMAN	601111870F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4506	17645	30633	3.73	6.0E-81	BE256829.1	EST_HUMAN	601111870F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
5397	18559	31569	2.29	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5397	18559	31570	2.29	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8437	22811	36076	1.24	6.0E-81	AA36017.1	EST_HUMAN	EST189129 Fetal lung II Homo sapiens cDNA 5' end
12747	25495	32030	3.38	6.0E-81	BF678022.1	EST_HUMAN	602163666F1 NIH_MGC_33 Homo sapiens cDNA clone IMAGE:4294801 5'
12747	25495	32031	3.38	6.0E-81	BF678022.1	EST_HUMAN	602163666F1 NIH_MGC_33 Homo sapiens cDNA clone IMAGE:4294801 5'
2281	15423	28557	2.98	5.0E-81	BE289042.1	EST_HUMAN	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
8807	21688	35226	3.06	5.0E-81	AB007823.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8807	21688	35227	3.06	5.0E-81	AB007823.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8848	22888	38467	1.25	5.0E-81	MB0316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
8848	22888	38468	1.25	5.0E-81	MB0316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
11883	24871	38568	1.76	6.0E-81	9506634	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
720	13902	25943	0.64	4.0E-81	AI521435.1	EST_HUMAN	h6b0a12.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:O85560 O85560
1867	15013	28121	1.54	4.0E-81	AW779812.1	EST_HUMAN	h6b0d02.x1 NCI_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3035907 3' similar to SW:COFG_BOVIN
3239	16413	28428	3.91	4.0E-81	AB037068.1	NT	PS3620 COATOMER GAMMA SUBUNIT:
3718	16878	28884	0.88	4.0E-81	AW004008.1	EST_HUMAN	Homo sapiens mRNA for KIAA1345 protein, partial cds
4276	17421	30408	2.94	4.0E-81	AF263306.1	NT	we90h03.x1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR:O43815 O43815
4276	17421	30409	2.94	4.0E-81	AF263306.1	NT	STR1A.TIN.:
							STR1A.TIN.:
7427	20504	33974	0.91	4.0E-81	4757893	NT	Homo sapiens calcium channel, voltage-dependent, L type, alpha 2delta subunit (CACNA2) mRNA
7659	20631	34106	0.59	4.0E-81	11420544	NT	Homo sapiens eis variant gene 1 (ETV1), mRNA
8482	21563	36098	2.36	4.0E-81	X06989.1	NT	Human mRNA for amyloid A4(751) protein
8742	21821	35355	2.2	4.0E-81	U20187.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3



Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8742	21821	35356	2.2	4.0E-81	U20187.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha subunit gene, exons 2 and 3
9427	22601	36087	3.35	4.0E-81	AB018001.1	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
10306	23341	36946	1.4	4.0E-81	U142528.1	NT	Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA
10374	23409	37016	0.85	4.0E-81	U1439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
10374	23409	37019	0.65	4.0E-81	U1439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11481	24520	38189	4.74	4.0E-81	U759085	NT	Homo sapiens vesicle trafficking protein vsc22b (SEC22B), mRNA
11481	24520	38190	4.74	4.0E-81	U759085	NT	Homo sapiens vesicle trafficking protein vsc22b (SEC22B), mRNA
12200	26039	31682	8.38	4.0E-81	U1417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12200	26039	31683	8.38	4.0E-81	U1417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12786	25532	32009	1.63	4.0E-81	U141787	NT	Homo sapiens beta-uridylate phosphorylase (LOC51733), mRNA
12786	25532	32010	1.63	4.0E-81	U141787	NT	Homo sapiens beta-uridylate phosphorylase (LOC51733), mRNA
1286	25823	31978	4.21	4.0E-81	U1417974	NT	Homo sapiens transcobalamin II, macrocytic anemia (TCND2), mRNA
1286	25823	31978	4.21	4.0E-81	U1417974	NT	Homo sapiens transcobalamin II, macrocytic anemia (TCND2), mRNA
1286	14452	27517	9.06	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1286	14452	27517	9.06	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2444	15572	28701	1.72	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A), complete cds
3055	16231	28230	6.11	3.0E-81	U4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
3055	16231	28231	6.11	3.0E-81	U4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
2894	16073	28080	2.29	2.0E-81	BE784336.1	EST_HUMAN	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
2894	16073	28081	2.29	2.0E-81	BE784336.1	EST_HUMAN	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
3873	17032	30031	0.8	2.0E-81	AW611542.1	EST_HUMAN	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
8144	21226	34746	0.89	2.0E-81	8923839	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
13129	17032	30031	5.88	2.0E-81	AW611542.1	EST_HUMAN	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
4639	17774	30754	2.86	1.0E-81	AA040370.1	EST_HUMAN	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
4768	17903	30885	9.54	1.0E-81	BE047988.1	EST_HUMAN	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
5241	18383	31331	0.8	1.0E-81	989844	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
5351	18479	38821	6.18	1.0E-81	U87828.1	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
5469	18659	31648	3.8	1.0E-81	U1432868	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
5469	18659	31649	3.8	1.0E-81	U1432868	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
6619	18813	31881	0.76	1.0E-81	AA255569.1	EST_HUMAN	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA
6771	18953	32284	3.18	1.0E-81	U52351.1	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN), mRNA

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5771	18983	32285	3.18	1.0E-81 U52351.1	NT	NT	Homo sapiens arm-repeat protein NPREA/pneurojuncin (CTNND2) mRNA, partial cds
6274	19448	32797	1.81	1.0E-81 BF67484.1	EST_HUMAN	EST_HUMAN	602137684F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274535 5'
6877	20029	33439	1.09	1.0E-81 AJ139269.1	NT	NT	Homo sapiens caveolin-1/2 locus, Contig1, DYS522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7949	20589	34509	7.84	1.0E-81 AJ139269.1	NT	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
7972	21022	34535	0.61	1.0E-81 AJ260408.1	NT	NT	Homo sapiens GLI3 gene for GLI3 protein
8978	23017	36810	0.89	1.0E-81 BE988278.1	EST_HUMAN	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3830228 5'
8978	23017	36811	0.89	1.0E-81 BE988278.1	EST_HUMAN	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3830228 5'
10174	23211	36804	5.13	1.0E-81 BE564307.1	EST_HUMAN	EST_HUMAN	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3695483 5'
							ect14d08.61 Strathgene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:858427 3' similar to SW:YB36 YEAST P38126 HYPOTHETICAL 60.5 KD PROTEIN IN RPS101-PPS13 INTERGENIC REGION.
10308	23343	36948	0.81	1.0E-81 AA630714.1	EST_HUMAN	EST_HUMAN	601577339F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3838280 5'
10310	23345	36950	3.72	1.0E-81 BE744545.1	EST_HUMAN	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10310	23346	36951	3.72	1.0E-81 BE744545.1	EST_HUMAN	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10728	23769	37367	1.41	1.0E-81 AW697550.1	EST_HUMAN	EST_HUMAN	CN8-NIND056-140400-147-812 NIND059 Homo sapiens cDNA
10884	23888	37619	0.49	1.0E-81 AW260322.1	EST_HUMAN	EST_HUMAN	2822127 Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822127 5'
11182	24261	37886	1.97	1.0E-81 8923688	NT	NT	Homo sapiens golgin-like protein (GLP), mRNA
11347	24409	38061	1.56	1.0E-81 AW944986.1	EST_HUMAN	EST_HUMAN	WFO-CT0006-250589-019 CT0006 Homo sapiens cDNA
11347	24409	38062	1.96	1.0E-81 AW944986.1	EST_HUMAN	EST_HUMAN	WFO-CT0006-250589-019 CT0006 Homo sapiens cDNA
11362	24414	38068	2.83	1.0E-81 AW789167.1	EST_HUMAN	EST_HUMAN	RC3-UM0046-290200-011-408 UM0046 Homo sapiens cDNA
11362	24414	38069	2.93	1.0E-81 AW789167.1	EST_HUMAN	EST_HUMAN	RC3-UM0046-290200-011-408 UM0046 Homo sapiens cDNA
11350	18490	31528	2.46	1.0E-81 AW60558.1	EST_HUMAN	EST_HUMAN	EST372728 IMAGE resequences, IMAGE Homo sapiens cDNA
11812	24802	38501	1.89	1.0E-81 BF204253.1	EST_HUMAN	EST_HUMAN	60186774F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
12417	26285	32086	3.6	1.0E-81 11418138	NT	NT	Homo sapiens photobin (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA
13	13251	26251	1.59	8.0E-82 AF161406.1	NT	NT	Homo sapiens HSPC288 mRNA, partial cds
108	13251	26251	1.56	8.0E-82 AF161406.1	NT	NT	Homo sapiens HSPC288 mRNA, partial cds
274	13492	26523	1.58	8.0E-82 U08986.1	NT	NT	Human CRFB4 gene, partial cds
837	14015	27070	1.87	8.0E-82 U08986.1	NT	NT	Human CRFB4 gene, partial cds
910	14086	27150	1.84	8.0E-82 U08986.1	NT	NT	Human CRFB4 gene, partial cds
1520	14873	27735	2.24	8.0E-82 AB037748.1	NT	NT	Homo sapiens glutathione peroxidase 5 (epithelial androgen-related protein) (GPX5), transcript variant 2, mRNA
1690	14842	27927	1.39	8.0E-82	NT	NT	Homo sapiens glutathione peroxidase 5 (epithelial androgen-related protein) (GPX5), transcript variant 2, mRNA
4198	17348	30339	0.74	8.0E-82	NT	NT	Homo sapiens glutathione peroxidase 5 (epithelial androgen-related protein) (GPX5), transcript variant 2, mRNA
4358	17501	30483	0.83	8.0E-82	NT	NT	Homo sapiens hypothetical protein FLJ20481 (FLJ20481), mRNA

### Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exam SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1481	14834		1.18	7.0E-82	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086.5
2825	16829	28049	1.62	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000762.3
1705	14857	27944	22.54	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
5613	16807	31874	0.87	4.0E-82	BF331591.1	EST_HUMAN	QV2-HT0540-120900-362-708 HT0540 Homo sapiens cDNA
5913	18807	31875	0.87	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-708 HT0540 Homo sapiens cDNA
5876	16063	32374	1.1	4.0E-82	M25833.1	NT	Human von Willebrand factor gene, exon 9
12016	26000	38702	4.71	4.0E-82	A1937310.1	EST_HUMAN	wp75609.x1 NC1 CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2467824.3 similar to TR:075278
12883	25455		3.78	4.0E-82	AF029707.2	NT	wp75609.x1 NC1 CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2467824.3 similar to TR:075278
288	13508	28540	16.3	3.0E-82		NT	Homo sapiens amyloid beta (A4) precursor protein (precursor nexn-11, Alzheimer disease) (APP), mRNA
721	13903	26944	2.6	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-013-702 BN0120 Homo sapiens cDNA
810	13889	27043	8.44	3.0E-82	6174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
693	14089	27134	6.31	3.0E-82		NT	Homo sapiens amyloid beta (A4) precursor protein (precursor nexn-11, Alzheimer disease) (APP), mRNA
1086	14252		15.73	3.0E-82	AA725648.1	EST_HUMAN	at23905.s1 Soares, Isatis_NHT Homo sapiens cDNA clone 1343648.3
1386	14641	27617	1.22	3.0E-82	AW875073.1	EST_HUMAN	RC6-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA
1494	14647	27728	6.56	3.0E-82	AL163293.2	NT	Homo sapiens chromosome 21 segment HS21C085
1850	15033	28164	2.14	3.0E-82	BE813332.1	EST_HUMAN	RC1-BN0005-280700-018-g04 BN0005 Homo sapiens cDNA
2092	15202	28318	1.11	3.0E-82		NT	Homo sapiens edénylate cyclase activating polypeptide 1 (pituitary) receptor type I (ADCYAP1R1) mRNA
3345	16518		2.42	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
8346	21427	34952	0.86	3.0E-82	11425206	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8753	21832	35371	0.89	3.0E-82	11432889	NT	Homo sapiens contractin 6 (CNTN6), mRNA
8753	21832	35372	0.89	3.0E-82	11432889	NT	Homo sapiens contractin 6 (CNTN6), mRNA
10029	23087	38665	4.01	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
10029	23087	38666	4.01	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
610	13789	26818	2.49	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
610	13789	26819	2.49	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1720	14870	27862	2.23	2.0E-82	AL046390.1	EST_HUMAN	DKFZ43M117.1 434 (synonym: hncs) Homo sapiens cDNA clone DKFZ43M117.5
3949	17107	30104	0.93	2.0E-82	D81875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4131	17284	30278	0.89	2.0E-82	U78833.1	NT	Homo sapiens integral membrane serine protease Sepsase mRNA, complete cds
4348	17491	30473	0.9	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4680	17815	30803	1.52	2.0E-82	AB029018.1	NT	Homo sapiens mRNA for KIAA1099 protein, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4680	17815	30804	1.62	2.0E-82	AB029073.1	NT	Homo sapiens mRNA for KIAA1098 protein, partial cds
4692	16121	31100	2.85	2.0E-82	AF045555.1	NT	Homo sapiens wbcscr1 (WBCSCR1) and wbcscr3 (WBCSCR3) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5191	18313	31280	1.56	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5191	18313	31281	1.56	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5597	18782	31827	2.89	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
6304	16477	32832	4.93	2.0E-82	AF234882.1	NT	Homo sapiens FANCA1 splice variant a (FANCA1) mRNA, complete cds
7858	26222		1.19	2.0E-82	AI476428.1	EST_HUMAN	tm21905.x1 Soares_NEL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157272
7858	21038	34550	0.8	2.0E-82	8823130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8500	21591	35117	1.81	2.0E-82	11321570	NT	Homo sapiens slit (Drosophila) homolog 3 (SLIT3), mRNA
8869	21948	35462	0.59	2.0E-82	7687340	NT	Homo sapiens microchidia (mouse) homolog (MORC), mRNA
8869	21948	35463	0.58	2.0E-82	7687340	NT	Homo sapiens microchidia (mouse) homolog (MORC), mRNA
10315	23350	36956	1.16	2.0E-82	Y09032.1	NT	Homo sapiens endogenous retrovirus-K, LTR U5 and gag gene
10315	23350	36957	1.16	2.0E-82	Y09032.1	NT	Homo sapiens endogenous retrovirus-K, LTR U5 and gag gene
11547	24603	38279	1.74	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNEP), mRNA
11547	24603	38280	1.74	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNEP), mRNA
11588	24841	38322	2.6	2.0E-82	U80798.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11588	24841	38323	2.6	2.0E-82	U80798.1	NT	Homo sapiens CAGF9 mRNA, partial cds
12230	25171		2.81	2.0E-82	N94950.1	EST_HUMAN	z01008.r1 Soares_fetal_liver_spleen_TNFS_S1 Homo sapiens cDNA clone IMAGE:429588
12818	25545		3.72	2.0E-82	AA011278.1	EST_HUMAN	z01008.r1 Soares_fetal_liver_spleen_TNFS_S1 Homo sapiens cDNA clone IMAGE:429588
605	13794	28913	1.59	1.0E-82	11949921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1236	14394		3.19	1.0E-82	BE885106.1	EST_HUMAN	601510859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207
1314	14470	27636	1.38	1.0E-82	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
1315	14471	27637	0.8	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
9143	22222	35765	0.9	1.0E-82	AB037838.1	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
9853	22893	36474	0.51	1.0E-82	AB014662.1	NT	Homo sapiens mRNA for KIAA0662 protein, partial cds
10451	23486		1.4	1.0E-82	BF615839.1	EST_HUMAN	UH-HBW1-4004-03-0-UJ.st NCI_CGAP_Suab7 Homo sapiens cDNA clone IMAGE:3084033
10451	23486		2.49	1.0E-82	AL163308.2	NT	Homo sapiens chromosome 21 segment HS21C009
11258	24327	37896	1.49	1.0E-82	AL163346.2	NT	Homo sapiens chromosome 21 segment HS21C0049
5307	18424	31394	1.05	9.0E-83	AF224569.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8912	21991	35530	4.99	8.0E-83	BF672220.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291561
10481	23516	37128	0.72	9.0E-83	BE283347.1	EST_HUMAN	601117160F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3397734
1446	14589	27676	2.97	8.0E-83	BE383073.1	EST_HUMAN	601273346F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1715	15992	27956	10.59	8.0E-83	N66951.1	EST_HUMAN	244812.s1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:295823 3'
1386	14543	27918	1.2	7.0E-83	AW385579.1	EST_HUMAN	QV4L.T0016-271289-088.H11.LT0016 Homo sapiens cDNA no12h01.s1 NCI CGAP_Phet Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element:
2926	16105		1.64	7.0E-83	AA584653.1	EST_HUMAN	7p37a07.x1 NCI CGAP_P28 Homo sapiens cDNA clone IMAGE:3647883 3' similar to 1R:Q9Y316 Q9Y316 D1207H1.1 ;
4936	18089		6.85	7.0E-83	BF221813.1	EST_HUMAN	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
6176	15362	32699	0.95	7.0E-83	11428657	NT	Homo sapiens Glycoprotein IIb (GP1Ib) gene, exons 2-29
416	13611	26650	1.39	6.0E-83	M33320.1	NT	Human platelet Glycoprotein IIb (GP1Ib) gene, exons 2-29
1828	14676	28071	1.79	8.0E-83	AW573038.1	EST_HUMAN	h131h03.x1 Scores NFL_T GBC.S1 Homo sapiens cDNA clone IMAGE:2833526 3' similar to SW:YBEB_HAEN P4471 HYPOTHETICAL PROTEIN H10034. ;
3082	19256	29277	0.68	6.0E-83	AW618405.1	EST_HUMAN	QV4.ST0234-181199-037-005 ST0234 Homo sapiens cDNA
3116	16292		0.7	8.0E-83	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3653	16816	29828	0.92	6.0E-83	11430241	NT	Homo sapiens hypophyseal protein FLJ10379 (FLJ10379), mRNA
5408	18610	31592	1.73	6.0E-83	4507666	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
6147	18324	32690	1.31	6.0E-83	AL010770.1	NT	Homo sapiens hyperion gene, exons 1-50
7871	20737	34215	2	6.0E-83	11422024	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
9878	22918	36503	3.51	6.0E-83	14505314	NT	Homo sapiens myomesin (My-protein) 2 (165kD) (MYOM2), mRNA
9871	23010	36604	0.71	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
9971	23010	36605	0.71	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
11821	24810		2.31	6.0E-83	AA486105.1	EST_HUMAN	ab14e10.s1 Stragene Lung (#937210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR12 THIR repetitive element ;
12178	25139		4.14	6.0E-83	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
969	14142		1.24	5.0E-83	U17883.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
2108	16989		3	5.0E-83	AF006305.1	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
3728	16893	28993	0.91	5.0E-83	AL133207.2	NT	Novel human gene mapping to chromosome X
4015	17172	30180	0.73	5.0E-83	4893190	NT	Homo sapiens deoxyribonuclease I (DNASEI), mRNA
4564	17692	30672	0.61	5.0E-83	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
6190	18312	31278	13.87	5.0E-83	4557013	NT	Homo sapiens cathepsin (CAT) mRNA
5190	18312	31278	13.87	5.0E-83	4557013	NT	Homo sapiens cathepsin (CAT) mRNA
657	13843	26870	1.87	4.0E-83	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
1022	14193		4.09	3.0E-83	AA368311.1	EST_HUMAN	EST175542 Placenta1 Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9

[illegible]

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11168	24238	37871	1.64	2.0E-83	AL134432.1	EST_HUMAN	DKFZ547J135.1 547 (synonym: mbr1) Homo sapiens cDNA clone DKFZ547J135.5
12859	25570		3.26	2.0E-83	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
1444	14597	27673	2.26	1.0E-83	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase3-oxoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1444	14697	27674	2.26	1.0E-83	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase3-oxoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
2076	16216	28335	1.15	1.0E-83	4503652	NT	Homo sapiens fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1) mRNA
2722	15840	28951	1.21	1.0E-83	BE883690.1	EST_HUMAN	Homo sapiens cell recognition molecule Caspr2 (KIAA0968), mRNA
3281	16425	29443	0.72	1.0E-83	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0968), mRNA
3872	17129	30132	7.78	1.0E-83	AF053788.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP90 mRNA, partial cds
4369	17502	30484	2.22	1.0E-83	Z25822.1	NT	H. sapiens gene for mitochondrial dodecenoyl-CoA delta-isomerase, exon 3
5008	18137	31111	2.74	1.0E-83	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
6835	18988	33397	1.59	1.0E-83	A1027614.1	EST_HUMAN	0x89008.x1 Score: _testis_NHT Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:U64241.QM
3897	17056	30068	3.62	7.0E-84	BE801209.1	EST_HUMAN	PROTEIN (HUMAN):
1323	14479	27544	2.86	6.0E-84	BE83894.1	EST_HUMAN	601676023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958853 5'
1323	14479	27545	2.98	6.0E-84	BE83894.1	EST_HUMAN	RC2-FN0119-200500-011-905 FN0119 Homo sapiens cDNA
2471	15598	28723	17.98	6.0E-84	AA176574.1	EST_HUMAN	RC2-FN0119-200500-011-905 FN0119 Homo sapiens cDNA
5354	18481		2.18	6.0E-84	AL042833.2	EST_HUMAN	aes6603.s1 Stratigene echizo brain S11 Homo sapiens cDNA clone IMAGE:871020 3'
6635	18829	31905	1.91	6.0E-84	AA897399.1	EST_HUMAN	DKFZp434H0322_r1 434 (synonym: hase3) Homo sapiens cDNA clone DKFZp434H0322 5'
6777	18959	32273	0.89	6.0E-84	11428718	NT	847603.s1 Scores: NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gb:U14338
6777	18959	32273	0.89	6.0E-84	11428718	NT	VITAMIN K-DEPENDENT PROTEIN 6 PRECURSOR (HUMAN):
6777	18959	32273	0.89	6.0E-84	11428718	NT	Homo sapiens acetyl LDL receptor, SREC-scavenger receptor expressed by endothelial cells (SREC), mRNA
6777	18959	32273	0.89	6.0E-84	11428718	NT	Homo sapiens acetyl LDL receptor, SREC-scavenger receptor expressed by endothelial cells (SREC), mRNA
7642	20711	34190	3.14	6.0E-84	BE101571.1	EST_HUMAN	PMO-L-T0018-190500-004-F02 L-T0018 Homo sapiens cDNA
7888	20822	34428	1.05	6.0E-84	AF038391.1	NT	Homo sapiens pre-miRNA splicing factor (PRP18) mRNA, complete cds
8284	21346	34861	2	6.0E-84	BE170199.1	EST_HUMAN	PM4-L-T0054-160500-004-e10 F-T0054 Homo sapiens cDNA
732	13914	28956	1.32	5.0E-84	AA382811.1	EST_HUMAN	EST160304 Testis 1 Homo sapiens cDNA 5' end
3076	16255		1.91	5.0E-84	AF109718.1	NT	EST160304 Testis 1 Homo sapiens cDNA 5' end
6232	18407	32756	0.62	5.0E-84	AA167678.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11839	24827	38516	2.85	5.0E-84	11428740	NT	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (REFX3), mRNA
11852	24838	38640	1.88	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
11852	24838	38641	1.98	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
1407	14591	27835	1.34	4.0E-84	AB037735.1	NT	Homo sapiens mRNA for KIAA1314 protein, partial cds
1443	14598	27872	4.47	4.0E-84	AI68531.1	EST_HUMAN	wa76cd4.x1 Soares NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:2302085 3' similar to SW_NPDC_HUMAN O43847 NADPHYSIN PRECURSOR;
6084	18182	31187	0.66	4.0E-84	4505928	NT	Homo sapiens polyomerase (DNA-directed), alpha (70kD) (POLA2), mRNA
5085	18183	31188	1.62	4.0E-84	AF089601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
6377	18579	31448	1.82	4.0E-84	AF022635.1	NT	Homo sapiens multidrug resistance protein (MRP), exon 13
5680	18874	32182	1.8	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5890	18974	32183	1.8	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
6388	18987	32928	2.14	4.0E-84	AF056650.1	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
7825	20880	34381	13.68	4.0E-84	11421326	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
9112	22181	35735	1.12	4.0E-84	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9112	22181	35736	1.12	4.0E-84	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
11158	24228	37859	4.78	4.0E-84	AB032855.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
326	13540	26572	2.16	3.0E-84	AF026200.1	NT	Homo sapiens Bach1 protein homolog mRNA, partial cds
1178	14341	27395	1.53	3.0E-84	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2016	16155	28260	2.38	3.0E-84	6453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
2063	16203	28319	2.38	3.0E-84	AI096830.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
3843	17002	30005	5.53	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLR51) mRNA, complete cds
11118	24180		6.78	3.0E-84	AI693801.1	EST_HUMAN	wu20d05.x1 Soares Dieckgreffe, codon, NHCD Homo sapiens cDNA clone IMAGE:2520585 3' similar to gb1L05083 60S RIBOSOMAL PROTEIN L18A (HUMAN);
2172	15307	28435	6.48	2.0E-84	BE96397.1	EST_HUMAN	GM1-B10765-190800-272-b08 B10785 Homo sapiens cDNA
2172	15307	28436	6.48	2.0E-84	BE96397.1	EST_HUMAN	GM1-B10765-190800-272-b08 B10785 Homo sapiens cDNA
3008	16185	29209	8.21	2.0E-84	AF036933.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
3027	16203	29228	1.22	2.0E-84	X88211.1	NT	H. sapiens DNA for endogenous retroviral like element
5843	18837	31914	0.93	2.0E-84	BF511575.1	EST_HUMAN	UI-H-B14-ae1-a-02-Q-UI.1 NCI CGAP_Su88 Homo sapiens cDNA clone IMAGE:3084863 3'
5843	18837	31915	0.93	2.0E-84	BF511575.1	EST_HUMAN	UI-H-B14-ae1-a-02-Q-UI.1 NCI CGAP_Su88 Homo sapiens cDNA clone IMAGE:3084863 3'
6774	19929	33325	0.92	2.0E-84	AI288074.1	EST_HUMAN	ys58e11.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:209324 3'
8247	21329		1.55	2.0E-84	AI288074.1	EST_HUMAN	q8b7c09.x1 NCI CGAP_L165 Homo sapiens cDNA clone IMAGE:1895728 3'
8578	21860	35200	0.58	2.0E-84	AI163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8578	21860	35201	0.58	2.0E-84	AI163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8546	22611	36178	1.24	2.0E-84	AU120230.1	EST_HUMAN	AU120280 HEMBB1 Homo sapiens cDNA clone HEMBB1000339 5'



Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8993	22672	36564	0.64	2.0E-84	H22841.1	EST_HUMAN	ym49t1.1t Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:61383 5' similar to SP-APOH_RAT
12449	25316	32092	1.81	2.0E-84	BF448006.1	EST_HUMAN	P26644 BETA-2-GI YCOOPROTEIN1:
12449	25316	32093	1.81	2.0E-84	BF448006.1	EST_HUMAN	ma30a02.x1 Lupsk1, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
322	13638	26568	1.5	1.0E-84	AF114483.1	NT	ma30a02.x1 Lupsk1, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
663	13765	26781	10.87	1.0E-84	4507952	NT	TR:Q9UGS3 Q9UGS3 D1766G23.1:
738	13920	27642	1.19	1.0E-84	AA984379.1	EST_HUMAN	TR:Q9UGS3 Q9UGS3 D1766G23.1:
1321	14277	27642	2.83	1.0E-84	BE392137.1	EST_HUMAN	ma30a02.x1 Lupsk1, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
2114	15252	28371	3.11	1.0E-84	AA720851.1	EST_HUMAN	TR:Q9UGS3 Q9UGS3 D1766G23.1:
2288	15430	28582	1.53	1.0E-84	AL228041.1	EST_HUMAN	ma30a02.x1 Lupsk1, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
3845	17005	30007	2.78	1.0E-84	AA720851.1	EST_HUMAN	TR:Q9UGS3 Q9UGS3 D1766G23.1:
4538	17676	30659	5.89	1.0E-84	AL043314.2	EST_HUMAN	ma30a02.x1 Lupsk1, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
4821	17954	30840	3.03	1.0E-84	AL043314.2	EST_HUMAN	TR:Q9UGS3 Q9UGS3 D1766G23.1:
5031	17676	30659	3.56	1.0E-84	AL228041.1	NT	ma30a02.x1 Lupsk1, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
6043	18226	32549	0.88	1.0E-84	11434422	NT	TR:Q9UGS3 Q9UGS3 D1766G23.1:
6319	19491	32849	2.84	1.0E-84	ST3482.1	NT	ma30a02.x1 Lupsk1, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
7020	20166	33576	1.42	1.0E-84	AL049794.1	NT	TR:Q9UGS3 Q9UGS3 D1766G23.1:
7020	20166	33577	1.42	1.0E-84	AL049794.1	NT	ma30a02.x1 Lupsk1, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
7296	20339	33789	2.53	1.0E-84	AL049794.1	NT	TR:Q9UGS3 Q9UGS3 D1766G23.1:
7637	20706	34186	10.45	1.0E-84	8383984	NT	ma30a02.x1 Lupsk1, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
7737	20798	34287	1.07	1.0E-84	11430846	NT	TR:Q9UGS3 Q9UGS3 D1766G23.1:
7777	20798	34287	2.34	1.0E-84	11430846	NT	ma30a02.x1 Lupsk1, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
8736	22800	36606	2.79	1.0E-84	5031884	NT	TR:Q9UGS3 Q9UGS3 D1766G23.1:
8872	22811	36606	0.6	1.0E-84	AF224511.1	NT	ma30a02.x1 Lupsk1, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
8894	18488	31527	1.6	1.0E-84	4507848	NT	TR:Q9UGS3 Q9UGS3 D1766G23.1:
8894	18488	31528	1.6	1.0E-84	4507848	NT	ma30a02.x1 Lupsk1, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
12325	25236	32088	2.62	1.0E-84	11417812	NT	TR:Q9UGS3 Q9UGS3 D1766G23.1:
12438	25311	32088	3.77	1.0E-84	11418185	NT	ma30a02.x1 Lupsk1, sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
889	14161		1.94	9.0E-85	AL163209.2	NT	TR:Q9UGS3 Q9UGS3 D1766G23.1:

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1098	14263	27319	2.88	8.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1098	14263	27320	2.88	8.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1608	14762	27841	1.12	8.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1608	14762	27842	1.12	8.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1709	14850	27949	3.59	9.0E-85	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
3870	17028		0.8	8.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4366	17509	30490	0.92	8.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5001	18130	31105	0.89	8.0E-85	5901978	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
5032	18160	31137	1.16	8.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C068
13046	14880	27949	1.78	9.0E-85	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
1159	14323	27378	4.64	7.0E-85	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
11943	24628		6.61	7.0E-85	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
11702	24699	38391	2.56	6.0E-85	11439573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11702	24699	38392	2.56	6.0E-85	11439573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
12060	25041	38750	2	8.0E-85	AA403053.1	EST_HUMAN	z162b01.r1 Scores: testis, NHT Homo sapiens cDNA clone IMAGE:728889 5' similar to TR:G1335789
2410	15540	28668	4.08	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4582	17690		0.71	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-e isoform (CACNA1I) mRNA, complete cds
5587	18764	31804	1.59	5.0E-85	BF03674.1	EST_HUMAN	601458646F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3862402 5'
5587	18764	31805	1.59	5.0E-85	BF03674.1	EST_HUMAN	601458646F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3862402 5'
11381	24442	38101	2.31	6.0E-85	AF224699.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
13127	17690		1.72	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-e isoform (CACNA1I) mRNA, complete cds
6276	18450	32788	1.39	4.0E-85	BF07810.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248087 5'
6276	18450	32789	1.39	4.0E-85	BF07810.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248087 5'
8021	21074	34688	3.43	4.0E-85	BE882304.1	EST_HUMAN	601506022F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3806940 5'
10788	23831		1.8	4.0E-85	BE079263.1	EST_HUMAN	RC1-BT0623-120200-011-c07 BT0623 Homo sapiens cDNA
1327	14484	27561	0.91	3.0E-85	AF098167.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1821	14970	28082	4.8	3.0E-85	T97486.1	EST_HUMAN	yes3g09.r1 Scores: fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:121504 5'
6018	18148	31125	1.03	3.0E-85	11024685	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5019	18148	31128	1.03	3.0E-85	11024595	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
5080	18208	31180	0.91	3.0E-85	7383442	NT	Homo sapiens olfactory receptor, family 12, subfamily D, member 2 (OR12D2), mRNA
5517	18716	31729	6.36	3.0E-85	11436001	NT	Homo sapiens lactoferrin, proline rich protein (LPRP), mRNA
6210	18385	32734	0.72	3.0E-85	11422024	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
6202	18436	32782	4.92	3.0E-85	7662309	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
6262	19436	32783	4.82	3.0E-85	7662309	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
7091	20186		7.96	3.0E-85	AL404488.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7635	20627	34103	0.84	3.0E-85	11416870	NT	Homo sapiens GTPase regulator associated with the focal adhesion kinase p125(FAK); KIAA0621 protein (KIAA0621), mRNA
8059	21139	34659	1.44	3.0E-85	U44961.1	NT	Homo sapiens DENN mRNA, complete cds
8706	21786	35319	0.48	3.0E-85	11525929	NT	Homo sapiens CGI-58 protein (LOC61108), mRNA
8178	22286	35798	4.39	3.0E-85	11430889	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
9506	22772	36343	0.84	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B* (SNRPB2), mRNA
9509	22772	36344	0.84	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B* (SNRPB2), mRNA
10700	23733	37338	0.72	3.0E-85	AF098642.1	NT	Homo sapiens phospholipid scramblase mRNA, complete cds
11799	24789	38484	1.48	3.0E-85	5031680	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
12989	25948		3.02	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
985	14157	27218	0.62	2.0E-85	7657266	NT	Homo sapiens KIAA0929 protein Max2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1065	14231	27289	2.35	2.0E-85	AF24640.1	NT	Homo sapiens Interactin 2 (SH3D1B), mRNA, complete cds
1436	14589	27862	1.19	2.0E-85	7708205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
1451	14604	27882	13.02	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2), mRNA
1451	14604	27883	13.02	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2), mRNA
2304	16436	28668	2.92	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2884	14523		4.22	2.0E-85	7657488	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3087	16283	29280	3.67	2.0E-85	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4464	17584	30574	4.66	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG), mRNA
4697	17822	30810	0.74	2.0E-85	4826977	NT	Homo sapiens reelin (RELN), mRNA
5030	18159	31136	1.21	2.0E-85	AL163294.2	NT	Homo sapiens chromosome 21 segment HS21C084
6473	22530	36094	1.78	2.0E-85	AI760830.1	EST_HUMAN	w67n08.x1 NCI_CGAP Kid12 Homo sapiens cDNA clone IMAGE:2396431 3' similar to contains element
9849	22889	38469	0.82	2.0E-85	AI914459.1	EST_HUMAN	wd46d03.x1 Soares NFL_T GBC_S1 Homo sapiens cDNA clone IMAGE:2331481 3'
10469	23504	37118	0.94	2.0E-85	AI88634.1	EST_HUMAN	winsd412.x1 NCI_CGAP U2 Homo sapiens cDNA clone IMAGE:2443607 3'
2360	16491		3.66	1.0E-85	BE794308.1	EST_HUMAN	601691416f1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2497	16594	28719	9.39	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
2497	16594	28720	8.36	1.0E-85	BE618392.1	EST_HUMAN	601462817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
7983	21032	34645	0.61	1.0E-85	BE082851.1	EST_HUMAN	MRQ-8T0284-221199-002-103 BT0284 Homo sapiens cDNA
9884	23023	36618	2.13	1.0E-85	BE257917.1	EST_HUMAN	601106738F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350553 5'
10416	23450	37055	0.76	1.0E-85	AW613535.1	EST_HUMAN	RC1-ST0186-081099-011-405 ST0186 Homo sapiens cDNA
11184	24235	37865	2.79	1.0E-85	AA778785.1	EST_HUMAN	Z4503.31 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
11184	24235	37866	2.79	1.0E-85	AA778785.1	EST_HUMAN	Z4503.31 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
11245	24314	37853	1.86	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128440 5'
11245	24314	37854	1.86	1.0E-85	BF311552.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128440 5'
12068	25049	38757	3.29	1.0E-85	AA198420.1	EST_HUMAN	q56a07.x1 NCI CGAP_Bn25 Homo sapiens cDNA clone IMAGE:1860468 3'
12330	25404	32045	4.68	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12801	25404	32045	2.92	1.0E-85	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1460	14613	32774	25.01	9.0E-86	BE274217.1	EST_HUMAN	801120718F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867690 5'
6254	19428	32774	0.62	8.0E-86	11424140	NT	Homo sapiens similar to CDC28 protein kinase 1 (H_spleen) (LOC83041), mRNA
233	13454	28480	2.2	7.0E-86	7662247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
960	14133	27192	1.03	7.0E-86	AA860801.1	EST_HUMAN	q18108.s1 Soares_papillary_tumor_NH-PPA Homo sapiens cDNA clone IMAGE:1403559 3'
960	14133	27193	1.03	7.0E-86	AA860801.1	EST_HUMAN	q18108.s1 Soares_papillary_tumor_NH-PPA Homo sapiens cDNA clone IMAGE:1403559 3'
6326	19497	32853	0.97	7.0E-86	9968886	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
6326	19497	32854	0.87	7.0E-86	9968886	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
7116	18542	31489	6.43	7.0E-86	11421737	NT	Homo sapiens Tax1 (human T-cell leukemia virus type 1) binding protein 1 (TAX1BP1), mRNA
8943	22022	35562	3.98	7.0E-86	138557.1	NT	Homo sapiens galactose oxidase (GALC) gene, exon 15
8901	22941		1.13	7.0E-86	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
9860	22939	36595	1.68	7.0E-86	11526307	NT	Homo sapiens Digeorge syndrome critical region gene 6 (DGCR6), mRNA
11204	24273	37809	1.44	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H_sapiens) (LOC63170), mRNA
11204	24273	37810	1.44	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H_sapiens) (LOC63170), mRNA
12117	25087	38802	1.89	7.0E-86	11418903	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
1322	14478	27543	1.87	6.0E-86	4605492	NT	Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH), mRNA
217	13438	28471	2.15	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458930 6'
6159	18335	32680	11.61	4.0E-86	BE285433.1	EST_HUMAN	601176885F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458930 5'
11517	13438	28471	2.34	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458930 5'
4404	17547	30531	0.94	3.0E-86	BE667703.1	EST_HUMAN	601443262F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847455 5'
5713	18806	32201	6.18	3.0E-86	AW340946.1	EST_HUMAN	x282h12.x1 NCI CGAP_LU24 Homo sapiens cDNA clone IMAGE:2871719 3'
8457	21538	35067	1.21	3.0E-86	AV722329.1	EST_HUMAN	AV722328 HTB Homo sapiens cDNA clone HTBBS004 5'
10425	23460	37065	3.54	3.0E-86	BE886479.1	EST_HUMAN	601509386F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10425	23460	37086	3.54	3.0E-86	BE886478.1	EST_HUMAN	601506686F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
11720	23906	37529	4.87	3.0E-86	AI656240.1	EST_HUMAN	U1802X1 NC1 CGAP_P128 Homo sapiens cDNA clone IMAGE:2261371 3'
11803	24793	39491	1.37	3.0E-86	AV690469.1	EST_HUMAN	AV690469 GKC Homo sapiens cDNA clone GKCBSE02 5'
12300	25971		3.38	3.0E-86	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636733 5'
277	13495	26525	1.68	2.0E-86	AA306264.1	EST_HUMAN	EST1177232 Jurkat T-cells VI Homo sapiens cDNA 5' end
427	13622		2.69	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1217	14378	27437	3.33	2.0E-86	N59977.1	EST_HUMAN	Y219a08.t1 Sceres_multiple_sclerosis_ZNBMSP Homo sapiens cDNA clone IMAGE:283478 5'
2265	15398	28526	8.53	2.0E-86	8935487	NT	Human endogenous retrovirus, complete genome
2342	15473	28607	1.56	2.0E-86	AB033103.1	NT	Homo sapiens mRNA for KIAA1277 protein, partial cds
3502	16689	29679	1.61	2.0E-86	AV666142.1	EST_HUMAN	EST378216 MAGE_resequences_MAGI Homo sapiens cDNA
3840	16989	30001	2.29	2.0E-86	AF168778.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAT-delta) mRNA, complete cds
3840	16989	30002	2.29	2.0E-86	AF159776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAT-delta) mRNA, complete cds
4161	17303		2.69	2.0E-86	AV615742.1	EST_HUMAN	h887608.X1 NC1 CGAP_G08 Homo sapiens cDNA clone IMAGE:2816542 3'
4910	18040	31030	3.21	2.0E-86	AF036480.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
5993	18178	32489	1.32	2.0E-86	Z18411.1	NT	H. sapiens mRNA encoding phospholipase c
5993	18178	32500	1.32	2.0E-86	Z18411.1	NT	H. sapiens mRNA encoding phospholipase c
7221	25837	33501	0.78	2.0E-86	11419429	NT	Homo sapiens similar to oocyte-specific pyrophosphatase/phosphodiesterase 3 (H. caplens) (LOC63214), mRNA
8199	21281	34803	0.58	2.0E-86	U84744.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
8772	21651	35392	2.62	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma)-2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
8772	21651	35393	2.52	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma)-2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
8104	22183	35728	0.68	2.0E-86	10853870	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
8518	22584	36153	1.86	2.0E-86	11422084	NT	Homo sapiens chromosome segregation 1 (yeast homolog) like (CSE1L), mRNA
10684	23698	37307	2.8	2.0E-86	11546848	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37308	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37309	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37310	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37311	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37312	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37313	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37314	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37315	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37316	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37317	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37318	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37319	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37320	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37321	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37322	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37323	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37324	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37325	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37326	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37327	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37328	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37329	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37330	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37331	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37332	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37333	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37334	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37335	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37336	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37337	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37338	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37339	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37340	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37341	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37342	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37343	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37344	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37345	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37346	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37347	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37348	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37349	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37350	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37351	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37352	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37353	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37354	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37355	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37356	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37357	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37358	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37359	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37360	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37361	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37362	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37363	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37364	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37365	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37366	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37367	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37368	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37369	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37370	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37371	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37372	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37373	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37374	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37375	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37376	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37377	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37378	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37379	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37380	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37381	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37382	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37383	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37384	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37385	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37386	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37387	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37388	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37389	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37390	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37391	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37392	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37393	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37394	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37395	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37396	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37397	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37398	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37399	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37400	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37401	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37402	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37403	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37404	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37405	2.9	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NIPAS3), mRNA
10684	23698	37406					

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3231	16405	28417	1.68	1.0E-86	3453649	NT	Homo sapiens fibulin 5 (FBLN5) mRNA
3307	16481	28502	2.39	1.0E-86	U0492.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3368	16540	29553	1.74	1.0E-86	AL163200.2	NT	Homo sapiens chromosome 21 segment HS21C009
3368	16540	29554	1.74	1.0E-86	AL163200.2	NT	Homo sapiens chromosome 21 segment HS21C009
4380	17523	30504	5.41	1.0E-86	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4743	17876	30861	0.94	1.0E-86	4507334	NT	Homo sapiens synaplanin 1 (SYN1), mRNA
5670	18864	32149	1.85	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
11805	18864	32149	1.53	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5472	18672		1.84	8.0E-87	AF150703.1	EST_HUMAN	SWK1CJ MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
7606	20676	34150	1.82	8.0E-87	4757721	NT	qbt7c08 x1 Soares fetal heart NbhH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to
7606	20676	34151	1.82	8.0E-87	4757721	NT	SWK1CJ MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
492	13686	26720	49.59	8.0E-87	X62245.1	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
2369	15500	28626	3.27	7.0E-87	BF063211.1	EST_HUMAN	O. cuniculus mRNA for elongation factor 1 alpha
2369	15500	28627	3.27	7.0E-87	BF063211.1	EST_HUMAN	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
6530	18694	33087	1.38	7.0E-87	AW890336.1	EST_HUMAN	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
8384	21465	34990	3	7.0E-87	BF352776.1	EST_HUMAN	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
9653	21088	34610	0.66	7.0E-87	BE71261.1	EST_HUMAN	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
10276	23311	36907	3.38	7.0E-87	AL043314.2	EST_HUMAN	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
10276	23311	36908	3.38	7.0E-87	AL043314.2	EST_HUMAN	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
10898	25965		0.53	7.0E-87	AI061565.1	EST_HUMAN	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
11129	24201	37825	6.59	7.0E-87	K03002.1	NT	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
11129	24201	37826	6.59	7.0E-87	K03002.1	NT	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
3615	16779	28794	1.19	6.0E-87	7657213	NT	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
6551	18713	33088	1.47	6.0E-87	AB029004.1	NT	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
10863	24044		4.48	6.0E-87	11432444	NT	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
1184	14347	27404	1.62	5.0E-87	AA362311.1	EST_HUMAN	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
12603	14347	27404	2.56	5.0E-87	AA362311.1	EST_HUMAN	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
988	14160	27220	1.37	4.0E-87	AL163210.2	NT	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
1189	14361	27420	7.91	4.0E-87	AB037835.1	NT	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
1461	14614	27686	1.31	4.0E-87	R78733.1	EST_HUMAN	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
2088	16226	28348	2.28	4.0E-87	AB007325.1	NT	7H8502.x1 NCJ CGAP Co16 Homo sapiens cDNA clone IMAGE:3322779 3'

Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2143	16279	28402	1.29	4.0E-87	R78133.1	EST_HUMAN	y80f10.1 Scores placenta NB2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element
2143	16279	28403	1.29	4.0E-87	R78133.1	EST_HUMAN	y80f10.1 Scores placenta NB2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element
2483	16820	28738	0.99	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51828), mRNA
2493	16820	28739	0.99	4.0E-87	7706299	NT	Homo sapiens CGI-60 protein (LOC51828), mRNA
3663	16718	29732	3.61	4.0E-87	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (triturax (Drosophila) homolog); translocated to 4 (MLL14) mRNA
6662	18759	31798	4.6	4.0E-87	000321	SWISSPROT	ETS-RELATED PROTEIN 71 (ETS TRANSLLOCATION VARIANT 2)
6669	18059	32366	0.58	4.0E-87	U85429.1	NT	Human transcription factor NFAT3 mRNA, complete cds
6170	19346	32692	4.34	4.0E-87	BE247294.1	EST_HUMAN	TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia Baydar-HQSC project=TCBAP1E4051 cDNA clone TCBAP4051
7848	20803	34408	0.71	4.0E-87	11425291	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
7848	20803	34407	0.71	4.0E-87	11425291	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
7850	21000	34510	3.84	4.0E-87	148524.1	NT	Homo sapiens tuberin (TSC2) gene, exon 10
11437	24488	38165	3.42	4.0E-87	M60678.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12705	26023	31671	1.27	4.0E-87	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12705	26023	31672	1.27	4.0E-87	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12889	25663		68.7	4.0E-87	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RX1), mRNA
2838	16950	29067	14.35	2.0E-87	4885420	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMGA4) mRNA
3884	17043	30042	1.02	2.0E-87	AU116935.1	EST_HUMAN	AU116935 HEMBA1 Homo sapiens cDNA clone HEMBA100307 5'
5033	18161	31138	3.2	2.0E-87	BF37631.1	EST_HUMAN	CNO-TN0038-150900-652-H08 TN0038 Homo sapiens cDNA
6076	18204	31176	0.8	2.0E-87	BE176478.1	EST_HUMAN	RCS-HT0580-200300-031-G04 HT0580 Homo sapiens cDNA
6778	18970	32275	12.22	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
6778	18970	32276	12.22	2.0E-87	BE734190.1	EST_HUMAN	601569041F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843730 5'
6468	18623		4.87	2.0E-87	BE507193.1	EST_HUMAN	601341363F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683348 5'
6838	18991	33399	0.79	2.0E-87	NA81281.1	EST_HUMAN	yw21e07.1 Scores fetal liver spleen 1NFJS Homo sapiens cDNA clone IMAGE:243398 5'
6920	20235	33668	0.75	2.0E-87	AV654143.1	EST_HUMAN	AV654143 GLO Homo sapiens cDNA clone IMAGE:3631511 5'
7324	20406	33868	1.35	2.0E-87	BE294432.1	EST_HUMAN	601176032F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3631511 5'
7374	20453	33918	0.7	2.0E-87	11433048	NT	Homo sapiens nucleic acid domain and RLD 2 (HERC2), mRNA
7611	20681	34157	38.59	2.0E-87	NA81281.1	EST_HUMAN	yw21e07.1 Scores fetal liver spleen 1NFJS Homo sapiens cDNA clone IMAGE:243398 5'
7864	20918	34424	36.3	2.0E-87	NA81281.1	EST_HUMAN	yw21e07.1 Scores fetal liver spleen 1NFJS Homo sapiens cDNA clone IMAGE:243398 5'
8589	21670	36208	3.35	2.0E-87	X52851.1	NT	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
9988	23027		4.86	2.0E-87	BE33136.1	EST_HUMAN	601273715F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610539 5'

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Table 4  
Single Exon Probe Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1209	15989		2.2	1.0E-87	7705683	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA
1463	14816	27898	1.81	1.0E-87	AW361877.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
1463	14816	27699	1.51	1.0E-87	AW361877.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
3801	16982	28966	5.18	1.0E-87	Y00062.1	NT	Human mRNA for T-cell cytochrome
3828	16988	28991	2.3	1.0E-87	4758827	NT	Homo sapiens neuritin III (NRXN3), mRNA
6356	19526	32883	1.63	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
6356	19526	32884	1.63	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
7333	20414	33876	1.08	1.0E-87	4508786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
7558	20830	34105	1.05	1.0E-87	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7707	20772	34257	0.92	1.0E-87	4508786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
8307	21389	34912	9.85	1.0E-87	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
9110	22189	35732	0.95	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
0110	22189	35733	0.95	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
9833	22873	36456	2.92	1.0E-87	BE618183.1	EST_HUMAN	RC6-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
9833	22873	36457	2.92	1.0E-87	BE618183.1	EST_HUMAN	RC6-BN0276-050700-012-E02 BN0276 Homo sapiens cDNA
10584	23619	37225	0.88	1.0E-87	M34426.1	NT	Human L-plastin mRNA, 5' end
10970	24050	37683	2.11	1.0E-87	5729867	NT	Homo sapiens heci domain and RLD 2 (HERC2), mRNA
11247	24316		1.66	1.0E-87	D10083.1	NT	Homo sapiens RCH1 gene, retrovirus-like element
12701	26190		2.37	1.0E-87	7657832	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
13228	26798	31890	1.22	1.0E-87	AF169356.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 9
13228	26798	31891	1.22	1.0E-87	AF169356.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 9
1130	14235	27350	8.48	8.0E-88	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1380	14635	27609	2.94	8.0E-88	AB037920.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1380	14635	27610	2.94	8.0E-88	AB037920.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
2189	16324	28449	0.88	8.0E-88	7681701	NT	Homo sapiens DKFZP586P1522 protein (DKFZP586P1522), mRNA
3717	16878	29883	1	8.0E-88	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
4384	17527	30508	2.97	8.0E-88	X91920.1	NT	H. sapiens ECE-1 gene (exon 9)
4384	17527	30509	2.97	8.0E-88	X91920.1	NT	H. sapiens ECE-1 gene (exon 9)
9223	22301	35845	4.04	6.0E-88	AF093528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1875	15019		1.22	3.0E-88	7661887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2704	15822	28639	3.65	5.0E-88	N88399.1	EST_HUMAN	K9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
3094	16240	28260	0.82	5.0E-88	AF114488.1	NT	Homo sapiens intercalin short isoform (ITSN) mRNA, complete cds



Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3076	16251	28272	0.71	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3075	16251	28273	0.71	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3476	16643		2.78	5.0E-88	AF169321.1	EST_HUMAN	repetitive element contains short isoform (ITSN) mRNA, complete cds
3625	16789	29806	0.75	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
4839	17682	30970	0.71	5.0E-88	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
6910	20226	33856	2.67	5.0E-88	AF10932.1	EST_HUMAN	Yn06610.1 Scores infant brain 1NIB Homo sapiens cDNA clone IMAGE:47129 5'
8114	21166	34715	2.67	5.0E-88	AF163264.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
8512	22577	36143	0.53	5.0E-88	BF080206.1	EST_HUMAN	602154858F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295775 5'
1360	14515	27590	0.99	4.0E-88	BF081229.1	EST_HUMAN	PM1-TN0028-050800-004710 TN0028 Homo sapiens cDNA
5244	18365	31333	0.65	4.0E-88	BF0714.1	EST_HUMAN	PM1-TN0028-050800-004710 TN0028 Homo sapiens cDNA
7392	20470	33836	1.7	4.0E-88	11416385	NT	802149702F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4290975 5'
11150	24221	37849	1.64	4.0E-88	4502694	NT	Homo sapiens transforming growth factor, beta-induced, 68KD (TGFB1) mRNA
11779	24769	38464	1.72	4.0E-88	7661947	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
11778	24769	38465	1.72	4.0E-88	7661947	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
750	13931	28974	1.25	3.0E-88	11545800	NT	Homo sapiens K1AA0152 gene product (K1AA0152) mRNA
1855	15001		3.09	3.0E-88	4508020	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634) mRNA
3073	16189	28214	6.08	3.0E-88	N66961.1	EST_HUMAN	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
4355	17498	30477	0.81	3.0E-88	4501912	NT	246812.51 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
4355	17498	30478	0.81	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4800	17737		4.81	3.0E-88	11429300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220) mRNA
5414	18618	31680	2.78	3.0E-88	11429300	NT	Homo sapiens velsin-containing protein (VCP) mRNA
5703	18898	32188	3.63	3.0E-88	9968888	NT	Homo sapiens polyoma virus PTA1, cell surface receptor (PRV1) mRNA
6822	18012	32318	3.9	3.0E-88	11420697	NT	Homo sapiens viral simian leukemia virus oncogene homolog A (ras related) (RALA) mRNA
6280	19463	32915	0.72	3.0E-88	11417370	NT	Homo sapiens interleukin 13 (IL13) mRNA
6643	26828	33050	0.84	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK) mRNA
6643	26828	33081	0.84	3.0E-88	11419210	NT	Homo sapiens putative activator of S phase kinase (ASK) mRNA
7211	20076	33489	15.52	3.0E-88	AF278265.1	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
7712	20777	34283	5.53	3.0E-88	11438400	NT	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5) mRNA
8105	21187	34707	9.3	3.0E-88	11421728	NT	Homo sapiens myoblasten cofactor biosynthesis protein A and myoblasten cofactor biosynthesis protein C
8390	21471	34997	1.58	3.0E-88	AF034574.1	NT	mRNA, complete cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9834	21077	34989	2.14	3.0E-88	11526262	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
10132	23170	38767	0.76	3.0E-88	AB016228.1	NT	Homo sapiens mRNA for RALDH2-1, complete cds
10132	23170	38768	0.76	3.0E-88	AB016228.1	NT	Homo sapiens mRNA for RALDH2-1, complete cds
10102	23189	38794	0.6	3.0E-88	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
12424	26301		2.49	3.0E-88	11417974	NT	Homo sapiens transcobalamin II, macrocytic anemia (TCN2), mRNA
12438	26300	31676	1.63	3.0E-88	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13223	25798	31889	1.31	3.0E-88	11526140	NT	Homo sapiens proteinase, serine, 7 (enterokinase) (PRSS7), mRNA
1061	14227	27283	6.85	2.0E-88	7305198	NT	Homo sapiens Calenillin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1853	14808	27891	4.24	2.0E-88	AF246218.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1789	14838	28031	6.93	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3554	16718	29733	2.9	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4545	17683	30695	1.93	2.0E-88	5031688	NT	Homo sapiens dyx1n, axonemal, light polypeptide 4 (DNAL4), mRNA
6032	19216	32536	4.88	1.0E-89	AW139365.1	EST_HUMAN	U1-H-B1-acc-d-04-0-U1.s1 NCJ CGAP Sub3 Homo sapiens cDNA clone IMAGE:2718760.3'
6032	19215	32537	4.98	1.0E-89	AW139365.1	EST_HUMAN	U1-H-B1-acc-d-04-0-U1.s1 NCJ CGAP Sub3 Homo sapiens cDNA clone IMAGE:2718760.3'
6783	18938	33334	21.66	1.0E-89	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
6783	18938	33335	21.66	1.0E-89	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
7271	20354	33807	1.52	1.0E-89	AA989034.1	EST_HUMAN	wq70a12.x1 NCJ CGAP GCB1 Homo sapiens cDNA clone IMAGE:2476806.3'
7334	20415	33877	3.7	1.0E-89	AA488981.1	EST_HUMAN	aa54a11.s1 NCJ CGAP GCB1 Homo sapiens cDNA clone IMAGE:824732.3' similar to WIPB0272.2
8331	21413	34839	0.51	1.0E-88	AF135183.1	NT	CE008851
9443	22559	36122	0.76	1.0E-88	AA190398.1	EST_HUMAN	Homo sapiens RecQ helicase 5 (RECQ5) gene, alternative splice products, complete cds
9778	22818	36398	2.83	1.0E-88	AL043314.2	EST_HUMAN	zpb7cd2.11 Strabagene HeLa cell s3 897216 Homo sapiens cDNA clone IMAGE:627170.5' similar to SW.FOL1_HUMAN P10266 RETROVIRUS-RELATED POL POL.VPROTEIN :
11730	23916	37541	3.35	1.0E-88	AA891478.1	EST_HUMAN	DKFZp434N0323.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323.5'
12665	25442		4.28	1.0E-88	AL163248.2	NT	os91g03.s1 NCJ CGAP GCB1 Homo sapiens cDNA clone IMAGE:1812766.3' similar to gb.M16342
13232	25800	31650	1.54	1.0E-88	AW457190.1	EST_HUMAN	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);
11194	24263	37808	8.14	9.0E-89	11421238	NT	os91g03.s1 NCJ CGAP GCB1 Homo sapiens cDNA clone IMAGE:2737084.3'
2795	15910	28019	1.75	8.0E-89	BE311557.1	EST_HUMAN	U1-H-B13-alk-b-03-0-U1.s1 NCJ CGAP Sub5 Homo sapiens cDNA clone IMAGE:2737084.3'
7072	20125	53541	1.14	8.0E-89	11421514	NT	Homo sapiens transgelin 2 (TAGLN2), mRNA
446	13642	26880	1.41	7.0E-89	7657213	NT	80114240951 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506186.5'
448	13642	26881	1.41	7.0E-89	7657213	NT	Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphrin) 3A (F1, sepiens) (LOC63232), mRNA
5005	18134	31108	2.71	7.0E-89	4557380	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
							Homo sapiens complement component 8, beta polypeptide (C8B), mRNA

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Probes Expressed[illegible]

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
128	13616	26656	0.73	2.0E-89	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
129	13616	26657	0.73	2.0E-89	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
421	13616	26656	0.89	2.0E-89	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
421	13616	26657	0.89	2.0E-89	7706870	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
543	13736	26760	0.63	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1342 protein, partial cds
2945	16122	29135	1.53	2.0E-89	AI222095.1	EST_HUMAN	q956-c8.x1 Soares, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:U04131
4263	17408	30394	1.18	2.0E-89	AF088997.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
4269	17414	30402	5.14	2.0E-89	X58742.1	NT	Homo sapiens liposomatase-related function protein (TRF4-2) mRNA, partial cds
4269	17414	30403	5.14	2.0E-89	X58742.1	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4469	17609	30897	1.13	2.0E-89	AL163203.2	NT	H. sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4619	17756	30738	1	2.0E-89	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5459	18659	31842	1.39	2.0E-89	BE541744.1	EST_HUMAN	Homo sapiens GGT gene, exon 5
5598	18793	32412	3.65	2.0E-89	AB007546.1	NT	601065996F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452423 5'
5909	18998	32865	1.5	2.0E-89	U09365.1	NT	Homo sapiens gene for LECT2, complete cds
6339	18509	32865	0.79	2.0E-89	AL163265.2	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
7847	20902	34405	6.28	2.0E-89	U81004.1	NT	Homo sapiens chromosome 21 segment HS21C005
8119	21201	34722	3.11	2.0E-89	11428801	NT	Human G124 (GT24) mRNA, partial cds
8612	21692	35228	0.9	2.0E-89	AJ245503.1	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
9453	22659	36136	0.72	2.0E-89	AB037754.1	NT	Homo sapiens partial mRNA for PEX5 related protein
10015	23053	36847	1.22	2.0E-89	AF170814.1	NT	Homo sapiens mRNA for KIAA1333 protein, partial cds
10015	23053	36848	1.22	2.0E-89	AF170814.1	NT	Homo sapiens CABP6 (CABP6) gene, exon 5
11855	24734	38426	2.53	2.0E-89	11434411	NT	Homo sapiens CABP6 (CABP6) gene, exon 5
11871	24859	38554	3.52	2.0E-89	11433673	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
12017	25001	38703	1.64	2.0E-89	U10692.1	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
12877	25584		4.25	2.0E-89	AF156981.1	NT	Human MAG-7 antigen (MAGE7) pseudogene, complete cds
11877	24855	38561	6.88	1.0E-89	BF186052.1	EST_HUMAN	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
11877	24855	38561	6.88	1.0E-89	BF186052.1	EST_HUMAN	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
11877	24855	38561	6.88	1.0E-89	BF186052.1	EST_HUMAN	htr1d09.x1 NCJ CGAP_K111 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778
11877	24855	38561	6.88	1.0E-89	BF186052.1	EST_HUMAN	SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN;
11877	24855	38561	6.88	1.0E-89	BF186052.1	EST_HUMAN	htr1d09.x1 NCJ CGAP_K111 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:O54778 O54778
11877	24855	38561	6.88	1.0E-89	BF186052.1	EST_HUMAN	SOLUTE CARRIER FAMILY 22-LIKE 2 PROTEIN.

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
8422	21603	36035	1.07	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046	
8422	21603	36036	1.07	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046	
1089	14254	27309	4.38	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046	
1089	14254	27309	2.91	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046	
1361	16035	27581	3.26	8.0E-90	BE670681.1	EST_HUMAN	7a36f08.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'	
1361	16035	27582	3.28	8.0E-90	BE670681.1	EST_HUMAN	7a36f08.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'	
8787	21839	35377	0.6	8.0E-90	BE177830.1	EST_HUMAN	RC1-HT0599-120400-022-808 HT0598 Homo sapiens cDNA	
10939	24021	37654	1.38	8.0E-90	AI222095.1	EST_HUMAN	cg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPETIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;	
10939	24021	37655	1.38	8.0E-90	AI222095.1	EST_HUMAN	cg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSPETIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;	
859	14036		6.51	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	
8619	21699		2.14	7.0E-90	AA782677.1	EST_HUMAN	al63d08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:3858924 3'	
9169	22244	35787	2.13	7.0E-90	BE682626.2	EST_HUMAN	601656837.R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858924 3'	
9169	22244	35788	2.13	7.0E-90	BE682626.2	EST_HUMAN	601656837.R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858924 3'	
10220	23256	36844	0.46	7.0E-90	AV273794.1	EST_HUMAN	KX24602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814028 3'	
10340	23375	36985	4.2	7.0E-90	H69849.1	EST_HUMAN	YB6604.s1 Soares_fetal liver spleen_NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;	
10340	23375	36986	4.2	7.0E-90	H69849.1	EST_HUMAN	YB6604.s1 Soares_fetal liver spleen_NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP:C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC;	
10872	23706	37314	0.82	7.0E-90	BF528099.1	EST_HUMAN	802071208.F1 NC1_CGAP_Brd4 Homo sapiens cDNA clone IMAGE:4214257 5'	
3136	16312	28324	1.16	8.0E-90	X918261.1	NT	H. sapiens ECE-1 gene (exon 6)	
3136	16312	28325	1.16	8.0E-90	X918261.1	NT	H. sapiens ECE-1 gene (exon 6)	
4342	17485	30467	11.21	8.0E-90		8822388	NT	H. sapiens ECE-1 gene (exon 6)
4342	17485	30468	11.21	8.0E-90		8822388	NT	H. sapiens ECE-1 gene (exon 6)
6105	18285	32618	2.84	8.0E-90	U77700.1	NT	Homo sapiens HSGCN1 mRNA, partial cds	
6105	18285	32619	2.84	8.0E-90	U77700.1	NT	Homo sapiens HSGCN1 mRNA, partial cds	
8522	21603	35140	4.01	6.0E-90		4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
8522	21603	35141	4.01	6.0E-90		4504794	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
159	13394		27.59	6.0E-90	AB035344.1	NT	Homo sapiens TOL8 gene, exon 1-10b	
1219	14380	27439	6.22	5.0E-90	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1864	16010	28116	1.07	5.0E-90	AI222035.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:104131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
1864	15010	28117	1.07	5.0E-90	AI222035.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:104131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
2622	15745	28659	2.37	5.0E-90	AF114487.1	NT	Homo sapiens interleukin long isoform (ILSN) mRNA, complete cds
4662	17787	30784	4.51	5.0E-90	4506354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4663	17818	30806	0.78	5.0E-90	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5708	18901	32188	2.85	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5726	18919		0.72	5.0E-90	AF008515.1	NT	Homo sapiens EVI5 homolog mRNA, complete cds
5810	19000	32307	1.32	5.0E-90	AB015617.1	NT	Homo sapiens ELKS mRNA, complete cds
6868	18901	32196	1.88	5.0E-90	Z18411.1	NT	H. sapiens mRNA encoding phospholipase c
6869	20021	33430	0.95	5.0E-90	8910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
6869	20021	33431	0.95	5.0E-90	8910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7364	20443	33906	2.04	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7364	20443	33906	2.04	5.0E-90	AF113708.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
7736	20787	34286	7.98	5.0E-90	4657288	NT	Homo sapiens adenylate cyclase 8 (ADCY8) mRNA
8488	21668	35107	4.89	5.0E-90	11345483	NT	Homo sapiens hypophthal protein FLJ13222 (FLJ13222), mRNA
8882	22922	36506	1.17	5.0E-90	11418429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
10498	23523	37133	0.71	5.0E-90	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10683	23697	37306	9.68	5.0E-90	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
10723	23756	37362	0.53	5.0E-90	7682051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10723	23756	37363	0.53	5.0E-90	7682051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
12846	25659		1.77	5.0E-90	AB011399.1	NT	Homo sapiens gene for A-E-8, complete cds
13000	25849		4.54	5.0E-90	AI623368.1	EST_HUMAN	at78105.x1 Bartschad aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2128781 3'
313	13528	28562	2.04	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
313	13528	28562	2.04	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
313	13528	28563	2.04	4.0E-90	AF231920.1	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1110	14275	27332	4.36	4.0E-90	4505316	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
1724	14874	27966	13.42	4.0E-90	X89033.1	NT	H. sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
2923	16101	29114	0.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2923	16101	29115	0.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3088	16284	29281	0.83	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3089	16284	29282	0.83	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4779	17914	30900	3.63	4.0E-90	D81675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4819	18049	31037	2.1	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4839	18069	31047	1.91	4.0E-90	M95867.1	NT	Human prothrombin converting enzyme (NEC2) gene, exon 8
12885	16101	29114	1.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12885	16101	29115	1.74	4.0E-90	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
8036	21119	34638	0.81	3.0E-90	BF516163.1	EST_HUMAN	UH-BW1-amyb-04-0-U1.s1 NC1_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839.3'
8036	21119	34639	0.81	3.0E-90	BF516163.1	EST_HUMAN	UH-BW1-amyb-04-0-U1.s1 NC1_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839.3'
11930	24919	38619	28.7	2.0E-90	BE537913.1	EST_HUMAN	601335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3453834.5'
220	13442	28473	4.5	2.0E-90	BE537913.1	EST_HUMAN	601067379F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834.5'
1200	14362	27421	6.48	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1200	14362	27422	6.48	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
3948	17106	30103	2.95	2.0E-90	A1138213.1	EST_HUMAN	q654c02.x1 Scores placenta, blood vessels, 2NbpHP8c6W Homo sapiens cDNA clone IMAGE:1713410.5'
4811	17944	30830	1.05	2.0E-90	AB006627.1	NT	similar to SW-OLF3 MOUSE P23273 OLFACTOR RECEPTOR OR3 ;
6029	18158	31135	10.16	2.0E-90	5729855	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
5888	19084	32395	0.6	2.0E-90	11625601	NT	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
5896	19084	32396	0.6	2.0E-90	11625601	NT	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
5803	19092	32406	3.86	2.0E-90	AW672886.1	EST_HUMAN	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
8993	23032	36623	0.99	2.0E-90	11427320	NT	ba49d05.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2869881.5' similar to TR.O79208 O75208
8993	23032	36624	0.99	2.0E-90	11427320	NT	HYPOTHETICAL 35.5 KD PROTEIN. ;
8993	23032	36624	0.89	2.0E-90	11427320	NT	Homo sapiens similar to laminin receptor 1 (LR1D), ribosomal protein SA (H. sapiens) (LOC63484), mRNA
10166	23202	36795	1.48	2.0E-90	AU118985.1	EST_HUMAN	Homo sapiens similar to laminin receptor 1 (LR1D), ribosomal protein SA (H. sapiens) (LOC63484), mRNA
10165	23202	36796	1.48	2.0E-90	AU118985.1	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795.5'
11758	23944	37971	3.08	2.0E-90	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
287	13505	26539	4.1	1.0E-90	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
385	15953	26528	2.28	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
386	15953	26528	1.56	1.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
713	13895	26932	1.92	1.0E-90	AL237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
713	13895	26933	1.92	1.0E-90	AL237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial

### Single Exon Probes Expressed in Placenta

Single Exon Probes Expressed in Placenta							Top Hit Descriptor
Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit A-session Nc.	Top Hit Database Source	Top Hit Descriptor
748	13929	26971	17.83	1.0E-80	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
748	13929	26972	17.83	1.0E-80	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1134	14299	27560	2.25	1.0E-80	AF096154.1	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KL7), mRNA
1334	14491	27561	3.46	1.0E-80	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1334	14491	27561	3.46	1.0E-80	AF096154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1701	14853	267	2.67	1.0E-80	BE378984.1	EST_HUMAN	807159563372 NIH_MGC_53 Homo sapiens cDNA clone IMAGE3511118 5'
1951	15094	28195	3.73	1.0E-80	11420514	NT	Homo sapiens similar to SALL1 (zeal Drosophila-like) (LOC57167), mRNA
2915	16093	29106	6.46	1.0E-80	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3954	17112	30112	0.58	1.0E-80	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3954	17112	30113	0.59	1.0E-80	AB020710.1	NT	Homo sapiens soluble intracellular 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
4543	17691	30663	1.68	1.0E-80	AF167340.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
6762	18093	32286	2.08	1.0E-80	AB014533.1	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
6959	19145	32460	0.9	1.0E-80	11426910	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7220	20085	33500	0.73	1.0E-80	UG1834.1	NT	Human retina-derived POU-domain factor-1 mRNA, complete cds
7849	20904	34408	2.31	1.0E-80	11428758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
9021	22100	35840	3	1.0E-80	11422098	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
9483	22550	36148	0.82	1.0E-80	AF163884.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
9516	22581	36149	1.4	1.0E-80	11422109	NT	Homo sapiens CGI-15 protein (LOC51009), mRNA
9516	22581	36149	1.4	1.0E-80	11422109	NT	Homo sapiens CGI-15 protein (LOC51009), mRNA
4313	17439	30444	8.29	8.0E-81	D12245.1	EST_HUMAN	Homo sapiens CG1-15 protein (LOC51009), mRNA
4313	17439	30444	8.29	8.0E-81	D12245.1	EST_HUMAN	Homo sapiens CG1-15 protein (LOC51009), mRNA
6501	21662	35118	1.14	7.0E-91	11418234	NT	Homo sapiens makorin, ring finger protein, 1 (MKRN1), mRNA
10807	23542	37153	0.65	7.0E-91	AI090415.1	EST_HUMAN	CA-BT043-000289-075 B17043 Homo sapiens cDNA
3563	16728	28744	1.85	6.0E-91	AA070294.1	EST_HUMAN	z99b04.s1 Soares fetal liver spleen, 1NF5, S1 Homo sapiens cDNA clone IMAGE448015 3'
4639	17775	30755	1.14	6.0E-91	AU143539	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4639	17775	30755	1.14	6.0E-91	AU143539	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4930	18060	31042	0.67	5.0E-81	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4930	18060	31043	0.67	5.0E-81	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
6760	19806	33300	1.25	5.0E-91	AI073895.1	EST_HUMAN	au909.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE2518121 3' similar to
8400	21481	35009	1.33	5.0E-91	BF314582.1	EST_HUMAN	SW-ASFG FLAME Q47898 N4 (BETA-NACETYLGLUCOSAMINYLA-ASPARAGINASE PRECURSOR
8950	22039	35581	1.47	6.0E-91	AV645878.1	EST_HUMAN	AV645878 GLC Homo sapiens cDNA clone GLCBY08 3'



### Single Exon Probes Expressed in Placenta

Single Exon Probes Expressed in T. lewisii						
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source
8860	22039	35582	1.47	5.0E-91	AV648878.1	EST_HUMAN
12871	25631		1.61	5.0E-91	AI1593566.1	EST_HUMAN
3272	16446	29466	1.58	4.0E-91	AF156776.1	NT
3272	16446	29466	1.58	4.0E-91	AF156776.1	NT
11171	24242	37875	3.22	4.0E-91	AL163284.2	NT
12376	26267	32074	3.27	4.0E-91	M77994.1	EST_HUMAN
12376	26267	32119	3.27	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
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12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
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12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1	EST_HUMAN
12885	25457	32019	1.16	4.0E-91	M77994.1</	

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9488	22545	36108	0.73	3.0E-91	AB011663.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
11480	24539	38207	1.49	3.0E-91	AB029003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
11480	24539	38208	1.49	3.0E-91	AB029003.1	NT	Homo sapiens mRNA for KIAA1080 protein, partial cds
13037	18489	31430	8.54	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 8
13037	18489	31431	8.54	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
49	13288	26300	2.94	1.0E-91	AF163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1274	14431	27502	2.74	1.0E-91	AF146746.1	EST_HUMAN	U1-H318-akc-01-0-U1-01 NQ CGAP Sub5 Homo sapiens cDNA clone IMAGE:2735280 3'
5529	18728	31742	0.78	1.0E-91	J1434402	NT	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA
6883	20211	33640	1.86	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NQ CGAP Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'
6883	20211	33641	1.86	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NQ CGAP Brn67 Homo sapiens cDNA clone IMAGE:4157804 5'
12130	25110	38814	1.49	1.0E-91	AV763053.1	EST_HUMAN	AV763053 MDS Homo sapiens cDNA clone MDSSEC05 5'
12840	26114		1.5	1.0E-91	H15212.1	EST_HUMAN	Ym30603.1 Scores infant brain T1NB Homo sapiens cDNA clone IMAGE:49597 5'
1270	14428	27498	5.77	8.0E-92	AF001689.1	NT	Homo sapiens NKGD2 gene, exon 10
1270	14428	27497	5.77	8.0E-92	AF001689.1	NT	Homo sapiens NKGD2 gene, exon 10
6308	18426	31398	0.66	9.0E-92	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
6308	18426	31398	0.66	9.0E-92	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
6579	18774	31820	5.86	8.0E-92	JD93007.1	NT	Human Nax/K+ ATPase alpha-subunit mRNA, partial cds
6722	18915	32210	2.82	8.0E-92	J11427149	NT	Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA
6583	19745	33127	3.77	8.0E-92	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
8041	21124	34644	0.65	8.0E-92	AJ250566.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
8041	21124	34646	0.55	9.0E-92	AJ250566.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
8569	21650	35192	1.53	8.0E-92	AB040545.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
8569	21650	35192	1.53	8.0E-92	AB040545.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9474	22531	36095	1.83	8.0E-92	W26387.1	EST_HUMAN	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
95	13330	26357	6.83	8.0E-92	BE386363.1	EST_HUMAN	2633 Homo sapiens cDNA randomly primed sublibrary Homo sapiens cDNA
296	13613	26547	3.09	8.0E-92	BE386363.1	EST_HUMAN	601275513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614887 5'
1868	18012	28119	1.43	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (DGKG), mRNA
1868	18012	28120	1.43	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (DGKG), mRNA
6508	18707	31722	0.69	8.0E-92	AB046820.1	NT	Homo sapiens mRNA for KIAA1600 protein, partial cds
6508	18707	31722	0.69	8.0E-92	AB046820.1	NT	Homo sapiens mRNA for KIAA1600 protein, partial cds
5915	18809	31877	0.8	8.0E-92	AF28417.1	NT	Homo sapiens FIVE domain-containing dual specificity protein phosphatase FIVE-DSP2 mRNA, complete cds
6677	19836	33225	1.28	8.0E-92	AF000979.1	NT	Homo sapiens MCP-4 gene
6680	19836	33228	0.91	8.0E-92	AF179428.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit variant 1 (REV3L) mRNA, complete cds
8283	21365		0.55	8.0E-92	11416861	NT	Homo sapiens AIM-1 protein (LOC61151), mRNA
8620	21700	35236	5.05	8.0E-92	LD4183.1	NT	Human lens membrane protein (mp18) gene, exon 11

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8620	21700	35236	5.05	8.0E-92	U04163.1	NT	Human lens membrane protein (Imp19) gene, exon 11
8721	21801	35337	0.71	8.0E-92	11428569	NT	Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA
9282	22339	35888	2.53	8.0E-92	AB014611.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
10232	23267	36857	0.91	8.0E-92	Y13628.1	NT	Homo sapiens mRNA for MBNL protein
11043	24121	37755	2.86	8.0E-92	AF074363.1	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
11642	24722	38415	1.93	8.0E-92	4503340	NT	Homo sapiens dihydropyrimidinase S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DUST)
12740	25491	32028	1.59	8.0E-92	11434704	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
68	13305	26328	1.91	7.0E-92	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
246	16008	26498	1.71	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
246	16008	26498	1.71	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
604	13783	27533	1.68	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Seprase truncated isoform mRNA, complete cds
1309	14465	27533	1.94	7.0E-92	4502384	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2260	16393	28519	3.85	7.0E-92	5031570	NT	Homo sapiens ARF2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2280	16393	28520	3.85	7.0E-92	5031570	NT	Homo sapiens ARF2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2630	15763	28668	6.13	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds
2787	15903	29010	6.84	7.0E-92	6005738	NT	Homo sapiens NRAS-related gene (D1S155E), mRNA
3426	18466	29609	0.7	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3426	18466	29610	0.7	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4710	17845	30828	1.19	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
4710	17845	30828	1.19	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
4710	17845	30828	1.19	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
5294	18403	31371	0.98	7.0E-92	4508118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
6376	18578	31448	6.51	7.0E-92	AA448206.1	EST_HUMAN	Zy66d12.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:781175 5'
2176	15313	28441	0.98	3.0E-92	11434814	NT	Homo sapiens Meckel-Gruber disease (splanchnicoblastic ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3) (MLD), mRNA
2176	15313	28441	0.98	3.0E-92	11434814	NT	Homo sapiens Meckel-Gruber disease (splanchnicoblastic ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3) (MLD), mRNA
2824	16838	29048	2.74	3.0E-92	BE009714.1	EST_HUMAN	Homo sapiens Meckel-Gruber disease (splanchnicoblastic ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3) (MLD), mRNA
5897	19182	32504	3.96	3.0E-92	AA378336.1	EST_HUMAN	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902839 5'
11002	24081	37716	3.26	3.0E-92	X15804.1	NT	EST191020 Synovial sarcoma Homo sapiens cDNA 6' end similar to ribosomal protein S13
11002	24081	37716	3.26	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
11002	24081	37716	3.26	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12878	28188		1.67	3.0E-92	BF367138.1	EST_HUMAN	RC1-GN0021-240800-012-a11 GN0021 Homo sapiens cDNA
26	13264	26266	1.54	2.0E-92	4507464	NT	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA
183	13405	26433	4.28	2.0E-92	11422848	NT	Homo sapiens hypothetical protein d1462023.2 (D1462023.2), mRNA
183	13405	26434	4.28	2.0E-92	11422848	NT	Homo sapiens hypothetical protein d1462023.2 (D1462023.2), mRNA
768	13949	26997	5.48	2.0E-92	BE289160.1	EST_HUMAN	601118337f1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304.5'
768	13949	26998	5.48	2.0E-92	BE289160.1	EST_HUMAN	601118337f1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304.5'
1752	14901		1.62	2.0E-92	S76653.1	NT	mtg-mnas-related [human, Genomic, 2416 nt]
1990	15132	28238	2.53	2.0E-92	AB18119.1	EST_HUMAN	wk27d07.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549.3' similar to TTR:Q12844
1990	15132	28237	2.53	2.0E-92	AB18119.1	EST_HUMAN	Q12844 BREACKPOINT CLUSTER REGION PROTEIN;
1990	15132	28237	2.53	2.0E-92	AB18119.1	EST_HUMAN	wk27d07.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549.3' similar to TTR:Q12844
2020	15161	28285	1.01	2.0E-92	4507464	NT	Q12844 BREACKPOINT CLUSTER REGION PROTEIN;
2020	15161	28286	1.01	2.0E-92	4507464	NT	wk27d07.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549.3' similar to TTR:Q12844
2108	15245	28360	5.35	2.0E-92	4506960	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
2725	15843	28954	22.38	2.0E-92	6912457	NT	Homo sapiens syndecan 4 (amphiglycan, ryudocan) (SDC4) mRNA
3701	16862	28864	1.02	2.0E-92	AF231619.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
3701	16862	28865	1.02	2.0E-92	AF231619.1	NT	Homo sapiens chromosome 21 unknown mRNA
3777	16938	29944	7.02	2.0E-92	6903180	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
4403	17548	30330	1.17	2.0E-92	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
6108	18236		4.1	2.0E-92	AL040437.1	EST_HUMAN	DKFZp434C0414.1 434 (synonym: hlae3) Homo sapiens cDNA clone DKFZp434C0414.5'
5879	19069	32377	0.64	2.0E-92	AF016355.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6431	19589		7.19	2.0E-92	4504758	NT	Homo sapiens Integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL), mRNA
6748	19804	33297	2.0	2.0E-92	AB028897.1	NT	Homo sapiens mRNA for KIAA1088 protein, partial cds
7627	20397		0.61	2.0E-92	U67760.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
7657	20697		0.64	2.0E-92	U67760.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
8056	22135	35680	1.28	2.0E-92	AW340174.1	EST_HUMAN	hcd2h02.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2808371.3' similar to TTR:O02711
10997	24076	37709	4.68	2.0E-92	31434800	NT	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
11257	24328	37865	3.22	2.0E-92	31434759	NT	Homo sapiens zinc finger protein 188 (ZNF188), mRNA
11409	24470	38134	5.71	2.0E-92	AW836290.1	EST_HUMAN	GM4-LT0026-161289-082-g08 LT0026 Homo sapiens cDNA
11409	24470	38135	5.71	2.0E-92	AW836290.1	EST_HUMAN	GM4-LT0026-161289-082-g08 LT0026 Homo sapiens cDNA
12758	25502	32035	8.46	2.0E-92	AB029076.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds

Table 4

### Single Exon Probes Expressed in Placenta

Single Exon Probes Expressed in Placenta							Top Hit Descriptor
Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Acceesion No.	Top Hit Database Source	
12782	25524	32005	1.36	2.0E-92	AF106856.1	NT	Homo sapiens adenylsuccinate lyase gene, complete cds
13068	15843	28954	73.88	2.0E-92	6912457	NT	Homo sapiens calcitriol binding protein 1 (KIAA0330). mRNA
1897	15040	28150	2.95	1.0E-92	AF78078.1	EST_HUMAN	Y80608.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:1455/4.5'
1897	15040	28151	2.95	1.0E-92	AF78078.1	EST_HUMAN	Y80608.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:1455/4.5'
2135	16271	28392	35.12	1.0E-92	4506668	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
8441	21522	35051	0.82	1.0E-92	BE43862.3.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107487.3 similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ; contains Alu repetitive element; contains element MER17 repetitive element ;
8365	22440	35999	3.24	1.0E-92	AI360356.1	EST_HUMAN	tg01502.x1 NCI CGAP CLL1 Homo sapiens

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7892	20944	34450	3.52	6.0E-93	AF067138.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
8804	21883	35422	0.73	5.0E-93	AF657628	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8804	21883	35423	0.73	5.0E-93	AF57526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9822	22862	36443	2.02	5.0E-93	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10012	23050	36844	1.35	5.0E-93	U032168	NT	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA
10275	23310	36806	1.78	5.0E-93	AF069313.2	NT	Homo sapiens WSB1 protein (WSB1) mRNA, complete cds
11084	24140	37775	1.92	5.0E-93	U1439599	NT	Homo sapiens nucleobindin 2 (NUCB2) mRNA
12851	26781	31821	2.31	5.0E-93	U1417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
80	13325		6.93	4.0E-93	AA459933.1	EST_HUMAN	z55068.s1 Soares, Jeeits, JNHT Homo sapiens cDNA clone IMAGE:785688 3' similar to SW:CLPA_RAT
458	13653	26690	2.38	4.0E-93	U457878	NT	P97387 CALPONIN, ACIDIC ISOFORM:
468	13653	26691	2.38	4.0E-93	U457879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
783	13872	27024	1.16	4.0E-93	U757454	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
783	13872	27025	1.16	4.0E-93	U757454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRC domain (PES1) mRNA
1210	14371	27431	2.12	4.0E-93	U892958	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRC domain (PES1) mRNA
2033	15174	28284	4.37	4.0E-93	AF047677.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
2318	15450	28582	1.19	4.0E-93	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
2672	15792	28809	1.16	4.0E-93	U766972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1) mRNA
3656	16818	29831	0.73	4.0E-93	U7703396	NT	Homo sapiens tumor antigen SLP-8p (HCC8) mRNA
4159	17310	30306	1.51	4.0E-93	U4504654	NT	Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA
5136	16818	28831	0.76	4.0E-93	U7703396	NT	Homo sapiens tumor antigen SLP-8p (HCC8) mRNA
5760	18952	32285	6.01	4.0E-93	U1428182	EST_HUMAN	y694c12.1 StrataGene liver (#937224) Homo sapiens cDNA clone IMAGE:78838 5' similar to similar to SP-A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN.
11398	24468	38123	10.47	4.0E-93	AF692051.1	EST_HUMAN	AV692051 GGC Homo sapiens cDNA clone GICDRF07 5'
3742	16903	28906	12.28	3.0E-93	U1690630.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
3742	16903	28907	12.26	3.0E-93	U1690630.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
4350	17493		2.0	3.0E-93	AF228898.1	NT	Homo sapiens lensin mRNA, complete cds
6686	18851	33242	1.31	3.0E-93	U1428182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog) like 2 (GCN5L2) mRNA
11040	24118	37752	2.88	3.0E-93	U1824839.1	EST_HUMAN	w602405.x1 NCI CGAP_GGC Homo sapiens cDNA clone IMAGE:2304489 3'
185	13418	26447	6.88	2.0E-93	U1824839.1	NT	Chlorocephus aethiops mRNA for ribosomal protein S4X, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
185	13418	26448	5.59	2.0E-93	AB015810.1	NT	Chlorocibac aethiops mRNA for ribosomal protein S4X, complete cds
333	13547	26578	13.77	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
334	13547	26578	6.74	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1946	14709	27884	3.9	2.0E-93	AF225966.1	NT	Homo sapiens tensin mRNA, complete cds
2199	16334	28461	2.23	2.0E-93	U40763.1	NT	Human CLK-associated RS cytidiphilic CARS-Cyp mRNA, complete cds
2555	16850	28806	1.02	2.0E-93	BE25282.1	EST_HUMAN	601117586F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5'
6254	18374	31340	1.18	2.0E-93	BE26320.1	EST_HUMAN	601116610F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357243 5'
5533	18730	31746	5.08	2.0E-93	AW064385.1	EST_HUMAN	EST376458 MAGEC resequenced, MAGEC Homo sapiens cDNA
5544	18741	31776	0.7	2.0E-93	4758153	NT	Homo sapiens deathness, autosomal dominant 5' (DFNA5), mRNA
5660	18854		0.94	2.0E-93	BF351459.1	EST_HUMAN	QV3-HT0513-280300-128-104 HT0513 Homo sapiens cDNA
5764	18946	32248	1.08	2.0E-93	11430039	NT	Homo sapiens hypophyseal protein (LOC51318), mRNA
5768	18960	32261	0.76	2.0E-93	U74313.1	EST_HUMAN	HSU74313 Human chromosome 14 Homo sapiens cDNA clone 1-86
6822	18975		1.2	2.0E-93	AW502002.1	EST_HUMAN	UHF-BN0-aks-9-09-0.U.11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078329 5'
11333	24388	38044	1.39	2.0E-93	AV721846.1	EST_HUMAN	AV721846 HTB Homo sapiens cDNA clone HTBAUB04 5'
11333	24388	38045	1.39	2.0E-93	AV721846.1	EST_HUMAN	AV721846 HTB Homo sapiens cDNA clone HTBAUB04 5'
12525	25358		1.78	2.0E-93	AA126735.1	EST_HUMAN	Z126C10, st Soares, pregnant, uterine, NHPUP Homo sapiens cDNA clone IMAGE:503348 3'
12824	25420		3.26	2.0E-93	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
12930	25613		5.34	2.0E-93	BF035827.1	EST_HUMAN	60145853F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
105	13341	26368	1.38	1.0E-93	AF238397.1	NT	Homo sapiens CTR1 pseudogene
105	13341	26369	1.38	1.0E-93	AF238397.1	NT	Homo sapiens CTR1 pseudogene
531	13724	26760	7.76	1.0E-93	7697016	NT	Homo sapiens CTR1 pseudogene
613	13802	28822	3.32	1.0E-93	AI148765.1	EST_HUMAN	064608.X1 NC1 CGAP CLL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR1Q62384 Q62384
895	14071	27136	3.43	1.0E-93	D67615.1	NT	ZINC FINGER PROTEIN, 1
1194	14359	27414	0.6	1.0E-93	4503872	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1265	14422	27487	7.22	1.0E-93	8923270	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67KD) (GAD1), transcript variant GAD87, mRNA
1265	14422	27488	7.22	1.0E-93	8923270	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67KD) (GAD1), transcript variant GAD87, mRNA
1376	14531	27604	9.7	1.0E-93	AI167108.1	NT	Homo sapiens hypophyseal protein FLJ20291 (FLJ20291), mRNA
2414	15544	28672	1.08	1.0E-93	AF231981.1	NT	Homo sapiens hypophyseal protein FLJ20291 (FLJ20291), mRNA
2576	15702	28763	3.06	1.0E-93	AF053086.1	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds
2833	14480	27546	1.32	1.0E-93	BE287369.1	EST_HUMAN	Homo sapiens long chain polynaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2833	14480	27547	1.32	1.0E-93	BE287369.1	EST_HUMAN	Homo sapiens long chain polynaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2833	14480	27547	1.32	1.0E-93	BE287369.1	EST_HUMAN	Homo sapiens long chain polynaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3000	16176	29167	5.86	1.0E-93	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
3287	18461		1.23	1.0E-93	AF231981.1	NT	Homo sapiens long chain polynunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4549	17687	30668	3.28	1.0E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6348	18461	31426	0.92	1.0E-93	AF123498.1	NT	Homo sapiens estrogen receptor alpha (ESR1) gene, exon 6
6348	18461	31427	0.92	1.0E-93	AF123498.1	NT	Homo sapiens estrogen receptor alpha (ESR1) gene, exon 6
6684	18878	32167	2.39	1.0E-93	U76509.1	NT	Homo sapiens glucocorticoid receptor (GR), intron D, and intron E
6684	18878	32168	2.39	1.0E-93	U76509.1	NT	Homo sapiens glucocorticoid receptor (GR), intron D, exon 5, and intron E
6885	19074	32383	1.2	1.0E-93	AF227138.1	NT	Homo sapiens candidate taste receptor T2R14 gene, complete cds
6037	18220	32543	10.78	1.0E-93	4557792	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Wilson disease) (NF1) mRNA
6326	19498	32855	4.8	1.0E-93	7682241	NT	Homo sapiens KIAA0672 gene product (KIAA0672), mRNA
6931	20246	33679	1.94	1.0E-93	11431580	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7400	20478	33940	3.24	1.0E-93	D42072.1	NT	Homo sapiens mRNA for NF1 N-isoform-exon11, complete cds
8455	21536	35066	2.29	1.0E-93	AB037632.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
8740	21819	35353	1.15	1.0E-93	Y10183.1	NT	H. sapiens mRNA for MEND protein
8850	21828	35468	1.14	1.0E-93	AF183032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds
9851	21094	34608	2.03	1.0E-93	AB040818.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
9656	21098	34612	1.14	1.0E-93	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9787	22827	36403	3.8	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 6)
9787	22827	36404	3.8	1.0E-93	X13474.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 6)
9826	22963	36555	1.24	1.0E-93	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhogAP
10346	23394	38994	0.59	1.0E-93	AL1433646	NT	Homo sapiens nyanidine receptor 3 (RYR3), mRNA
12820	26547		1.82	1.0E-93	AL230126.1	NT	Homo sapiens GGT1 gene, exon 1
12823	25608		3.71	1.0E-93	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
13108	26723	31941	1.36	1.0E-93	11417862	NT	Homo sapiens calchaurin binding protein 1 (KIAA0330), mRNA
13123	26173		1.42	1.0E-93	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
10819	23652		1.13	8.0E-94	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
4070	17226	30233	1.94	8.0E-94	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
6483	18682	31696	3.51	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
6483	18682	31699	3.51	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0612 protein, partial cds
6173	19349	32695	2.24	5.0E-94	AA72234.1	EST_HUMAN	Z871g06.st Soares_fetal_hart_NBH118W Homo sapiens cDNA clone IMAGE:406594.3
7150	20285	33728	1.45	5.0E-94	AI015800.1	EST_HUMAN	c863d05.st Soares_tal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1823389.3



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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8840	21819	35457	0.85	5.0E-94	BF528115.1	EST_HUMAN	602042183F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180023 5'
11215	24284	37822	1.43	5.0E-94	11423982	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
11215	24284	37823	1.43	5.0E-94	11423982	NT	Homo sapiens adenylate kinase 2 (AK2), mRNA
12503	28177	31536	3.6	5.0E-94	T83395.1	EST_HUMAN	Yd88b04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:116239 3'
1890	16034		16.48	4.0E-94	U95094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2723	16841	28952	0.89	4.0E-94	4506008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
3762	16923	28926	1.12	4.0E-94	AW187361.1	EST_HUMAN	Xt89f12.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
3762	16923	28926	1.12	4.0E-94	AW187351.1	EST_HUMAN	Xt89f12.X1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701679 3'
4840	17973	30963	3.06	4.0E-94	AI591312.1	EST_HUMAN	Mt11f10.X1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TRQ16265 Q15265 PROTEIN TYROSINE PHOSPHATASE 1
6597	19757	33144	1.48	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6597	19757	33145	1.48	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
7052	20105	26833	0.9	3.0E-94	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
739	13921	26861	1.13	3.0E-94	4502506	NT	Homo sapiens complement component 5 (C5) mRNA
1779	14928	28022	12.9	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1779	14928	28022	12.9	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1813	14962	28055	3.16	3.0E-94	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
4306	17449	30435	0.67	3.0E-94	AA464506.1	EST_HUMAN	ZW63G08.L1 Soares_fetal testis_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:774762 5'
4437	17577	30657	0.72	3.0E-94	AA781836.1	EST_HUMAN	as5h08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376163 3'
6798	18968	32292	3.21	3.0E-94	11498288	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6279	19453	32801	1.13	3.0E-94	AB011536.1	NT	Homo sapiens mRNA for MECF2, partial cds
6591	18743	33125	0.83	3.0E-94	11528228	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
7978	21027	34541	0.96	3.0E-94	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
8383	21474	35001	0.96	3.0E-94	AF152309.1	NT	Homo sapiens protocadherin alpha 13 (PCDH-alpha13) mRNA, complete cds
8787	21866	35408	4.41	3.0E-94	AB014578.1	NT	Homo sapiens mRNA for KIAA0679 protein, partial cds
8781	22631	38410	7.29	3.0E-94	AF081942.1	NT	Homo sapiens glycoprotein-11, mRNA, complete cds
11362	24423	38079	1.94	3.0E-94	4757821	NT	Homo sapiens exonal transport of synaptic vesicles (ATSV) mRNA
11876	24680	38662	2.11	3.0E-94	U26711.1	NT	Homo sapiens chb-b truncated form 1 lacking leucine zipper mRNA, complete cds
8954	22993	36587	0.67	2.0E-94	AI910393.1	EST_HUMAN	Wt50h11.X1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2301813 3'
8954	22993	36588	0.67	2.0E-94	AI910393.1	EST_HUMAN	Wt50h11.X1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2301813 3'
153	13378	26410	3.07	1.0E-94	BE285714.1	EST_HUMAN	601175f02F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531036 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3158	16333	28342	2.05	1.0E-94	BE253433.1	EST_HUMAN	601111696f1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3158	16333	28343	2.05	1.0E-94	BE253433.1	EST_HUMAN	601111696f1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4478	17618	30800	1.11	1.0E-94	9506692	NT	Homo sapiens hypothetical protein (FLJ20746), mRNA
6198	16373	32724	0.69	1.0E-94	AE000269.1	NT	Escherichia coli K-12 MG1655 seqlon 169 of 400 of the complete genome
6399	16565	32925	1.91	1.0E-94	AL040518.1	EST_HUMAN	DKFZp434G0314_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434G0314 5'
6405	16574	32936	0.82	1.0E-94	H08270.1	EST_HUMAN	Y87022.1 Soares infant brain IN18 Homo sapiens cDNA clone IMAGE:45053 5'
6848	19807	33184	0.68	1.0E-94	AV72692.1	EST_HUMAN	AV725992 HTC Homo sapiens cDNA clone HCCBF05 5'
8304	21386	34808	0.8	1.0E-94	AL183204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8304	21386	34809	0.8	1.0E-94	AL183204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8456	22572	36138	2.17	1.0E-94	AL183204.2	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
8990	23029	36620	1.35	1.0E-94	BE780478.1	EST_HUMAN	601468748f1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872099 5'
11321	24384	38028	3.11	1.0E-94	U85590.1	NT	Homo sapiens IL-1 receptor antagonist IL-1RA (IL-1RN) gene, alternatively spliced forms, complete cds
11697	24650	38334	1.88	1.0E-94	AI272244.1	EST_HUMAN	ap22602.x1 Schiller oligodendrogloma Homo sapiens cDNA clone IMAGE:1656122 3' similar to TRQ62845
12051	25032	38738	1.34	1.0E-94	11418071	NT	Q62845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR.1
12639	13378	28410	2.02	1.0E-94	BE295714.1	EST_HUMAN	601175762f1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
12668	13378	28410	1.73	1.0E-94	BE295714.1	EST_HUMAN	601175762f1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
1506	14659	27741	6.05	9.0E-95	AF027302.1	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABCS0) mRNA, complete cds
3224	16398	29409	1.09	9.0E-95	7882027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3224	16398	29410	1.09	9.0E-95	7882027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5521	18718	31733	1.46	9.0E-95	X82569.1	NT	Mmusculus glyt1 gene (exons 1c and 2)
5521	18718	31734	1.46	9.0E-95	X82569.1	NT	Mmusculus glyt1 gene (exons 1c and 2)
8446	21527	35054	1.58	9.0E-95	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
148	13374	28407	2.8	8.0E-95	AF154330.1	NT	Homo sapiens carbamyl phosphate synthetase 1 mRNA, complete cds
4658	17784	30779	1.68	8.0E-95	AF700998.1	EST_HUMAN	we08604.x1 NC_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340506 3' similar to gb:K00558
4658	17784	30780	1.68	8.0E-95	AF700998.1	EST_HUMAN	we08604.x1 NC_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340506 3' similar to gb:K00558
7087	20181	33605	0.73	8.0E-95	11418376	NT	TUBULIN ALPHA-1 CHAIN (HUMAN).
7380	20468	33934	1.4	8.0E-95	11426529	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
7390	20468	33935	1.4	8.0E-95	11426529	NT	Homo sapiens proteasome (prosome, macropain) 28S subunit, non-ATPase, 11 (PSMD11), mRNA
8391	21472	34988	2.08	8.0E-95	AF032897.1	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
8965	22707	38273	1.98	8.0E-95	11420944	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds

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9565	22707	36274	1.98	8.0E-95	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
10053	23081	36693	2.46	8.0E-95	5174844	NT	Homo sapiens prolins dehydrogenase (proline oxidase) (PRODH), mRNA
10063	23121		2.92	8.0E-95	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cde
10440	23475	37078	0.81	8.0E-95	9845523	NT	Homo sapiens early growth response 2 (Krox-20 (Drosophila) homolog) (EGR2), mRNA
10853	24035	37670	1.39	8.0E-95	AF112152.1	NT	Homo sapiens developmental arteries and neural crest EGF-like protein mRNA, complete cds
11773	24765	38461	1.72	8.0E-95	10864024	NT	Homo sapiens HGF-binding transcription factor Zhengfei (ZF), mRNA
11982	24957	38669	1.32	8.0E-95	7019572	NT	Homo sapiens zincfin (ZNF), mRNA
11982	24957	38670	1.32	8.0E-95	7019572	NT	Homo sapiens zincfin (ZNF), mRNA
12867	25598		17.21	8.0E-95	AA629056.1	EST_HUMAN	zif4b01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1, L1 repetitive element;
286	13504	26537	6.07	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
286	13504	26538	6.07	7.0E-95	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
2519	15645	28767	1.37	7.0E-95	M75973.1	NT	Human hepatocyte growth factor gene, exon 8
2619	16645	28768	1.37	7.0E-95	M75973.1	NT	Human hepatocyte growth factor gene, exon 8
4466	17628	30608	15.92	7.0E-95	M95708.1	NT	Homo sapiens LY-6-like protein (CD59), mRNA, complete cds
4835	17873		1.09	7.0E-95	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9418	22482	36058	0.62	4.0E-95	BE439625.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
215	13438	28468	0.82	3.0E-95	AV648361.1	EST_HUMAN	AV648361 GLC Homo sapiens cDNA clone GLCBI01 3'
6666	18766	31784	1.62	3.0E-95	BF62604.1	EST_HUMAN	602071146F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4214147 5'
5791	26911	32285	0.94	3.0E-95	4603354	NT	Homo sapiens dedicator of cyto-kinesis 1 (DOCK1), mRNA
7315	20397	33859	0.73	3.0E-95	AA412321.1	EST_HUMAN	z87d01.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730273 5'
7315	20397	33860	0.73	3.0E-95	AA412321.1	EST_HUMAN	z87d01.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730273 5'
7525	20598	34071	2.01	3.0E-95	AW856121.1	EST_HUMAN	EST1370191 IMAGE resequences, IMAGE Homo sapiens cDNA
7525	20598	34072	2.01	3.0E-95	AW856121.1	EST_HUMAN	EST1370191 IMAGE resequences, IMAGE Homo sapiens cDNA
9555	22620	38180	1.62	3.0E-95	7692289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9555	22620	36181	1.62	3.0E-95	7692289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
8949	22897	36581	0.86	3.0E-95	BF213446.1	EST_HUMAN	60184212F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4070451 5'
1676	14828	27911	3.52	2.0E-95	7692027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1676	14828	27912	3.52	2.0E-95	7692027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1995	16139	28242	73.27	2.0E-95	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Scribble/Tundus dystrophy pseudoinflammatory) (TIMP3), mRNA
1898	15139	28246	3.87	2.0E-95	BE393973.1	EST_HUMAN	60131216F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658892 5'
2467	15824	28743	1.5	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19), mRNA
2467	15824	28744	1.5	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19), mRNA

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2636	15681	28784	3.62	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2582	15707	28828	1.34	2.0E-95	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
2662	15794		0.99	2.0E-99	R16245.1	EST_HUMAN	Y649408.s1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:53393 3'
3226	16400	28412	2.1	2.0E-95	AF015482.1	NT	Homo sapiens Usurin-gamma mRNA, complete cds
3655	16818	28828	3.6	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3655	16818	28830	3.6	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3708	16867	28870	0.81	2.0E-95	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
3844	17004	30006	0.62	2.0E-95	A1290264.1	EST_HUMAN	qnm1602.x1 Soares_NIHMPU_S1 Homo sapiens cDNA clone IMAGE:1880548 3' similar to WIP:123G7.4 CE03705
4481	17621	30602	1.38	2.0E-95	7667185	NT	Homo sapiens hypothetical protein (HS922B1A), mRNA
5151	18273	31242	3.6	2.0E-95	7661978	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5230	18352	31321	0.99	2.0E-95	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5597	18792	31840	4.12	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51056), mRNA
5597	18792	31841	4.12	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51056), mRNA
5815	19005	32310	1.24	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5815	19005	32311	1.24	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5855	18045	32352	0.63	2.0E-95	11525983	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
6270	18444	32793	3.86	2.0E-95	M59724.1	NT	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7
6579	18741	33122	0.9	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3, variant hepatic nuclear factor (TCF2), mRNA
6579	18741	33123	0.9	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3, variant hepatic nuclear factor (TCF2), mRNA
6700	18658	33248	3.25	2.0E-95	AF26737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
6803	20218	33647	1.47	2.0E-95	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
6843	22419	35973	1.48	2.0E-95	11421795	NT	Homo sapiens ribophorin II (RPN2), mRNA
10592	23627	37236	0.56	2.0E-95	11434330	NT	Homo sapiens KIAA1065 protein (KIAA1065), mRNA
10592	23627	37236	0.56	2.0E-95	11434330	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRIA), mRNA
10592	23627	37236	0.56	2.0E-95	11434330	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRIA), mRNA
11138	24210	37836	1.35	2.0E-95	7661993	NT	Homo sapiens Siae20-related serine/threonine kinase (KIAA0204), mRNA
12002	24987	38691	1.69	2.0E-95	7662298	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12002	24987	38692	1.69	2.0E-95	7662298	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12703	25083		1.57	2.0E-95	AF161420.1	NT	Homo sapiens HSPC302 mRNA, partial cds
12608	25407	32047	2.31	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

Single Exon Probes Expressed in Tissues

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Table 4  
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7163	20298	33740	0.91	6.0E-96	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cde
7684	20749	34231	0.76	5.0E-96	AB024334.1	NT	Homo sapiens mRNA for 14-3-3gamma, complete cds
8297	21379	34900	1.97	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
8297	21379	34901	1.87	6.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 6
12083	29063	38769	1.33	5.0E-96	7661973	NT	Homo sapiens KIAA0175 gene product (KIAA0175), mRNA
4306	17451		15.95	3.0E-96	H69566.1	EST_HUMAN	y87h12.1 Soares fetal liver spleen INF15 Homo sapiens cDNA clone IMAGE:212327 5'
426	13623		6.76	2.0E-96	4603098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
766	13947	26994	1.1	2.0E-96	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1834	14981	28079	1.03	2.0E-96	7706205	NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
4880	18011	30995	1.56	2.0E-96	BE148074.1	EST_HUMAN	RC3-H1T0230-040500-116-902 HT0230 Homo sapiens cDNA
7620	20690	34165	0.59	2.0E-96	BF369731.1	EST_HUMAN	QV4-GN0120-250900-427-512 GN0120 Homo sapiens cDNA
7620	20690	34166	0.59	2.0E-96	BF369731.1	EST_HUMAN	QV4-GN0120-250900-427-512 GN0120 Homo sapiens cDNA
9181	22259		4.9	2.0E-96	AV689461.1	EST_HUMAN	AV689461 GKCC Homo sapiens cDNA clone GKCFM07 5'
12288	26214		2.54	2.0E-96	AW246140.1	EST_HUMAN	2819351 5'prime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2819351 5'
636	13623	28945	0.88	1.0E-96	4828963	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
636	13623	28946	0.88	1.0E-96	4828963	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
688	13872	26905	3.08	1.0E-96	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1822	14971	28063	9.97	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGE resequences, MAGE Homo sapiens cDNA
5331	18444	28064	1.59	1.0E-96	5453913	NT	EST367124 MAGE resequences, MAGE Homo sapiens cDNA
7105	18532	31487	1.18	1.0E-96	0912735	NT	Homo sapiens phospholipid transfer protein (PLTP) mRNA
7194	20059	33470	0.71	1.0E-96	0912455	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
8407	21488	35017	0.9	1.0E-96	7661803	NT	Homo sapiens guanine nucleotide exchange factor for Rap1 (KIAA0277), mRNA
8407	21488	35018	0.9	1.0E-96	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8913	21992	35531	21.44	1.0E-96	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC83214), mRNA
9031	22130	35674	2.22	1.0E-96	AF274833.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10362	23397	37007	0.68	1.0E-96	AB033148.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
10362	23397	37008	0.68	1.0E-96	AB033148.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
12274	13823	26946	3.29	1.0E-96	4828963	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
12274	13823	26946	3.29	1.0E-96	4828963	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
3405	16575	28990	0.72	6.0E-97	BF245240.1	EST_HUMAN	801863712P1 NIH_MGC 5' Homo sapiens cDNA clone IMAGE:4081202 5'
7730	20782		3.4	6.0E-97	BE141839.1	EST_HUMAN	IL5-HT0117-011089-004-DD7 HT0117 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9134	22213	35757	0.75	6.0E-97	BE898012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
9134	22213	35758	0.75	6.0E-97	BE898012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
10821	23854	37475	0.65	6.0E-97	AA320332.1	EST_HUMAN	EST122872 Adipose tissue, white II Homo sapiens cDNA 5' end
10821	23854	37476	0.65	6.0E-97	AA320332.1	EST_HUMAN	EST122872 Adipose tissue, white II Homo sapiens cDNA 5' end
11692	24690	38381	2.42	6.0E-97	X13903.1	NT	Human mRNA for alpha-actinin
8204	21286	34809	1.73	6.0E-97	AL04314.2	EST_HUMAN	DKFZp434A0323.1 434 (synonym: hsc3) Homo sapiens cDNA clone IMAGE:767758 3' similar to TR:G1304125
8336	21417	34943	11.21	6.0E-97	AA418026.1	EST_HUMAN	z67612.s1 Scaree_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:767758 3' similar to TR:G1304125
8877	22817	36502	3.12	5.0E-97	BF154912.1	EST_HUMAN	RCO-B10812-250900-032-e09 BT0812 Homo sapiens cDNA
11840	24829	38519	1.68	5.0E-97	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-502 HT0241 Homo sapiens cDNA
11840	24829	38520	1.68	5.0E-97	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-502 HT0241 Homo sapiens cDNA
962	14135	27198	2.13	4.0E-97	BE00436.1	EST_HUMAN	GM0-BU0106-170300-293-e06 BN0108 Homo sapiens cDNA
1059	15102	28202	1.41	4.0E-97	5453672	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
6883	18877	32168	0.92	4.0E-97	4557326	NT	Homo sapiens epolipoprotein H (beta-2-glycoprotein I) (APOH) mRNA
6862	20190	33615	8.47	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form
6862	20190	33616	8.47	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase I, long form
7161	20294	33737	1.09	4.0E-97	7710125	NT	Homo sapiens ligase III, DNA, ATP-dependent (LIG3), transcript variant alpha, mRNA
7214	20079	33492	0.82	4.0E-97	11422165	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8329	21411	34937	1.06	4.0E-97	4557708	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2), mRNA
8553	21634	35171	1.43	4.0E-97	11421793	NT	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA
8779	21858	35401	0.51	4.0E-97	11431060	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
8820	21898	35438	0.82	4.0E-97	11423233	NT	Homo sapiens cyclochrome P450, subfamily VB, polypeptide 1 (CYP4B1), mRNA
9449	22665	36128	1.06	4.0E-97	AB011168.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9449	22665	36129	1.06	4.0E-97	AB011168.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
10652	23886	37296	0.55	4.0E-97	11431060	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
11435	24496	38162	1.89	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11435	24496	38163	1.89	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11719	23906	37628	4.61	4.0E-97	AB042567.1	NT	Homo sapiens mRNA, similar to rat myomegalin, complete cds
12472	25325		5.26	4.0E-97	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (G1SE1), mRNA
253	13473	26504	1.58	3.0E-97	AB032398.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
897	14073	27138	7.16	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
897	14073	27139	7.16	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1473	16039	27712	1.94	3.0E-97	4788813	NT	Homo sapiens N-nryx (and STA1) inhibitor (NMI), mRNA
2506	15988	28755	2.4	3.0E-97	UG255.1	NT	Homo sapiens beta-primin-actinin (BAM22) gene, exon 7
3333	16506	28523	0.96	3.0E-97	5174478	NT	Homo sapiens pericentri (PCNT) mRNA
4902	18032	31021	22.23	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
6557	19719	33095	2.72	1.0E-97	BE566166.1	EST_HUMAN	601339520F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3681821.5'
7039	20092	33509	0.69	1.0E-97	5453881	NT	Homo sapiens phosphorylase kinase, gamma 1 (muscle) (PHKG1) mRNA
9866	23005	36600	1.02	1.0E-97	R10887.1	EST_HUMAN	yf3cd08.st Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134.3'
10945	24027	37663	2.84	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
11589	24642	38324	1.38	1.0E-97	AA563761.1	EST_HUMAN	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
11766	23942	37668	8.3	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
11766	23942	37668	8.3	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S16 (RPS16), mRNA
11766	23942	37668	8.3	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S16 (RPS16), mRNA
1324	14089	27163	2.34	9.0E-98	BE030793.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
1305	14481	27528	1.32	9.0E-98	8383082	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
6432	18600		0.79	9.0E-98	AJ250713.1	NT	Homo sapiens CLDN12 gene for claudin-12
8020	21072	34853	4.13	9.0E-98	AB046956.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
8020	21072	34854	4.13	9.0E-98	AB046956.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
8109	21191	34711	5.62	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
8109	21191	34712	5.62	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
9316	22382	35643	1.78	9.0E-98	X08986.1	NT	Human mRNA for amyloid A4(75) protein
9425	22498	36064	1.12	9.0E-98	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
9492	22549	39112	1.0	9.0E-98	AB037766.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
9540	22605		0.81	9.0E-98	AF057726.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 8
9687	22708	38278	1.28	9.0E-98	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3), mRNA
9687	22708	38277	1.28	9.0E-98	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3), mRNA
10467	23502	37115	0.67	9.0E-98	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
10576	28610	37215	0.5	9.0E-98	11431544	NT	Homo sapiens proteinase-activated receptor 3 (PAR3), mRNA
11253	24322	37992	2.62	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11253	24322	37993	2.62	9.0E-98	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
12487	14008	27163	4.97	9.0E-98	BE030793.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA



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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1403	14557	27631	0.93	8.0E-98	AB033769.1	NT	Homo sapiens hPAD- $\alpha$ 1 mRNA for peptidylglycine deaminase type I, complete cds
1591	14743	27825	1.1	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1591	14743	27826	1.1	8.0E-98	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1765	14914	28008	2.79	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1769	14914	28010	2.79	8.0E-98	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3896	17055	30055	8.45	8.0E-98	J04469.1	NT	Homo sapiens mitochondrial creatine kinase (CKMT) gene, complete cds
6207	19382	32732	0.96	6.0E-98	BE86593.1	EST_HUMAN	601507503F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909097 5'
2247	15380	28508	1.35	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
2873	16793	28910	2.1	3.0E-98	AB014507.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2807	16921		5.04	3.0E-98	AA077198.1	EST_HUMAN	7818H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7818H01
7085	20179	33602	1.99	3.0E-98	11418210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7085	20179	33603	1.99	3.0E-98	11418210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
8951	22030	35571	4.07	3.0E-98	H46998.1	EST_HUMAN	X017909.1 Soares adult brain N25HB557 Homo sapiens cDNA clone IMAGE:178240 5'
8487	22563	36116	0.64	3.0E-98	8922099	NT	Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA
10087	23125	36726	1.82	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
10087	23125	36727	1.82	3.0E-98	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone 18
10691	23724	37330	0.89	3.0E-98	BE900454.1	EST_HUMAN	601673686F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956517 5'
11195	24284	37899	2.55	3.0E-98	U65306.1	NT	Human tumefactor precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
11819	24808	38504	2.22	3.0E-98	A155975.1	EST_HUMAN	qb80h02.x1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:1708451 3'
13138	25739		3.01	3.0E-98	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
754	13935	26390	0.67	2.0E-98	BE261094.1	EST_HUMAN	601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'
2141	15277	28398	4.06	2.0E-98	BE294281.1	EST_HUMAN	601172858F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2311	15443	28578	2.21	2.0E-98	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4411	17553	30538	0.82	2.0E-98	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4459	17599	30577	4.23	2.0E-98	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4948	18078	31052	1.39	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATTRN) gene, exon 16
4948	18078	31053	1.39	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATTRN) gene, exon 16
5492	18691	31708	4.76	2.0E-98	7708512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6793	18948	33347	1.7	2.0E-98	4605788	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A), mRNA
7801	20857	34348	1.25	2.0E-98	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
7801	20857	34349	1.25	2.0E-98	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
8807	21886	35428	4.44	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8807	21886	35427	4.44	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8889	21888	35503	0.8	2.0E-88	L76883.1	NT	Homo sapiens NIKAT4b mRNA, complete cds
8889	21888	35504	0.8	2.0E-88	L76883.1	NT	Homo sapiens NIKAT4b mRNA, complete cds
8737	22802	36376	1.56	2.0E-88	X12891.1	NT	H. sapiens angliases gene exon 3 (EC 3.5.3.1)
10624	23658		1.65	2.0E-88	7708868	NT	Homo sapiens AIN-1 protein (LOC61161), mRNA
12130	25116		1.61	2.0E-88	AB040913.1	NT	Homo sapiens mRNA for KIAA1593 protein, partial cds
12492	25340	32082	2.23	2.0E-88	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
418	13613	26653	27.52	1.0E-88	AI892007.1	EST_HUMAN	W36804.X1 NC1 CGAP_U11 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW:RL2B_HUMAN
407	13662	28698	3.27	1.0E-88	AW69811.1	EST_HUMAN	P28318 60S RIBOSOMAL PROTEIN L23A ;
1840	14898	28086	26.16	1.0E-88	N49813.1	EST_HUMAN	P40-BN0085-100300-001-c08 BN0085 Homo sapiens cDNA
5432	18532	31810	3.3	1.0E-88	AA195354.1	EST_HUMAN	PMO-BN0085-100300-001-c08 BN0085 Homo sapiens cDNA
5687	18881	32172	0.87	1.0E-88	BE380627.1	EST_HUMAN	PMO-BN0085-100300-001-c08 BN0085 Homo sapiens cDNA
5687	18881	32173	0.87	1.0E-88	BE380627.1	EST_HUMAN	PMO-BN0085-100300-001-c08 BN0085 Homo sapiens cDNA
8189	22277	35815	0.59	1.0E-88	AF141349.1	NT	PIR:S54204 S54204 ribosomal protein L28 - human ;
8189	22277	35816	0.59	1.0E-88	AF141349.1	NT	PIR:S54204 S54204 ribosomal protein L28 - human ;
5939	18125	32438	1.05	9.0E-89	AI805004.1	EST_HUMAN	Y23105.1 Scars fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243585 5' similar to
5939	18125	32439	1.05	9.0E-89	AI805004.1	EST_HUMAN	PIR:S54204 S54204 ribosomal protein L28 - human ;
6165	19341	32888	4.01	9.0E-89	AW68636.1	EST_HUMAN	QV-BT073-191298-012 BT073 Homo sapiens cDNA
11384	24445	36105	1.85	9.0E-89	AI479829.1	EST_HUMAN	QV-BT073-191298-012 BT073 Homo sapiens cDNA
11384	24445	36106	1.85	9.0E-89	AI479829.1	EST_HUMAN	EST380711 MAGe resequences, MAGJ Homo sapiens cDNA
11700	24697	38389	1.72	9.0E-89	AA134804.1	EST_HUMAN	IM69H07.X1 NC1 CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BJD_HUMAN
8924	22003	35542	1.19	8.0E-89	9835487	NT	IM69H07.X1 NC1 CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BJD_HUMAN
6668	19142	32458	9.26	7.0E-89	AF056808.1	NT	P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
11809	24896	38399	1.91	7.0E-89	AF001896.1	NT	P55957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
484	13678	26713	0.72	6.0E-89	U10951.1	NT	TR:G682994 G682994 GPI-ANCHORED PROTEIN P-137 ;
2198	15331	28456	6.2	6.0E-89	11430555	NT	Human endogenous retrovirus, complete genome
2198	15331	28457	6.2	6.0E-89	11430555	NT	Human G2 protein mRNA, partial cds
3995	17152	30160	2.8	6.0E-89	AW976364.1	EST_HUMAN	Homo sapiens cysine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
4870	18003	30886	1.42	6.0E-89	4502660	NT	Homo sapiens cysine-rich repeat-containing protein S52 precursor, (LOC51232), mRNA
							EST388473 MAGe resequences, MAGN Homo sapiens cDNA
							Homo sapiens CD34 antigen (CD34) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6732	18888	33280	0.94	6.0E-99	7706138	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
6816	18889	33376	0.74	6.0E-99	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
6816	18889	33377	0.74	6.0E-99	L43610.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8298	21378	34899	1.85	6.0E-99	X89101.1	NT	H. sapiens mRNA for estrogen receptor
8314	21396	34921	0.59	6.0E-99	6501589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8864	22043	35686	2.67	6.0E-99	AB036429.1	NT	Homo sapiens NDS14 mRNA for N-deacetylase/N-sulfatransferase 4, complete cds
8064	22143	35688	7.6	6.0E-99	AF080255.1	NT	Homo sapiens iodester protein mRNA, complete cds
8064	22143	35689	7.6	6.0E-99	AF080255.1	NT	Homo sapiens iodester protein mRNA, complete cds
9123	22202	35744	0.59	6.0E-99	11431894	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
9123	22202	35745	0.59	6.0E-99	11431894	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
10958	24039	37674	3.15	6.0E-99	11636259	NT	Homo sapiens BH3 interacting domain death agonist (BID), mRNA
11742	23928	37553	2.02	6.0E-99	9910279	NT	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
11742	23928	37554	2.02	6.0E-99	8910279	NT	Homo sapiens UDP-glucose:glycoprotein glucosyltransferase 1 (HUGT1), mRNA
2022	15193	28268	1	5.0E-99	Y11363.1	NT	H. sapiens MPA gene, exon 8
4886	17821	30809	1.81	5.0E-99	AF008300.1	NT	Homo sapiens T cell receptor beta locus, TORBVS3A2 to TORBV12S2 region
12502	25346		2.49	5.0E-99	BE880177.1	EST_HUMAN	601513167F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3974391 5'
8516	21587		4.95	3.0E-99	M85588.1	NT	Human E2AHLA fusion protein (E2AHLF) mRNA, complete cds
1268	14426		7.26	2.0E-99	AW274792.1	EST_HUMAN	X08808.x1 NCJ CGAP_HNB Homo sapiens cDNA clone IMAGE:2738874 3' similar to gb:M831212 MYOSIN LIGHT CHAIN ALKALI NON-MUSCLE ISOFORM (HUMAN);
3331	16504	29522	1.4	2.0E-99	M30838.1	NT	Human Ku (p70p80) subunit mRNA, complete cds
4865	17800	30787	1.82	2.0E-99	AF086703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7851	20806	34410	0.76	2.0E-99	AF28737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8904	21863	35523	10.79	2.0E-99	W23607.1	EST_HUMAN	zb46d06.r1 Soares_Fetal_lung.Nhl.L19W Homo sapiens cDNA clone IMAGE:306635 5' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
8953	22428	35986	0.76	2.0E-99	R78254.1	EST_HUMAN	y81b08.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145625 5'
11367	24428	38085	3.16	2.0E-99	AF247457.2	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
12081	25061	38787	1.64	2.0E-99	10863960	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
326	13639	28671	1.49	1.0E-99	AF114497.1	NT	Homo sapiens intercalin long isoform (ITSN) mRNA, complete cds
380	13696	28632	1.75	1.0E-99	11920150	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GBTF) (GABPA), mRNA
1492	14605	27684	3.61	1.0E-99	M30838.1	NT	Human Ku (p70p80) subunit mRNA, complete cds
1587	14738	27819	1.16	1.0E-99	AF192823.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1587	14738	27820	1.16	1.0E-99	AF192823.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1980	16123	28224	1.21	1.0E-99	4803730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1880	15123	28225	1.21	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
3164	16329	29339	0.83	1.0E-99	J03171.1	NT	Human interferon- $\alpha$ receptor (HuIFN- $\alpha$ Re) mRNA, complete cds
4489	17639	30621	2.64	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4489	17639	30622	2.64	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
6943	20266	33694	1.26	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
6943	20266	33695	1.25	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7289	25842	33827	0.81	1.0E-99	X98022.1	NT	H. sapiens E8-AP gene exon 2
8400	22474		0.75	1.0E-99	11419721	NT	Homo sapiens ALEX1 protein (LOC51309), mRNA
8720	22785	36356	1.7	1.0E-99	AW340174.1	EST_HUMAN	h02h02.x1 Series NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TRC002711
11403	24484	38128	2.56	1.0E-99	7427614	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN :
11403	24484	38128	2.66	1.0E-99	7427614	NT	Homo sapiens huntingtin interacting protein 1 (HIP1), mRNA
11462	24521	38191	1.68	1.0E-99	5901978	NT	Homo sapiens head shock transcription factor 2 binding protein (HSF2BP), mRNA
11659	24738	38428	2.83	1.0E-99	AB023222.1	NT	Homo sapiens mRNA for KIAA1009 protein, partial cds
11886	24981	38687	2.45	1.0E-99	11417181	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
12257	25183		4.62	1.0E-99	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1	13241	26241	1.7	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
2	13241	26241	2.81	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
70	13307	26328	1.82	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
70	13307	26330	1.82	1.0E-100	11418230	NT	Homo sapiens Testis-specific XK-related protein on Y (XKRY), mRNA
89	13324	26353	0.82	1.0E-100	AW276237.1	EST_HUMAN	xv78b11.x1 NC1_CGAP_Bm53 Homo sapiens cDNA clone IMAGE:2824605 3'
173	13397	26426	0.89	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C049
327	13841	26573	1.84	1.0E-100	AF163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
353	13964	26592	1.87	1.0E-100	TO5087.1	EST_HUMAN	EST102975 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFB0CR32
450	13846		2.24	1.0E-100	AF003328.1	NT	Homo sapiens X-linked arylidic endodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
502	13697		5.88	1.0E-100	X80831.1	NT	G.gallie DNA for ZNF80 gene homolog
622	13716	26742	1.21	1.0E-100	BE180509.1	EST_HUMAN	RC3_HT0625-040600-022-509 HT0625 Homo sapiens cDNA
1044	14210	27286	4.57	1.0E-100	7681868	NT	Homo sapiens DKFZP586N0122 protein (DKFZP586N0122), mRNA
1044	14210	27287	4.57	1.0E-100	7681868	NT	Homo sapiens DKFZP586N0122 protein (DKFZP586N0122), mRNA
1577	14730		1.3	1.0E-100	AW201565.1	EST_HUMAN	UH-HB11-efk-c-07-0-U1.s1 NC1_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
1681	14733	27814	1.66	1.0E-100	AI200857.1	EST_HUMAN	qf62f09.x1 Series _testis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COT1A P61061 CRYSTATIN :

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2315	15447		1.14	1.0E-100	DB3349.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2507	15634	28754	1.41	1.0E-100	X62468.1	NT	H. sapiens mRNA for IRN-gamma (pKC-0)
2771	16886	28986	2.5	1.0E-100	11418978	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
3063	16269		6.55	1.0E-100	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4328	17469	30496	1.67	1.0E-100	AF057354.1	NT	Homo sapiens myoblastin-related protein 1a mRNA, partial cds
4331	17494	30474	2.28	1.0E-100	4503792	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
6202	18323	31291	3.01	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5202	18323	31292	3.01	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
6404	18606	31578	1.74	1.0E-100	BF24428.1	EST_HUMAN	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5625	18819	31893	0.76	1.0E-100	AW076983.1	EST_HUMAN	601883164F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080999 5'
5818	19008	32314	1.45	1.0E-100	AU118192.1	EST_HUMAN	xa8201.x1 NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573305 3' similar to gbX12433
5884	19054	32361	1.78	1.0E-100	AF135136.1	NT	PROTEIN PHPS-1-2 (HUMAN);
6650	19146	32491	0.85	1.0E-100	X14890.1	NT	AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'
6292	19465	32817	0.9	1.0E-100	4567568	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
6292	19465	32818	0.9	1.0E-100	4567568	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
6628	19788	33174	5.62	1.0E-100	AU140214.1	EST_HUMAN	Human mRNA for plasma inter-alpha-trypsin inhibitor heavy chain H(3)
6824	19977	33384	1.36	1.0E-100	R10887.1	EST_HUMAN	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6908	20223	33653	1.77	1.0E-100	7382478	NT	AU140214 PLACE2 Homo sapiens cDNA clone PLACE200137 5'
6982	20210	33638	1.02	1.0E-100	AA498841.1	EST_HUMAN	Y38408 s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134 3'
6982	20210	33638	1.02	1.0E-100	AA498841.1	EST_HUMAN	Human sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
6982	20210	33638	1.02	1.0E-100	AA498841.1	EST_HUMAN	ae33b06.t1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418
6982	20210	33638	1.02	1.0E-100	AA498841.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN. ;
7026	20182	33583	1.18	1.0E-100	BF376478.1	EST_HUMAN	ae33b06.t1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418
7026	20182	33583	1.18	1.0E-100	BF376478.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN. ;
7026	20182	33583	1.18	1.0E-100	BF376478.1	EST_HUMAN	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
7033	20169	33591	6.2	1.0E-100	X04571.1	NT	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
8729	21809	35346	3.53	1.0E-100	BF103853.1	EST_HUMAN	Human mRNA for kidney epidermal growth factor (EGF) precursor
8766	21845		5.59	1.0E-100	AL163203.2	NT	601647337F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:3931310 5'
9216	22294	35837	0.47	1.0E-100	AU116951.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
9216	22294	35838	0.47	1.0E-100	AU116951.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9433	22507	36073	3.88	1.0E-100	AB040918.1	NT	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9510	22776		1.65	1.0E-100	A197288.1	EST_HUMAN	Homo sapiens mRNA for KIAA1485 protein, partial cds
9833	21076	34588	2.28	1.0E-100	AY888911.1	EST_HUMAN	w37g08.x1 NCI CGAP_P228 Homo sapiens cDNA clone IMAGE:2489920 3' similar to contains element
							MER22 repetitive element ;
							PMO-BN0065-100300-001-c03 BN0065 Homo sapiens cDNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8887	22736		0.84	1.0E-100	AU12720.1	EST_HUMAN	AU12720 NT2RP2 Homo sapiens cDNA clone NT2RP2001818 5'
0782	22822	36400	2.17	1.0E-100	AB046946.1	NT	Homo sapiens mRNA for KIAA1626 protein, partial cds
9782	22822	36401	2.17	1.0E-100	AB046946.1	NT	Homo sapiens mRNA for KIAA1626 protein, partial cds
10048	23086	36897	1.81	1.0E-100	AW630487.1	EST_HUMAN	h83c11.y1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2969396 5'
10048	23086	36898	1.81	1.0E-100	AW630487.1	EST_HUMAN	h83c11.y1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2969396 5'
10688	23721	37327	0.64	1.0E-100	BF347516.1	EST_HUMAN	602020554F1 NCI CGAP Brn67 Homo sapiens cDNA clone IMAGE:4159165 5'
10782	23815		1.39	1.0E-100	Y10391.1	NT	Human endogenous retrovirus HERV-K, pol gene
10966	24076	37708	6.64	1.0E-100	BF327292.1	EST_HUMAN	h83c11.y1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:4159165 5'
11564	24619	38300	1.56	1.0E-100	X94633.1	NT	H. sapiens CD97 gene exon 4
11564	24619	38301	1.55	1.0E-100	X94633.1	NT	H. sapiens CD97 gene exon 4
11635	24715	38406	3.91	1.0E-100	AF111703.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11635	24715	38408	3.91	1.0E-100	AF111703.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
11665	13241	28241	3.07	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
11665	13241	28241	3.07	1.0E-100	AL163247.2	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11977	24682		2.21	1.0E-100	AF268285.1	NT	Homo sapiens class gene, exon 12
12128	25108	38812	1.93	1.0E-100	AJ131034.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
12177	25137	38832	7.59	1.0E-100	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
12312	26037		1.78	1.0E-100	BF446549.1	EST_HUMAN	7q88H03.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:3' similar to TRQ21997 Q21997
12483	26341	32063	4.97	1.0E-100	11545732	NT	COSMID R151, [2] TR:Q9UAD8
12754	25500	32063	1.31	1.0E-100	11418123	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
13195	28778	31895	6.91	1.0E-100	11417074	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
79	13315	28342	0.92	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
79	13315	28343	0.92	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
704	13887	28919	1.4	1.0E-101	AB007816.2	NT	Homo sapiens mRNA for KIAA0448 protein, partial cds
722	13904	28945	8.12	1.0E-101	7110724	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
722	13904	28946	8.12	1.0E-101	7110724	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
792	13971	27023	1.37	1.0E-101	7657454	NT	Homo sapiens pascadillo (zebrinfish) homolog 1, containing BRCT domain (PES1), mRNA
876	14052	27117	1.35	1.0E-101	4503914	NT	Homo sapiens phosphoribosylaminoimidazole synthetase (GAR1), mRNA
848	14121	27182	0.85	1.0E-101	Z20656.1	NT	phosphoribosylaminoimidazole synthetase (GAR1), mRNA
1009	14180	27243	6.07	1.0E-101	BF881218.1	EST_HUMAN	Homo sapiens of cardiac alpha-myosin heavy chain gene
1077	14243	27259	1.39	1.0E-101	AJ221878.1	EST_HUMAN	602156474F1 NIH MGC_53 Homo sapiens cDNA clone IMAGE:4297291 5'
1674	14787	27848	1.44	1.0E-101	5921460	NT	qg99609.x1 Scores_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
							Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1614	14797	27850	1.44	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1785	14934	28028	1.57	1.0E-101	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1785	14934	28029	1.57	1.0E-101	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1899	16140	28247	2.07	1.0E-101	4502986	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1), mRNA
2110	15254	28379	2.70	1.0E-101	BE843070.1	EST_HUMAN	RC3-S10281-100000-016-H09 S10281 Homo sapiens cDNA
2425	16062	28880	1.2	1.0E-101	5728982	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2680	16800	28917	4.62	1.0E-101	XT2893.1	NT	H. sapiens EWS gene, exon 5
2802	15916	29025	9.27	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
2802	15916	29026	9.27	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
3020	16186		20.16	1.0E-101	AJ262312.1	NT	Homo sapiens genomic downstream Rhesus box
3273	16447	29467	2.97	1.0E-101	4886270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
3313	16486		2.3	1.0E-101	BF038327.1	EST_HUMAN	601458531.F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3962086 5'
3468	16635	29854	1.82	1.0E-101	AW965566.1	EST_HUMAN	EST377629 MAGC resequences, MAG1 Homo sapiens cDNA
3487	15916	29026	3.59	1.0E-101	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
3981	17138	30142	3.81	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
5147	18269	31239	1.14	1.0E-101		NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5147	18269	31240	1.14	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5248	18369	31336	0.6	1.0E-101	BE612654.1	EST_HUMAN	601452067.F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
5249	18369	31337	0.6	1.0E-101	BE612654.1	EST_HUMAN	601452067.F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
5433	18933	31611	1.84	1.0E-101	AW965139.1	EST_HUMAN	EST377212 MAGC resequences, MAG1 Homo sapiens cDNA
6126	18305	32649	4.07	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6126	18305	32646	4.07	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6834	19887	33366	0.86	1.0E-101	11450734	NT	Homo sapiens carbonic anhydrase VII (CA7), mRNA
7423	20500		1.26	1.0E-101	11545780	NT	Homo sapiens hypodermal protein FLJ22087 (FLJ22087), mRNA
7473	20548	34019	4.22	1.0E-101	AF206970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3), mRNA, alternative splice form 4, partial cds
7473	20548	34020	4.22	1.0E-101	AF206970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3), mRNA, alternative splice form 4, partial cds
7845	20714	34192	7.63	1.0E-101	AW0008475.1	EST_HUMAN	W55112.X1 NC1 CGAP Gas4 Homo sapiens cDNA clone IMAGE:2333487 3'
7749	20809		1.89	1.0E-101	BE27384.1	EST_HUMAN	601108217.F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3340901 5'
7900	20962	34469	6.64	1.0E-101	BE330739.1	EST_HUMAN	RC1-B10313-220700-018-f12 B10313 Homo sapiens cDNA
8097	21179	34696	0.74	1.0E-101	BE273821.1	EST_HUMAN	601121621.F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3343869 5'
8097	21179	34697	0.74	1.0E-101	BE273821.1	EST_HUMAN	601121621.F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3343869 5'
8245	21827	34843	1.0	1.0E-101	BF029174.1	EST_HUMAN	601764886.F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996837 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8517	21598	35132	0.71	1.0E-101	AW630070.1	EST_HUMAN	hnt4g10.y1 NCL CGAP GU1 Homo sapiens cDNA clone IMAGE:2868578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
8517	21598	35133	0.71	1.0E-101	AW630070.1	EST_HUMAN	hnt4g10.y1 NCL CGAP GU1 Homo sapiens cDNA clone IMAGE:2868578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
8212	22280	35832	1.1	1.0E-101	AA036800.1	EST_HUMAN	2c29g08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:371998 5' similar to PIR:S44640 S44640 YD8335.03c protein - yeast;
9631	22698	36167	0.99	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for pancreatic gamma-glutamyltransferase
9531	22598	38168	0.98	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1351 protein, partial cds
9681	21103	34819	17.36	1.0E-101	X60089.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9676	22638	36209	19.41	1.0E-101	8845492	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
9939	22998	36593	3.36	1.0E-101	BE818687.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875933 3'
9056	22698	36594	3.36	1.0E-101	BE818687.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875933 3'
10098	23138	36737	0.58	1.0E-101	10883980	NT	Homo sapiens janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10620	23654	37284	1.84	1.0E-101	11429127	NT	h077d11.x1 NCL CGAP Gae4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326 KERATIN, TYPE I, CYTOSKELETAL 18 (HUMAN);
10656	23660	37289	4.37	1.0E-101	AL670283.1	EST_HUMAN	h077d11.x1 NCL CGAP Gae4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326 KERATIN, TYPE I, CYTOSKELETAL 18 (HUMAN);
10696	23690	37300	4.37	1.0E-101	AL670283.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
10771	23804	37426	0.83	1.0E-101	BE873648.1	EST_HUMAN	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
10771	23804	37427	0.83	1.0E-101	BE873648.1	EST_HUMAN	Homo sapiens mRNA for KIAA0819 protein, partial cds
11371	24432	38089	1.31	1.0E-101	AB020628.1	NT	RC-BT163-290499-085 BT163 Homo sapiens cDNA
12058	25040	38748	1.85	1.0E-101	AB08168.1	EST_HUMAN	RC-BT163-290499-085 BT163 Homo sapiens cDNA
12059	25040	38749	1.85	1.0E-101	AB08168.1	EST_HUMAN	OV3-H10460-230200-101-d03 HT0460 Homo sapiens cDNA
12738	25489		2.24	1.0E-101	BE16357.1	EST_HUMAN	OV1-DT0068-240200-085-a01 DT0068 Homo sapiens cDNA
12783	25529		12.79	1.0E-101	AW839051.1	EST_HUMAN	Homo sapiens phosphatidylinositol 4-kinase 230 (p41k230) mRNA, complete cds
40	13278	26284	0.61	1.0E-102	AF012872.1	NT	Homo sapiens chromosome 21 segmentHS21C103
351	13562	26589	4.57	1.0E-102	AL168303.2	NT	601108232F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'
635	13820	26844	0.61	1.0E-102	BE352470.1	EST_HUMAN	Homo sapiens down-regulated in adenoma (DRA) mRNA
796	13975	27028	1.06	1.0E-102	4657634	NT	Human endogenous retroviral DNA (4-), complete retroviral segment
1141	14308	27362	1.9	1.0E-102	M109761.1	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1297	14453	27518	2.05	1.0E-102	11437148	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1297	14453	27519	2.06	1.0E-102	11437148	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1450	14603	27681	355.9	1.0E-102	BE408471.1	EST_HUMAN	601299925F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3629901 5'



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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2383	15514	28642	1.91	1.0E-102	AU124619.1	EST_HUMAN	am50c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:153954 3' similar to SW:GG95_HUMAN 008379 GOLGIN-95.1
2383	16514	28643	1.91	1.0E-102	AU124619.1	EST_HUMAN	am50c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:153954 3' similar to SW:GG95_HUMAN 008379 GOLGIN-95.1
3080	16288		0.74	1.0E-102	Y13932.1	NT	Homo sapiens PRKY exon 7
3133	16308	29322	1.47	1.0E-102	7661878	NT	Homo sapiens KIA0187 gene product (KIA0187), mRNA
3203	16378	28387	3.73	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
3203	16378	28388	3.73	1.0E-102	AU141005.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4347	17480	30472	1.74	1.0E-102	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C07
4533	17871	30655	2.57	1.0E-102	BE2513.10.1	EST_HUMAN	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5'
6224	18348	31316	1.28	1.0E-102	R88488.1	EST_HUMAN	y32c04.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:140934 5'
5487	18888	31704	1.6	1.0E-102	AF067133.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
5867	19037		6.87	1.0E-102	AB034531.1	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5905	18084	32408	3.25	1.0E-102	7705388	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5905	18084	32409	3.25	1.0E-102	7705388	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
5912	19100	32414	0.81	1.0E-102	11433046	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
6422	18581	32966	2.81	1.0E-102	AI458625.1	EST_HUMAN	ar8208.x1 Barrett colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137 Q13137 NDP52.1
7227	20080	33507	0.7	1.0E-102	AW451543.1	EST_HUMAN	UI-H-BI3-ell-d-10-0-JL s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736835 3'
7286	20368	33823	0.81	1.0E-102	BE728323.1	EST_HUMAN	601561505F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831241 5'
7314	20386	33858	1.02	1.0E-102	BE386106.1	EST_HUMAN	60127216F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618243 5'
7428	20508	33977	1.5	1.0E-102	AB023177.1	NT	Homo sapiens mRNA for KIAA0900 protein, partial cds
7510	20584	34057	8.03	1.0E-102	AJ238394.1	NT	Homo sapiens mRNA for Centaurin-alpha2 protein
7802	20858	34350	2.61	1.0E-102	AV710738.1	EST_HUMAN	AV710738 C4 Homo sapiens cDNA clone CUAAXD03 5'
8418	21488	35031	3.85	1.0E-102	BE763051.1	EST_HUMAN	QV3-NT0025-210600-236-108 NT0025 Homo sapiens cDNA
8691	21771	35302	1.71	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKC Homo sapiens cDNA clone GKCEE11 5'
8691	21771	35302	1.71	1.0E-102	AV694817.1	EST_HUMAN	AV694817 GKC Homo sapiens cDNA clone GKCEE11 5'
8802	21881	35419	0.81	1.0E-102	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8131	22210	35754	1.2	1.0E-102	BE388033.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
9131	22538	36102	1.2	1.0E-102	BE388033.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
8522	22587	36156	2	1.0E-102	T703931.1	EST_HUMAN	AV755442 BM Homo sapiens cDNA clone BMFAUD08 5'
8522	22587	36156	2	1.0E-102	T703931.1	EST_HUMAN	y473407.r1 Soares fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:67021 5'
8522	22587	36156	2	1.0E-102	T703931.1	EST_HUMAN	y473407.r1 Soares fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:67021 5'
8611	22666	36237	3.11	1.0E-102	AU124628.1	EST_HUMAN	AU124628 NT2RMA Homo sapiens cDNA clone NT2RMA4000308 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
10593	23628		0.84	1.0E-102	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
10847	23681	37281	0.67	1.0E-102	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165KD) (MYOM2), mRNA
10647	23681	37282	0.67	1.0E-102	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165KD) (MYOM2), mRNA
10887	23720	37325	3.26	1.0E-102	AI805037.1	EST_HUMAN	RC-B1074-260499-014 B1074 Homo sapiens cDNA
10687	23720	37326	3.26	1.0E-102	AI905037.1	EST_HUMAN	RC-B1074-260499-014 B1074 Homo sapiens cDNA
10748	23781	37394	1.5	1.0E-102	AA670786.1	EST_HUMAN	on57h04.s1 Soares, NFL_T_CBC, S1 Homo sapiens cDNA clone IMAGE:1560823 3' similar to SW/CAV2_HUMAN P51698 CAVEOLIN-2, [1]:
11323	24386	38030	1.37	1.0E-102	BE897488.1	EST_HUMAN	601438392F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924186 5'
11327	24390	38035	2.44	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11600	24653	38337	1.47	1.0E-102	AA686675.1	EST_HUMAN	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11680	24688	38378	2.47	1.0E-102	BF359243.1	EST_HUMAN	AK49110.s1 Soares, Isella, NHT Homo sapiens cDNA clone IMAGE:1408347 3'
12006	24994	38689	2.83	1.0E-102	U41302.1	NT	RC8-ET0072-150800-011-F01 ET00722 Homo sapiens cDNA
12182	25142		5.69	1.0E-102	AL163280.2	NT	Human chromosome 16 creatine transporter (SLC6A6) and (CDM) paralogous genes, complete cds
12775	25517	32000	5.67	1.0E-102	AW300862.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
12831	25553	32015	1.25	1.0E-102	11418158	NT	XK07C12X1 NC1_CGAP_Co20 Homo sapiens cDNA clone IMAGE:2668038 3'
71	13308	26331	0.85	1.0E-103	BE808158.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (thriforax (Drosophila) homolog), translocated to, 4 (MLL4), mRNA
71	13308	26332	0.85	1.0E-103	BE808158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
102	13338	26365	8.24	1.0E-103	D87078.2	NT	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
213	13436	26456	0.84	1.0E-103	5453793	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
1004	14175	27234	74.34	1.0E-103	AJ278348.1	NT	Homo sapiens nucleolar protein (KKEID repeat) (NOP56) mRNA
1272	14429	27500	7.08	1.0E-103	BE877541.1	EST_HUMAN	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1626	14778	27863	3.51	1.0E-103	AF012672.1	NT	601485388F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'
1984	15107	28207	1.02	1.0E-103	7857592	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds
2031	15172	28280	0.95	1.0E-103	4502428	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SMAP), mRNA
2031	15172	28281	0.95	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2379	15510	28638	1.95	1.0E-103	AU134691.1	EST_HUMAN	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2623	16848	28772	1.84	1.0E-103	AF060568.1	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2685	16905	28921	1	1.0E-103	N52770.1	EST_HUMAN	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3137	16313		2.78	1.0E-103	BE744722.1	EST_HUMAN	YW91D08.s1 Soares, placenta, 8weeks, 2NhpP8baw Homo sapiens cDNA clone IMAGE:259589 3'
3467	16834	28853	5.33	1.0E-103	AW288245.1	EST_HUMAN	601673113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834315 5'
							U-H-BW0-ajh-11-0-U1.s1 NC1_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733165 3'

Single Exon Probes Expressed in Placenta							Top Hit Descriptor:
Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	
3526	16691	29700	0.95	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3850	17010		5.46	1.0E-103	AF023891.1	NT	Maceca mulatta cyclophilin A mRNA, complete cds
3894	17053	30053	0.9	1.0E-103	AA485693.1	EST_HUMAN	clmient LTR10 repetitive element
3833	17092	30080	1.54	1.0E-103	U430878	NT	Homo sapiens neuropilin 1 (NRP1), mRNA
4110	17294	30264	4.63	1.0E-103	T23683.1	EST_HUMAN	sec340 b4HBM3A-Coll109+10-Big Homo sapiens cDNA clone b4HBM3A-Coll109+10-Big-73
5325	18438		0.63	1.0E-103	AA451613.1	EST_HUMAN	TR:G292362 G292352 COLLAGEN CHAIN RH
6056	18238	32563	0.9	1.0E-103	BF569522.1	EST_HUMAN	TR:G292362 G292352 COLLAGEN CHAIN RH
6063	18245	32571	1.67	1.0E-103	AF179995.1	NT	802186023F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310573 5'
6397	18566	32926	0.8	1.0E-103	U435053	NT	Homo sapiens septin 2 (SEP2) mRNA, partial cds
6397	18566	32927	0.8	1.0E-103	U435053	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6397	18748	33130	0.84	1.0E-103	AW945536.1	EST_HUMAN	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6687	18748	33131	0.84	1.0E-103	AW945536.1	EST_HUMAN	EST366538 IMAGE:366538, MACG Homo sapiens cDNA
6725	25631	33273	1.15	1.0E-103	AA781442.1	EST_HUMAN	EST1366838 IMAGE:1366838, MACG Homo sapiens cDNA
6768	19924	33318	0.91	1.0E-103	AF053450.1	NT	4p26d3, a1 Soares, testis, NHT Homo sapiens cDNA clone 1391452 3'
6859	20011	33422	1.66	1.0E-103	AI590071.1	EST_HUMAN	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4
6859	20011	33423	1.66	1.0E-103	AI590071.1	EST_HUMAN	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4
6987	18508	31621	1.77	1.0E-103	5032282	NT	tm58b05.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
6987	18508						Q13769 ANONYMOUS
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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exam SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8484	21669	35101	0.59	1.0E-103	T31080.1	EST_HUMAN	EST27183 Human Brain Homo sapiens cDNA 5' end similar to None
8822	21801	35440	1.05	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLAGE2 Homo sapiens cDNA clone PLAGE2000374 5'
8822	21801	35441	1.05	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLAGE2 Homo sapiens cDNA clone PLAGE2000374 5'
8900	21979	35518	1.34	1.0E-103	BF109244.1	EST_HUMAN	760603.X1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523954 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;
8307	22383	35834	3.18	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
8307	22383	35835	3.18	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9349	22425	35980	0.87	1.0E-103	AA581086.1	EST_HUMAN	nd13a02.s1 NCL_CGAP_Ov1 Homo sapiens cDNA clone IMAGE:800162 3' similar to gpL02426 265
10263	23286	36896	2.04	1.0E-103	Z31976.1	NT	PROTEASE SUBUNIT 4 (HUMAN);
10304	23339	36944	2.07	1.0E-103	AW963676.1	EST_HUMAN	H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
10443	23478	37083	10.78	1.0E-103	AB78956.1	EST_HUMAN	EST375749 IMAGE: ressequences, MAGI1 Homo sapiens cDNA
10876	23963	37591	1.52	1.0E-103	BE549706.1	EST_HUMAN	TR:O15046 Q15046 KIAA0338 ;
10971	24051	37684	9.5	1.0E-103	AU792759.1	EST_HUMAN	7b4103.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230813 3' similar to gbM69043 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN (HUMAN);
11072	24147	37785	2.45	1.0E-103	11424081	NT	002408.Y5 NCL_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1522283 5' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
11072	24147	37786	2.45	1.0E-103	11424081	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
11083	24157	37784	2.4	1.0E-103	AF14973.1	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
11083	24157	37785	2.4	1.0E-103	AF14973.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
11636	24735	38428	2.67	1.0E-103	AU136283.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
11731	23917	37642	4.1	1.0E-103	L43610.1	NT	AU136283 PLAGE1 Homo sapiens cDNA clone PLAGE1003923 5'
11889	24963		1.71	1.0E-103	AB024759.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
12044	25025	38730	2.28	1.0E-103	BE644611.1	EST_HUMAN	Homo sapiens TSA305 gene, exon 16
12178	25138		3.4	1.0E-103	AF224609.1	NT	766810.X1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER29.13 MER29 repetitive element ;
12209	25162		1.22	1.0E-103	11528291	NT	(UBE2D) genes, complete cds
12414	26293	32083	1.71	1.0E-103	AB011389.1	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
243	13465	28494	2.46	1.0E-104	AL031549.3	EST_HUMAN	Homo sapiens gene for A1-5, complete cds
243	13465	28495	2.48	1.0E-104	AL031549.3	EST_HUMAN	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
1837	15080	28182	1.92	1.0E-104	4502428	NT	DKFZ564H1072.J1 564 (synonym: hfb2) Homo sapiens cDNA clone DKFZ564H1072 5'
							DKFZ564H1072.J1 564 (synonym: hfb2) Homo sapiens cDNA clone DKFZ564H1072 5'
							Homo sapiens bone morphogenetic protein 8 (BMP8) mRNA

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2267	16400	28528	33.28	1.0E-104	AA132975.1	EST_HUMAN	z022c06.s1 Stratigene codon (#937204) Homo sapiens cDNA clone IMAGE:587828 5' similar to gb:214118.mat CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2277	16409	28640	4.56	1.0E-104	BE744628.1	EST_HUMAN	601677460.F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928438 5'
2442	15570	28698	9.73	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-112 CT0249 Homo sapiens cDNA
2442	15570	28699	9.73	1.0E-104	BF334221.1	EST_HUMAN	RC1-CT0249-110900-214-112 CT0249 Homo sapiens cDNA
2506	15633	28793	2	1.0E-104	6031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2634	16111	29126	17.98	1.0E-104	M34871.1	NT	Human lymphocytic antigen CD59/MEM43 mRNA, complete cds
2683	16159		2.15	1.0E-104	Y1151.1	NT	H.sapiens gene encoding phenylpyruvate tautomerase II
3337	16510	29526	0.99	1.0E-104	AU133926.1	EST_HUMAN	AU133926 OVARC1 Homo sapiens cDNA clone OVARC1000836 5'
3478	16645	29860	2.33	1.0E-104	AA318436.1	EST_HUMAN	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end
3630	16832	29861	0.65	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
4053	17209	30219	0.71	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
4248	17394	30383	0.71	1.0E-104	F11745.1	EST_HUMAN	HSC31A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07
4496	17636	30618	33.95	1.0E-104	X02791.1	NT	Human mRNA for fibronectin (FN precursor)
4732	17897	30849	1.2	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4732	17897	30850	1.2	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
6061	18243	32568	1.05	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6108	18289	32623	0.93	1.0E-104	AB017322.1	NT	Human Down Syndrome region of chromosome 21 DNA
6596	18730	33142	8.3	1.0E-104	AF768797.1	EST_HUMAN	Homo sapiens a1c3 mRNA for Aurora/ipl-1-related kinase 3, complete cds
6598	18766	33143	8.6	1.0E-104	AF768797.1	EST_HUMAN	KIAA0132 PROTEIN, contains element LTR7 repetitive element;
6766	18941	33338	0.74	1.0E-104	7708512	NT	KIAA0132 PROTEIN, contains element LTR7 repetitive element;
6942	20265	33692	3.39	1.0E-104	BE314182.1	EST_HUMAN	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6942	20265	33693	3.39	1.0E-104	BE314182.1	EST_HUMAN	601150451.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
7373	20452	33917	2.01	1.0E-104	BE314182.1	EST_HUMAN	601150451.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
7898	21875	35414	0.87	1.0E-104	BF509244.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8366	22443	36004	2.41	1.0E-104	BF448230.1	EST_HUMAN	U1-H-B14-gene-b-09-C-U1 st NC1 CGAP_L124 Homo sapiens cDNA clone IMAGE:3365948 3'
8463	22620	36082	0.46	1.0E-104	AA682308.1	EST_HUMAN	nef18g11.x1 NC1 CGAP_L124 Homo sapiens cDNA clone IMAGE:3365948 3'
8463	22620	36082	0.46	1.0E-104	AA682308.1	EST_HUMAN	nef18g11.x1 NC1 CGAP_L124 Homo sapiens cDNA clone IMAGE:3365948 3'
9494	22541		1.03	1.0E-104	T74219.1	EST_HUMAN	298106.s1 Soares fetal liver 11B Homo sapiens cDNA clone IMAGE:462897 3'
9515	22580	36146	5	1.0E-104	AF091395.1	NT	yc3102.1 Soares infant brain 11B Homo sapiens cDNA clone IMAGE:22440 5'
9515	22580	36147	5	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9515	22580	36147	5	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds

[illegible]

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5033	18181		5.34	1.0E-105	AL169208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5259	18378	31344	1.08	1.0E-105	AB020673.1	NT	Homo sapiens mRNA for KIAA0868 protein, complete cds
5445	18845	31623	1.18	1.0E-105	AF016704.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 2
5613	18711		1.12	1.0E-105	U1420134	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
7045	20098	33513	1.44	1.0E-105	BF314302.1	EST_HUMAN	601801028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 6'
7045	20098	33514	1.44	1.0E-105	BF314302.1	EST_HUMAN	601801028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7121	18547	31458	3.78	1.0E-105	11419108	NT	Homo sapiens GTPase activating protein-like (GAPL) mRNA
7121	18547	31459	3.78	1.0E-105	11419108	NT	Homo sapiens GTPase activating protein-like (GAPL) mRNA
7167	20300	33743	0.72	1.0E-105	AW051634.1	EST_HUMAN	EST1363669 MAGE resequences, MAGEB Homo sapiens cDNA
7436	20513	33988	0.72	1.0E-105	BE802618.1	EST_HUMAN	801677279F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2500628 5'
8043	21126	34647	0.63	1.0E-105	X12568.1	NT	Human mRNA for ddi proto-oncogene
8217	21299	34820	11.05	1.0E-105	T05087.1	EST_HUMAN	EST102915 Fetal brain, Striatum (cat336206) Homo sapiens cDNA clone HFBGR32
8692	21673	35211	1.83	1.0E-105	AW007194.1	EST_HUMAN	W650-10 X1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2500628 3' similar to SW:ACSA_PENCH P30833 ACETYL-COENZYME A SYNTHETASE ;
8128	22207	35750	0.82	1.0E-105	AW840671.1	EST_HUMAN	RC1-CN0008-070100-011-605 CN0008 Homo sapiens cDNA
8250	22327	35874	2.51	1.0E-105	AW016879.1	EST_HUMAN	U1-H-BIP-ab-b-12-0-UI-s1 NCI CGAP_Sub2 Homo sapiens cDNA
8404	22478	36041	0.83	1.0E-105	AW88272.1	EST_HUMAN	QV2-OT0062-140300-083-008 OT0062 Homo sapiens cDNA
8404	22478	36042	0.83	1.0E-105	BE867783.1	EST_HUMAN	QV2-OT0062-140300-083-008 OT0062 Homo sapiens cDNA
8767	22784	36333	0.75	1.0E-105	BE867783.1	EST_HUMAN	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
8767	22784	36334	0.75	1.0E-105	BE867783.1	EST_HUMAN	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
11173	24243	37876	4.82	1.0E-105	AF284322.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
11508	24584	38241	1.42	1.0E-105	DE354811	NT	Homo sapiens COL4A6 gene for $\alpha 6(IV)$ collagen, exon 31
11558	24614	38283	1.85	1.0E-105	7705836	NT	Homo sapiens Ran binding protein 11 (LOC61194), mRNA
11887	24875	38572	2.52	1.0E-105	AW027554.1	EST_HUMAN	WY7407 X1 Scores: thymus_NHFT Homo sapiens cDNA clone IMAGE:2535301 3' similar to TR:P87892
11887	24875	38572	2.52	1.0E-105	AW027554.1	EST_HUMAN	P87892 PROTEASE ;
11872	24957	38669	1.48	1.0E-105	BF430921.1	EST_HUMAN	7c18b10 X1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3574281 3' similar to TR:P87880 P87880
12111	26081	38794	1.3	1.0E-105	AF218886.1	NT	RIN1 ;
165	13380		0.88	1.0E-106	AW503208.1	EST_HUMAN	Homo sapiens attractin precursor (ATRIN) gene, exon 8
210	13433	26484	5.14	1.0E-106	AI056005.1	EST_HUMAN	U1-H-BIP-ab-b-12-0-UI-s1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
555	13748	28774	1.89	1.0E-106	AW965558.1	EST_HUMAN	W78601 X1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2215008 3'
820	13807	28828	0.8	1.0E-106	J00146.1	NT	EST1377629 MAGE resequences, MAGEI Homo sapiens cDNA
821	13807	28828	1.13	1.0E-106	J00146.1	NT	Human dihydropyridine reductase pseudogene (psl-hd1)
1554	14707	27787	8.84	1.0E-108	AF145712.1	NT	Human dihydropyridine reductase pseudogene (psl-hd1)
1554	14707	27787	8.84	1.0E-108	AF145712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds

Table 4  
Single Exon Probes Expressed in Placenta

Single Exon Probes Expressed in Tissues							Top Hit Descriptor
Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession N.	Top Hit Database Source	Top Hit Descriptor
1736	14885	27978	7.83	1.0E-106 U48724.1	NT	Human	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
1737	14906	28000	1.33	1.0E-106 U04510.1	NT	Human	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
1846	14992	28093	5.51	1.0E-106 AA627446.1	EST_HUMAN	Human	ng41c05.s1 NC1_CGAP_C03 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element;
1846	14992	28093	5.51	1.0E-106 AA627446.1	EST_HUMAN	Human	ng41c05.s1 NC1_CGAP_C03 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element;
1846	14992	28094	6.51	1.0E-106 AA527446.1	EST_HUMAN	Human	ng41c05.s1 NC1_CGAP_C03 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element LTR3 repetitive element;
2191	15328	28461	1.94	1.0E-106 BE144286.1	EST_HUMAN	Human	MR0-HT0165-140200-008-410 HT0165 Homo sapiens cDNA
2391	15522	28851	3.62	1.0E-106 4504184	NT	Human	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2574	15699	28821	2.19	1.0E-106 AF003528.1	NT	Human	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2687	15788	28904	1.83	1.0E-106 U64675.2	NT	Human	Homo sapiens sperm membrane protein BS-63 mRNA, complete cds
2089	15790	28908	2.01	1.0E-106 BE260201.1	EST_HUMAN	Human	801149783.F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3602461 6'
2815	15929	29041	8.05	1.0E-106 AU276526.1	EST_HUMAN	Human	q78h10.x1 Scares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1876307 3'
2886	14617	27700	1.84	1.0E-106 4504184	NT	Human	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2886	14617	27701	1.84	1.0E-106 4504184	NT	Human	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2839	18116	29128	1.18	1.0E-106 BE384236.1	EST_HUMAN	Human	601272675.F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3913818 5'
3007	18182	29204	5.7	1.0E-106 AB037747.1	NT	Human	Homo sapiens mRNA for KIAA1326 protein, partial cds
3248	18422	29438	2.5	1.0E-106 AB037747.1	NT	Human	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3248	18422	29438	2.5	1.0E-106 AB037747.1	NT	Human	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3248	18422	29439	2.5	1.0E-106 8922866	NT	Human	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3461	18628	29848	1.04	1.0E-106 AB008681.1	NT	Human	Homo sapiens gene for actinin receptor type IIb, complete cds
3527	16892	29701	1.07	1.0E-106 AB003104.1	NT	Human	Homo sapiens gene for actinin receptor type IIb, complete cds
3527	16892	29702	1.07	1.0E-106 AB003104.1	NT	Human	Homo sapiens mRNA for KIAA1278 protein, partial cds
4149	17301	30293	8.2	1.0E-106 AW974350.1	EST_HUMAN	Human	EST386876 IMAGE resequenced, MAGN Homo sapiens cDNA
4149	17301	30294	8.2	1.0E-106 AW974350.1	EST_HUMAN	Human	EST386876 IMAGE resequenced, MAGN Homo sapiens cDNA
4149	17301	30294	8.2	1.0E-106 AW974350.1	EST_HUMAN	Human	MR0-HT0165-140200-008-410 HT0165 Homo sapiens cDNA
4723	17858	30840	2.27	1.0E-106 BE144286.1	EST_HUMAN	Human	g24509.s1 Scares_NHMPU_S1 Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN
5485	18684	31701	2.95	1.0E-106 AA78155.1	EST_HUMAN	Human	PHPS1-2 (HUMAN);
5976	19161	32480	0.95	1.0E-106 AU130113.1	EST_HUMAN	Human	AU130113 NT2R2P3 Homo sapiens cDNA clone NT2R2P3-3000274 5'
5976	19161	32481	0.95	1.0E-106 AU130113.1	EST_HUMAN	Human	AU130113 NT2R2P3 Homo sapiens cDNA clone NT2R2P3-3000274 5'
6026	19209	32528	0.91	1.0E-106 AA434168.1	EST_HUMAN	Human	znc2812.s1 Scares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:770915 3'
6116	19286	32831	1	1.0E-106 AU143428.1	EST_HUMAN	Human	AU143428 Y78AA1 Homo sapiens cDNA clone Y78AA1001912 5'
6116	19286	32832	1	1.0E-106 AU143428.1	EST_HUMAN	Human	AU143428 Y78AA1 Homo sapiens cDNA clone Y78AA1001912 5'
6227	19402	32762	8.39	1.0E-106 BF678574.1	EST_HUMAN	Human	602154012.F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285067 5'



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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6336	19507	32864	0.81	1.0E-106	BE89712.1	EST_HUMAN	601439870F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6526	18507	32864	0.68	1.0E-108	BE89712.1	EST_HUMAN	601439870F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924641 5'
6649	19711	33087	16.91	1.0E-106	11646913	NT	Homo sapiens xylotransferase II (XT2), mRNA
6549	19711	33088	15.91	1.0E-106	11646913	NT	Homo sapiens xylotransferase II (XT2), mRNA
7528	20601	34075	5.69	1.0E-106	AA68378.1	EST_HUMAN	aa72e07.s1 Striatum schizo brain S11 Homo sapiens cDNA clone IMAGE:969732 3' similar to gb:U65873
7692	20654	34130	4.17	1.0E-106	11428917	NT	Homo sapiens XPM22 protein (LOC57108), mRNA
7672	20738	34216	1.94	1.0E-106	BE202722.1	EST_HUMAN	601105736F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:298345 5'
7787	20843	34335	8.06	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
7787	20843	34336	8.06	1.0E-106	11425503	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
7994	21044	34556	0.8	1.0E-106	AU118850	EST_HUMAN	AU118850 HEMBA1 Homo sapiens cDNA clone IMAGE:1000129 5'
8173	21265	34778	3.62	1.0E-106	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8173	21265	34777	3.62	1.0E-106	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8368	21449	34972	2.21	1.0E-106	AI523068.1	EST_HUMAN	ae08a07.x1 Barstead scoria HPLRB8 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:U06233
8830	21909	35447	0.64	1.0E-106	BE387930.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
8830	21909	35448	0.64	1.0E-106	BE387930.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
8903	21882	35522	2.77	1.0E-106	AI654123.1	EST_HUMAN	tye2a05.x1 NCL CGAP_KR11 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICAG_HUMAN
8252	22329	35876	0.83	1.0E-106	AW838831.1	EST_HUMAN	CM4.LT0059-150200-086-e06.LT0059 Homo sapiens cDNA
8348	22424	35978	2.34	1.0E-106	AA825307.1	EST_HUMAN	cc87e08.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354780 3'
8348	22424	35979	2.34	1.0E-106	AA825307.1	EST_HUMAN	cc87e08.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354780 3'
9488	22643	36106	0.77	1.0E-106	AU750447.1	EST_HUMAN	cn03e04.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn03e04.random
9628	22694	36255	1.94	1.0E-106	AU79569.1	EST_HUMAN	tm4102.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160698 3' similar to contains MSR1.13
9628	22694	36256	1.94	1.0E-106	AU79569.1	EST_HUMAN	tm4102.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160698 3' similar to contains MSR1.13
10205	23241	36832	0.6	1.0E-106	BE389234.1	EST_HUMAN	TAR1.PTR5 repetitive element1;
10289	23324	36928	1.09	1.0E-106	BF027310.1	EST_HUMAN	tm4102.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3604217 5'
10289	23324	36927	1.09	1.0E-106	BF027310.1	EST_HUMAN	TAR1.PTR5 repetitive element1;
10446	23481	37086	10.7	1.0E-106	AA604417.1	EST_HUMAN	60187874F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
10446	23481	37089	10.7	1.0E-106	AA604417.1	EST_HUMAN	60187874F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
10492	23627	37136	1.83	1.0E-106	AW363298.1	EST_HUMAN	np57b10.s1 NCL CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
							np57b10.s1 NCL CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
							RCO-CT0318-201199-031-e11 CT0318 Homo sapiens cDNA

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10497	23532	37141	0.66	1.0E-106	11436432	NT	Homo sapiens multimerin (MMRN), mRNA
10497	23532	37142	0.66	1.0E-106	11436432	NT	Homo sapiens multimerin (MMRN), mRNA
10678	23712	37320	0.65	1.0E-106	AL038886.1	EST_HUMAN	DKFZp434F0712.1 434 (synonym: HES3) Homo sapiens cDNA clone DKFZp434F0712.6
10807	23840	37464	4.26	1.0E-106	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11135	24207	37632	4.81	1.0E-106	BF032735.1	EST_HUMAN	601453461F1 NIH_MGC.66 Homo sapiens cDNA clone IMAGE:3857368 5'
11135	24207	37633	4.81	1.0E-106	BF032735.1	EST_HUMAN	601453461F1 NIH_MGC.66 Homo sapiens cDNA clone IMAGE:3857368 5'
11317	24380	38025	2.06	1.0E-106	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
11317	24380	38028	2.06	1.0E-106	J05200.1	NT	Human ryanodine receptor mRNA, complete cds
11694	24692	38383	1.35	1.0E-106	BE267335.1	EST_HUMAN	601109219F1 NIH_MGC.16 Homo sapiens cDNA clone IMAGE:3348997 5'
11837	24826	38514	1.89	1.0E-106	BE010832.1	EST_HUMAN	RCS-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
11837	24826	38515	1.89	1.0E-106	BE010832.1	EST_HUMAN	RCS-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
12263	25046		4.3	1.0E-106	AW410405.1	EST_HUMAN	h05111.x1 NIH_MGC.17 Homo sapiens cDNA clone IMAGE:2861644 5'
12464	25336	32069	1.97	1.0E-106	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC.72 Homo sapiens cDNA clone IMAGE:3918524 6'
12464	25336	32060	1.97	1.0E-106	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC.72 Homo sapiens cDNA clone IMAGE:3918524 6'
12717	25477		3.71	1.0E-106	BE99505.1	EST_HUMAN	R01-CT0249-090800-024-d05 CT0249 Homo sapiens cDNA
244	13466		4.52	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudocautosomal region, segment 11/2
276	13493		0.9	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
637	13922		1.03	1.0E-107	4828663	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
647	13832	28858	2.34	1.0E-107	AF166103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
636	14014	27069	1.02	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
808	14084	27149	1.38	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
891	14163	27223	6.71	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1307	14463	27631	1.08	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1600	14763	27836	3.81	1.0E-107	BF087405.1	EST_HUMAN	GV24HT0540-120900-389-605 HT0540 Homo sapiens cDNA
1791	14940	28033	6.42	1.0E-107	AF138275.1	NT	Homo sapiens cathepsin Z precursor (CTSZ) gene, exon 3
1887	15031	28138	1.52	1.0E-107	AB007822.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1887	15031	28139	1.52	1.0E-107	AB007822.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2282	15414	28646	3.77	1.0E-107	U13728.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2435	15563	28691	4.03	1.0E-107	AW842461.1	EST_HUMAN	PM1-CN0031-190100-001-403 CN0031 Homo sapiens cDNA
2435	15563	28692	4.03	1.0E-107	AW842461.1	EST_HUMAN	PM1-CN0031-190100-001-403 CN0031 Homo sapiens cDNA
3072	16248	28268	6.14	1.0E-107	AW842461.1	EST_HUMAN	PM1-CN0031-190100-001-403 CN0031 Homo sapiens cDNA
3072	16248	28269	6.14	1.0E-107	AW842461.1	EST_HUMAN	PM1-CN0031-190100-001-403 CN0031 Homo sapiens cDNA
3169	16344	28352	2.9	1.0E-107	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA

### Table 4

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3931	17060	30087	4.89	1.0E-107	AF020871.1	NT	Homo sapiens mycubulin (MTM1) gene, exon 8
5742	18935	32225	0.64	1.0E-107	AW988038.1	EST_HUMAN	EST381115 IMAGE:3849494 5'
5986	19171	32453	2.71	1.0E-107	BE867480.1	EST_HUMAN	601442558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849494 5'
7620	20593	34067	1.33	1.0E-107	AW603813.1	EST_HUMAN	U1-HF-BND-af-c-08-U1.1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3079310 5'
7520	20593	34068	1.33	1.0E-107	AW503913.1	EST_HUMAN	U1-HF-BND-af-c-08-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079310 5'
7698	20763	34247	1.36	1.0E-107	A1766078.1	EST_HUMAN	W556H04.X1 NCI_CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2284791 3'
7809	20981	34487	0.59	1.0E-107	A1404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7809	20981	34488	0.59	1.0E-107	A1404468.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
9587	22728	36289	0.99	1.0E-107	AU122469.1	EST_HUMAN	AU122469 MAMMA1 Homo sapiens cDNA clone MAMMA1002493 5'
10889	23973	37604	1.92	1.0E-107	BE168123.1	EST_HUMAN	QV1-H10516-140300-107-c10 H10516 Homo sapiens cDNA
10944	24026	37662	2.66	1.0E-107	A1922830.1	EST_HUMAN	g10d005.X1 NCI_CGAP_COLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICD1
11189	24238	37894	1.58	1.0E-107	L49141.1	NT	P05085 ALPHA-ACTININ 3, NON MUSCULAR:
11202	24271	37907	2.31	1.0E-107	BF666511.1	EST_HUMAN	Homo sapiens neurotrophin-specific protein (NSP) gene, exon 4
11603	24658	38341	3.81	1.0E-107	BE540550.1	EST_HUMAN	60212366F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281039 5'
11676	23504	37626	4.29	1.0E-107	11419701	NT	60106888F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5'
11678	23504	37627	4.29	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
12322	26100	31820	7.14	1.0E-107	AA001415.1	EST_HUMAN	Homo sapiens HSPC049 protein (HSPC049), mRNA
13211	25780	27210	1.24	1.0E-107	BE78169.1	EST_HUMAN	2245601.s1 Sources retina N24HR Homo sapiens cDNA clone IMAGE:361944 3' similar to contains THR.b1
977	14160	27210	1.72	1.0E-108	BE289042.1	EST_HUMAN	THR repetitive element:
1284	14450	27616	2.41	1.0E-108	Y18000.1	NT	60198265Z1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3937188 5'
2140	15278	28398	1.02	1.0E-108	BF028728.1	EST_HUMAN	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3332348 5'
2407	15338	28665	12.11	1.0E-108	A1866040.1	EST_HUMAN	Homo sapiens NF2 gene
2407	15338	28666	12.11	1.0E-108	A1866040.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
2407	15338	28668	12.11	1.0E-108	A1866040.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
2499	15626	28746	11.86	1.0E-108	BE206894.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
3025	16201	28224	0.64	1.0E-108	AF032897.1	NT	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
3430	16598	28614	0.64	1.0E-108	AF032897.1	NT	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
3430	16598	28615	0.64	1.0E-108	AF032897.1	NT	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4273	17418	30406	1.57	1.0E-108	AW664438.1	EST_HUMAN	h112a1.1x1 NCI CGAP_GUH Homo sapiens cDNA clone IMAGE:2872060 3' similar to SW-3BP1_MOUSE
4847	17783	30765	2.62	1.0E-108	U72901.1	NT	P65184 SH3-BINDING PROTEIN 3BP-1.
4847	17783	30766	2.62	1.0E-108	U72901.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4927	18057	31040	3.37	1.0E-108	7661976	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
5037	18165	31141	0.63	1.0E-108	AW504709.1	EST_HUMAN	Homo sapiens KIAA0187 gene product (KIAA0187) mRNA
6063	18191	31166	3.18	1.0E-108	AJ008005.1	NT	Homo sapiens PSN1 gene, alternative transcript
5598	18791	31839	1.24	1.0E-108	AW394094.1	EST_HUMAN	RCO-H10372-241199-031-c03 H10372 Homo sapiens cDNA
5644	18838	31916	2.56	1.0E-108	BE869016.1	EST_HUMAN	801444822F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3848980 5'
5644	18838	31917	2.56	1.0E-108	BE869016.1	EST_HUMAN	801444922F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3848980 5'
6048	19232		0.66	1.0E-108	BF012623.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 20
6125	19304	32644	0.74	1.0E-108	BF334831.1	EST_HUMAN	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6287	19441	32789	6.14	1.0E-108	AF284717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6287	19441	32790	6.14	1.0E-108	AF284717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6392	19561	32921	1.22	1.0E-108	AJ133289.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exon 1 and 2)
6489	18304	32844	1.08	1.0E-108	BF334831.1	EST_HUMAN	PM4-CT0403-240700-001-c10 CT0403 Homo sapiens cDNA
6753	19909	33302	0.64	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
6753	19909	33303	0.64	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7308	20390	33650	4.52	1.0E-108	11431857	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPCR5B) mRNA
7587	20687	34143	2.12	1.0E-108	4786333	NT	Homo sapiens delta-6 fatty acid desaturase (FADS6) mRNA
7846	20715	34193	1.32	1.0E-108	BE252607.1	EST_HUMAN	801113471F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354064 5'
7874	20739	34218	0.73	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4181037 5'
8264	21336	34219	0.73	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Bim87 Homo sapiens cDNA clone IMAGE:4181037 5'
8306	21388	34910	0.61	1.0E-108	AW408694.1	EST_HUMAN	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
8306	21388	34911	0.61	1.0E-108	AW408694.1	EST_HUMAN	U1-HF-BM0-ads-e-12-o-U1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
8247	22324	35869	0.77	1.0E-108	AF203977.1	NT	U1-HF-BM0-ads-e-12-o-U1.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
8287	22363	35912	0.46	1.0E-108	NA4974.1	EST_HUMAN	Homo sapiens ETS-family transcription factor EHF (EHF) mRNA, complete cds
10847	23880	37500	1.08	1.0E-108		NT	y35h10.1 Scores melanocyte 2NbhHM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR.A45773 A45773 keratin protein, long form - fruit fly.
							Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC83446), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10804	21037	34549	2.08	1.0E-108	BE635227.1	EST_HUMAN	601058769F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445361 5'
11066	18501	31537	2.67	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Gb1-associated microtubule-binding protein (GMAP-210)
11319	24382	38027	1.35	1.0E-108	AF228391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-18, and partial cds, alternatively spliced
11949	24605	38283	3.48	1.0E-108	AW986185.1	EST_HUMAN	EST378258 IMAGE resequenced, MAC1 Homo sapiens cDNA
11605	24638	38343	1.71	1.0E-108	AV708790.1	EST_HUMAN	AV708780 ADC Homo sapiens cDNA clone ADCAE03 5'
11605	24638	38344	1.71	1.0E-108	AV708790.1	EST_HUMAN	AV708780 ADC Homo sapiens cDNA clone ADCAE03 5'
11652	24731		2.77	1.0E-108	11441485	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
11688	15538	28665	2.89	1.0E-108	AI686040.1	EST_HUMAN	BB1610.X1 NC1_CGAP_P23 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
11688	15538	28666	2.89	1.0E-108	AI686040.1	EST_HUMAN	PROTEOLYCAN II PRECURSOR (HUMAN);
11712	24752	38448	1.72	1.0E-108	DS359.1	NT	BB1610.X1 NC1_CGAP_P23 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
12489	26344	32004	4.15	1.0E-108	AK02447.1	NT	PROTEOLYCAN II PRECURSOR (HUMAN);
12940	26918		5.08	1.0E-108	BF346356.1	EST_HUMAN	Homo sapiens COL4A6 gene for $\alpha 4(V)$ collagen, exon 23
43	13281	28287	1.01	1.0E-109	AW803116.1	EST_HUMAN	Homo sapiens mRNA for FLJ00037 protein, partial cds
66	13303	28328	1.17	1.0E-109	D88974.1	NT	602018571F1 NC1_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4154287 5'
225	13447	28475	3.34	1.0E-109	11422486	NT	IL2-UM0077-260400-079-D56 UM0077 Homo sapiens cDNA
236	13466	28482	2.77	1.0E-109	11438381	NT	Human mRNA for KIAA0220 gene, partial cds
478	13674	28705	2.28	1.0E-109	4507712	NT	Homo sapiens hypothetical protein FLJ11318 (FLJ11318), mRNA
611	13800	28820	14.77	1.0E-109	AB023216.1	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
611	13800	28820	14.77	1.0E-109	AB023216.1	NT	Homo sapiens tetrahydrocysteine repeat domain 2 (TTG2), mRNA
1037	14205	27282	1.82	1.0E-109	AI163249.2	NT	Homo sapiens mRNA for KIAA0989 protein, partial cds
1229	14389	27451	8.5	1.0E-109	M28699.1	NT	Homo sapiens chromosome 21 segment HS21C049
1230	14389	27451	8.38	1.0E-109	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
1673	14726	27806	0.89	1.0E-109	BE28673.1	EST_HUMAN	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1673	14726	27807	0.89	1.0E-109	BE28673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2858636 5'
1823	15066	28170	2.3	1.0E-109	D136432	NT	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2958636 5'
2314	15446	28580	5.48	1.0E-109	AL16324.2	NT	Homo sapiens chromosome 21 segment HS21C084
2326	16467	28589	3.65	1.0E-109	Y17123.1	NT	Homo sapiens chromosome 21 segment HS21C084
2687	15807	28923	18.35	1.0E-109	AI022328.1	EST_HUMAN	Homo sapiens SNF5011 gene, exon 6
2687	15807	28923	18.35	1.0E-109	AI022328.1	EST_HUMAN	ow65801.X1 Soares_fetal_liver_spleen_1NF.S_S1 Homo sapiens cDNA clone IMAGE:1654636 3' similar to
2687	15807	28924	18.35	1.0E-109	AI022328.1	EST_HUMAN	TR002197 002197 CIRCULATING CATHODIC ANTIGEN.;
2687	15807	28924	18.35	1.0E-109	AI022328.1	EST_HUMAN	ow65801.X1 Soares_fetal_liver_spleen_1NF.S_S1 Homo sapiens cDNA clone IMAGE:1654636 3' similar to
2687	15807	28924	18.35	1.0E-109	AI022328.1	EST_HUMAN	TR002197 002197 CIRCULATING CATHODIC ANTIGEN.;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2888	15808	28925	2.68	1.0E-109	4504208	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCY1A) mRNA
3125	16301	28314	3.37	1.0E-109	N85190.1	EST_HUMAN	J2818f Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3475	16842	28681	2.08	1.0E-109	AW883192.1	EST_HUMAN	CM3-NN0009-180400-150-f10 NN0009 Homo sapiens cDNA
3475	16642	28662	2.08	1.0E-109	AW883192.1	EST_HUMAN	CM3-NN0009-190400-180-f10 NN0009 Homo sapiens cDNA
3505	16770	28785	1.1	1.0E-109	AF240388.1	NT	Homo sapiens retinol dehydrogenase homology isoform-1 (RDH) mRNA, complete cds
3845	17104		1.31	1.0E-109	BE146144.1	EST_HUMAN	MRO-HT0209-110400-108-c04 HT0209 Homo sapiens cDNA
4284	17409	30395	4.35	1.0E-109	AI655417.1	EST_HUMAN	bs8e08.x1 NC1_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2239330 3' similar to WIPF53A2.8 CE16100.
4524	17683	30650	2.67	1.0E-109	4504208	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCY1A) mRNA
4722	17857	30838	1.7	1.0E-109	7682083	NT	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
5165	18287	31252	0.72	1.0E-109	BE283973.1	EST_HUMAN	60T186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:285636 5'
5165	18287	31253	0.72	1.0E-109	BE283973.1	EST_HUMAN	60T186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:285636 5'
5361	18584	31480	0.67	1.0E-109	AU137282.1	EST_HUMAN	AU137282 PLACE1 Homo sapiens cDNA clone IMAGE:106169 5'
5374	18577	31445	0.82	1.0E-109	BF67318.1	EST_HUMAN	60213644F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272922 5'
5428	18828	31604	2.82	1.0E-109	5174622	NT	Homo sapiens placental protein 11 (serine protease) (P11) mRNA
5724	18917		1.23	1.0E-109	BE178358.1	EST_HUMAN	RC1-HT0615-200400-022-c04 HT0615 Homo sapiens cDNA
6050	25817	32658	1.23	1.0E-109	BF37688.1	EST_HUMAN	RC1-HT0615-200400-022-c04 HT0615 Homo sapiens cDNA
6119	18917		1.41	1.0E-109	BE178358.1	EST_HUMAN	RC1-HT0615-200400-022-c04 HT0615 Homo sapiens cDNA
6721	19878	33269	0.85	1.0E-109	AI221395.1	EST_HUMAN	cg86h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842111 3'
6807	20222	33651	0.69	1.0E-109	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
6807	20222	33652	0.69	1.0E-109	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
7389	20467	33933	0.67	1.0E-109	AB046911.1	NT	Homo sapiens mRNA for KIAA1561 protein, partial cds
7738	20789	34288	3.75	1.0E-109	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7740	20801	34290	4.91	1.0E-109	BF182107.1	EST_HUMAN	60T180949SF1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
7740	20801	34291	4.91	1.0E-109	BF182107.1	EST_HUMAN	60T180949SF1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8366	21447	34970	1.35	1.0E-109	AL049184.1	NT	Novel human gene mapping to chromosome 13
8480	21561	35006	1.39	1.0E-109	AW749130.1	EST_HUMAN	PNC-BT0340-091299-002-c05 BT0340 Homo sapiens cDNA
8657	21936		2.84	1.0E-109	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
8832	22011	35548	4.36	1.0E-109	BE787540.1	EST_HUMAN	60T479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
8832	22011	35550	4.36	1.0E-109	BE787540.1	EST_HUMAN	60T479417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
8177	22255	35797	0.57	1.0E-109	BE145672.1	EST_HUMAN	IL0-HT0205-071189-142-g01 HT0205 Homo sapiens cDNA
9439	22513	36077	1.65	1.0E-109	HB4860.1	EST_HUMAN	ys80g08.l1 Soares retina N255FR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP-A53461 A53461 BLUETANIDE-SENSITIVE NAK-C1 COTRANSPORTER - SPINY.

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9550	22615	36184	0.64	1.0E-109	BE397086.1	EST_HUMAN	601288760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
9550	22615	36185	0.64	1.0E-109	BE397088.1	EST_HUMAN	601288760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
9550	22734	36304	1.37	1.0E-109	FO6804.1	EST_HUMAN	HSC1EC121 normalized Infant brain cDNA Homo sapiens cDNA clone c-1ec12
11013	24082	37730	1.8	1.0E-109	BE340908.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449589 5'
11013	24092	37731	1.8	1.0E-109	BE340909.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449599 5'
11046	24123	37577	18.68	1.0E-109	BF69483.1	EST_HUMAN	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5'
11387	24448	38109	1.57	1.0E-109	AU121370.1	EST_HUMAN	AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002690 5'
11651	24730	38422	2.18	1.0E-109	4502838	NT	Homo sapiens Cheddi-Highashi syndrome 1 (OHS1) mRNA
11693	24691	38382	4.5	1.0E-109	W16610.1	EST_HUMAN	z608b12.r1 Soares, fetal Lung NIH/19W Homo sapiens cDNA clone IMAGE:301439 5' similar to PIR:SA33669 SA33669 p64-hole stress-activated protein kinases - rat;
11884	24872	38569	1.64	1.0E-109	BE04560.1	EST_HUMAN	ht23105.x1 NCJ CGAP_LU24 Homo sapiens cDNA clone IMAGE:2855969 3' similar to TR:O92124 O92124 YGR163W MRNA HOMOLOGUE, COMPLETE CDS.;
11884	24934	38636	1.5	1.0E-109	AL118824.1	EST_HUMAN	DKFZ7611124.t1 761 (synonym: ham2) Homo sapiens cDNA clone DKFZ7611124 5'
11884	24969	38673	1.31	1.0E-109	11416618	NT	Homo sapiens single-minded (Drosophila) homolog 1 (SIM1), mRNA
12126	25106	38910	2.26	1.0E-109	AB007832.1	NT	Homo sapiens mRNA for KIAA0463 protein, partial cds
12397	15457	28589	2.32	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
12636	15457	28589	3.2	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
12762	25508	32038	8.39	1.0E-109	AB011399.1	NT	Homo sapiens gene for AIF-4, complete cds
3	13242	26242	1.4	1.0E-110	754804	NT	Homo sapiens deiodinase, deiodinase, type II (DIO2), transcript variant 2, mRNA
38	13276	26281	3.86	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
38	13276	26282	3.86	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
112	13242	26242	1.83	1.0E-110	754804	NT	Homo sapiens deiodinase, deiodinase, type II (DIO2), transcript variant 2, mRNA
305	13521	26555	1.31	1.0E-110	D87291.1	NT	Homo sapiens deiodinase, deiodinase, type II (DIO2), transcript variant 2, mRNA
640	13733	26757	1.04	1.0E-110	U84550.1	NT	Human dyx2b1/evx (DYN) gene, exon 20
1207	14368	27429	0.88	1.0E-110	5031620	NT	Homo sapiens calcitonin receptor-like (CALOR), mRNA
1308	14464	27532	1.02	1.0E-110	AB032353.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1973	15116	28217	1.65	1.0E-110	BE379477.1	EST_HUMAN	601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5'
2118	15256		1.66	1.0E-110	BF503896.1	EST_HUMAN	UH-B14-acc-b-05-0-UJ-s1 NCJ CGAP_S108 Homo sapiens cDNA clone IMAGE:3085784 3'
2803	16081		7.19	1.0E-110	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
3156	16331		1.48	1.0E-110	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L4-like ribosomal protein (L4L), and FTF3 (FTF3) genes, complete cds
3284	16438	28457	2.66	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3284	16438	28458	2.66	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
4320	17463	30448	1.09	1.0E-110	M15918.1	NT	Human autoimmune antigen small nuclear ribonucleoprotein E pseudogene

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4758	17893	30872	2.04	1.0E-110	AA017213.1	EST_HUMAN	ou32b10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627833 3' similar to SW:NI121
4777	17912	30897	3.01	1.0E-110	AA017212.1	EST_HUMAN	SW:NI121 RAT P52891 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121
5088	18216		2.28	1.0E-110	7682441	NT	Human sapiens KIAA1002 protein (KIAA1002), mRNA
5409	18611	31583	2.23	1.0E-110	BE288436.1	EST_HUMAN	601118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5'
5843	18033	32339	0.78	1.0E-110	BE621039.1	EST_HUMAN	601483677F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895785 5'
5860	18050	32357	8.61	1.0E-110	11419323	NT	Human sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6860	19050	32357	8.61	1.0E-110	11419323	NT	Human sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6868	25835	33421	5.43	1.0E-110	MA59112.1	NT	Human cysle fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
7179	20311	33764	0.59	1.0E-110	BE251430.1	EST_HUMAN	601108388F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350277 5'
7251	20334	33782	0.85	1.0E-110	U088981.1	NT	Human GS2 gene, exon 2
7281	20334	33783	0.85	1.0E-110	U088981.1	NT	Human GS2 gene, exon 2
7477	20352	34025	0.78	1.0E-110	AI560289.1	EST_HUMAN	h12408.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167407 3' similar to SW:ETV1_HUMAN
7583	20655	34131	16.19	1.0E-110	AV714276.1	EST_HUMAN	P50649 ETS TRANSLOCATION VARIANT 1 ;
7683	20655	34132	16.19	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB Homo sapiens cDNA clone DCBCE01 5'
7813	20883	34159	2.87	1.0E-110	AB020875.1	NT	Human sapiens mRNA for KIAA0868 protein, partial cds
7743	20804	34293	0.86	1.0E-110	AI137823.1	EST_HUMAN	AI137823 PLACET Homo sapiens cDNA clone PLACE1007511 5'
9536	22801	38174	1.09	1.0E-110	BE302594.1	EST_HUMAN	ba68801.Y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2805561 5' similar to TR:O77258 O77258
9777	22817	38395	2.46	1.0E-110	AW838394.1	EST_HUMAN	EG:114D9.2 PROTEIN.1 ;
10528	23564	37171	3.38	1.0E-110	11432732	NT	QV2L10033-020400-18-c04 LT0053 Homo sapiens cDNA
10986	24085	37700	3.2	1.0E-110	Y12337.1	NT	Human sapiens galectokinas 2 (GALK2), mRNA
11208	24278	37916	3.64	1.0E-110	BE734357.1	EST_HUMAN	Human sapiens galectokinas 2 (GALK2), mRNA
11208	24278	37917	3.64	1.0E-110	BE734357.1	EST_HUMAN	601656504F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11608	24681	38347	1.89	1.0E-110	MA100511.1	NT	601656504F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11728	23914	37839	1.7	1.0E-110	AA446529.1	EST_HUMAN	Human insulin receptor mRNA, complete cds
12211	25164		2.47	1.0E-110	BE691218.1	EST_HUMAN	zw67g02.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781298 5' similar to TR:G1146816
12341	25246		2.88	1.0E-110	AW062568.1	EST_HUMAN	G1146816 FCBP84 ;
12394	28400		2.88	1.0E-110	AB011399.1	NT	601439764F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924548 5'
12746	28113		6.01	1.0E-110	BE784546.1	EST_HUMAN	ILD-BT0163-040899-094-g10 BT0163 Homo sapiens cDNA
13071	16256		1.16	1.0E-110	BE608836.1	EST_HUMAN	Human sapiens gene for Af-6, complete cds
178	13402		11.82	1.0E-111	U43701.1	NT	PM3-NN1082-140900-006-f12 NN1082 Homo sapiens cDNA
							UI-H-B14-acc-b-05-0-UI-ST NCI CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
							Human ribosomal protein L23a mRNA, complete cds



Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
201	13424	28455	1.64	1.0E-111	3758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
733	13834		1.89	1.0E-111	BF033327.1	EST_HUMAN	601458631F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
762	13943	26889	4.13	1.0E-111	5393092	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1), mRNA
950	14123	27185	2.5	1.0E-111	M25142.1	NT	Human cardiac alpha-myosin heavy chain (MYH8) gene, exons 32 to 34
4288	17431	30418	1.15	1.0E-111	7681569	NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
4449	17589	30570	4.59	1.0E-111	K02288.1	NT	Human enkephalin B (enkb) gene, exon 4 and 3' flank and complete cds
5593	18786	31835	0.75	1.0E-111	AA151017.1	EST_HUMAN	247507.1 Soares, pregnant uterus, NBHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to
5693	18786	31836	0.75	1.0E-111	AA151017.1	EST_HUMAN	247507.1 Soares, pregnant uterus, NBHPU Homo sapiens cDNA clone IMAGE:505045 5' similar to
5749	18941	32242	0.88	1.0E-111	BE887809.1	EST_HUMAN	gbM23576 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5882	18052	32369	0.66	1.0E-111	U15989.1	NT	601443690F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847855 5'
6156	19332	32876	2.09	1.0E-111	A1344670.1	EST_HUMAN	Human two-handed zinc finger protein ZEB mRNA, partial cds
6818	19971	33379	0.86	1.0E-111	AL040762.1	EST_HUMAN	RELATED PROTEIN PAL-A (HUMAN);
6945	20258	33697	1.31	1.0E-111	AW294648.1	EST_HUMAN	DKFZp434C1815.1 434 (synonym: hsa3) Homo sapiens cDNA clone DKFZp434C1815 5'
7605	20676	34149	3.04	1.0E-111	BF368228.1	EST_HUMAN	UH-HW0-014-03-0-U1.61 NCI CGAP Sub6 Homo sapiens cDNA clone IMAGE:2728525 3'
7704	20769	34254	0.7	1.0E-111	AI761223.1	EST_HUMAN	IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA
7791	20847	34340	0.83	1.0E-111	U80017.1	NT	w86801.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2398465 3' similar to gb:J04813
8286	21368	34888	0.8	1.0E-111	AA278808.1	EST_HUMAN	CYTOKROME P450 IIIA5 (HUMAN);
8286	21368	34889	0.8	1.0E-111	AA278808.1	EST_HUMAN	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory
8383	21464	34889	0.63	1.0E-111	11431898	NT	protein (nrip) and survival motor neuron protein (smn) genes, complete cds
8435	21516	35047	3.66	1.0E-111	U68633.1	NT	2579g03.11 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410
8878	21957	35482	0.86	1.0E-111	11420516	NT	2579g03.11 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410
8975	22054	35587	0.64	1.0E-111	AK024633.1	NT	G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR ;
9008	22087		8.43	1.0E-111	X17033.1	EST_HUMAN	2579g03.11 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410
9085	22184	35708	15.93	1.0E-111	X17033.1	NT	G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR ;
9085	22184	35709	15.93	1.0E-111	X17033.1	NT	2579g03.11 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410
9289	22365	35914	3.37	1.0E-111	AF081336.1	NT	G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR ;
9518	22593	36182	0.54	1.0E-111	BF333210.1	EST_HUMAN	w86801.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398465 3' similar to gb:J04813

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10393	23360	37000	1.56	1.0E-111	AA604160.1	EST_HUMAN	aa68g02.s1 NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825170.3 similar to gb:U09235
10383	23418		1.04	1.0E-111	D10083.1	NT	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
10476	23514	37127	3.36	1.0E-111	AA131243.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
10995	24074	37707	1.34	1.0E-111	AW298497.1	EST_HUMAN	Z3101.1 Sceres, pregnant, uterus, NBHPU Homo sapiens cDNA clone IMAGE:503545.5
11299	24386	38006	3.29	1.0E-111	U68159.1	NT	UH-BWO-alc-d-07-0-UI.s1 NC1_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730276.3
12167	25130	38828	4.07	1.0E-111	11417901	NT	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
12741	25492	32028	4.72	1.0E-111	AV708482.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MAN1) mRNA
12881	25938	31855	4.82	1.0E-111	W22562.1	EST_HUMAN	AV708482 ADC Homo sapiens cDNA clone ADCA0808.5
13041	18504	31539	1.27	1.0E-111	AB035368.1	NT	72C9 Human retina cDNA Taps091-cleaved sublibrary Homo sapiens cDNA not directional
623	13810	26831	4.84	1.0E-112	U29103.1	NT	Homo sapiens mRNA for neuronin-1 alpha protein, complete cds
625	13810	26832	4.84	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
649	13834	26860	1.82	1.0E-112	BF508039.1	EST_HUMAN	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
649	13834	26861	1.82	1.0E-112	BF508039.1	EST_HUMAN	UH-BI4-alc-g-04-0-UI.s1 NC1_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023.3
1026	14167	27255	33.06	1.0E-112	AF157623.1	NT	UH-BI4-alc-g-04-0-UI.s1 NC1_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023.3
1087	14263	27308	1.49	1.0E-112	PS2742.1	SWISSPROT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1716	14868	27958	7.1	1.0E-112	7682125	NT	ZINC FINGER PROTEIN 135
1716	14868	27959	7.1	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
1863	15005	28115	1.11	1.0E-112	AF248540.1	NT	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
2577	15703	28823	2.83	1.0E-112	BE86939.1	EST_HUMAN	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
3147	16323		0.76	1.0E-112	4504116	NT	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
3444	16612	28630	0.61	1.0E-112	AI826511.1	EST_HUMAN	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
3680	17147	30153	0.63	1.0E-112	BE076073.1	EST_HUMAN	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
4726	17861	30843	0.68	1.0E-112	4504116	NT	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
4876	18007	30890	5.87	1.0E-112	AB037832.1	NT	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
4876	18007	30891	5.87	1.0E-112	AB037832.1	NT	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
5784	18976	32282	36.7	1.0E-112	NA60481	EST_HUMAN	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
6201	19378	32727	1.33	1.0E-112	AF148773.1	NT	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
6273	19447	32785	0.68	1.0E-112	AW502437.1	EST_HUMAN	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
6273	19447	32786	0.68	1.0E-112	AW502437.1	EST_HUMAN	Homo sapiens KIAA0440 protein (KIAA0440) mRNA
6378	18548	32904	0.83	1.0E-112	BE141686.1	EST_HUMAN	UH-BI4-alc-g-04-0-UI.s1 NC1_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023.3
6586	19749	33132	0.7	1.0E-112	BE672815.1	EST_HUMAN	UH-BI4-alc-g-04-0-UI.s1 NC1_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023.3

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6773	19928	33323	0.83	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
6773	19928	33324	0.83	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
6981	20209	33637	1.51	1.0E-112	BE574235.1	EST_HUMAN	602131405F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270921 5'
7305	20387	33847	0.88	1.0E-112	AL043298.1	EST_HUMAN	DKFZp434M0523 J1 434 (synonym: hncs3) Homo sapiens cDNA clone DKFZp434M0523 5'
7491	20566	34037	1.49	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7491	20566	34038	1.49	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
8367	21468	34895	1.78	1.0E-112	AU118031.1	EST_HUMAN	AU118051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5'
8158	22236	35781	2.64	1.0E-112	BE867635.1	EST_HUMAN	601443191F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
8158	22236	35782	2.64	1.0E-112	BE867635.1	EST_HUMAN	601443191F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
10097	23135	38736	2.37	1.0E-112	BF111413.1	EST_HUMAN	730g07.x1 Soares NSF_P8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to TR:Q9VW36 Q9VW35 CG9743 PROTEIN.1
11017	24098	37735	16.73	1.0E-112	AW68327.1	EST_HUMAN	MFE3-SND009-100400-105-B12 SND009 Homo sapiens cDNA
11103	24175	37810	1.31	1.0E-112	TS9387.1	EST_HUMAN	yt6d10.s1 Soares fetal liver spleen TNF.LS Homo sapiens cDNA clone IMAGE:112243 3' similar to SP:C40H1.1 CE00109 OVARIAN PROTEIN.1
11103	24175	37811	1.31	1.0E-112	TS9387.1	EST_HUMAN	yt6d10.s1 Soares fetal liver spleen TNF.LS Homo sapiens cDNA clone IMAGE:112243 3' similar to SP:C40H1.1 CE00109 OVARIAN PROTEIN.1
11191	24260	37896	3.14	1.0E-112	AJ249800.1	NT	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)
11359	24421	38077	2.24	1.0E-112	BE280478.1	EST_HUMAN	601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138989 5'
11428	24489	38153	2.28	1.0E-112	AT92603.1	EST_HUMAN	QK24C08.y6 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1868902 5' similar to TR:Q64362 Q64362 FUSED TOES.1
11428	24489	38164	2.28	1.0E-112	AT92603.1	EST_HUMAN	QK24C08.y6 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1868902 5' similar to TR:Q64362 Q64362 FUSED TOES.1
11460	24519	38188	4.78	1.0E-112	AW37870.1	EST_HUMAN	PMO-CT0237-141089-001-H02 CT0237 Homo sapiens cDNA
12096	23076	38783	1.66	1.0E-112	AT92603.1	EST_HUMAN	QK24C08.y6 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1868902 5' similar to TR:Q64362 Q64362 FUSED TOES.1
12096	23076	38784	1.66	1.0E-112	AT92603.1	EST_HUMAN	QK24C08.y6 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1868902 5' similar to TR:Q64362 Q64362 FUSED TOES.1
12727	25484		1.31	1.0E-112	AF106856.1	NT	Homo sapiens adenovocucinate lyase gene, complete cdo
761	13942	26987	6.82	1.0E-113	AJ355861.1	EST_HUMAN	ae05f01.x1 Schlier meningioma Homo sapiens cDNA clone IMAGE:1853625 3'
761	13942	26988	6.82	1.0E-113	AJ355861.1	EST_HUMAN	ae05f01.x1 Schlier meningioma Homo sapiens cDNA clone IMAGE:1853625 3'
865	14138	27199	2.83	1.0E-113	MT1865.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1572	14725	27605	3.23	1.0E-113	AJ355861.1	EST_HUMAN	ae05f01.x1 Schlier meningioma Homo sapiens cDNA clone IMAGE:1853625 3'

Table 4

## Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1893	16894	28240	1.63	1.0E-113	AF240775.1	NT	Homo sapiens eIF4E-transporter mRNA, complete cds
2161	15287	28422	1.49	1.0E-113	BF515218.1	EST_HUMAN	U1-H-BW1-ant403-0-U1:st NC1 CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876.3
3200	16375	28385	2.06	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
5178	16300	31263	38.66	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
5178	16300	31284	38.66	1.0E-113	5453562	NT	Homo sapiens activating transcription factor B (B-ATF), mRNA
5359	23930		2.4	1.0E-113	BE780838.1	EST_HUMAN	601469465F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872536 5'
5910	18805	31870	6.37	1.0E-113	AU127214.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP200807 5'
6045	18228	32552	3.54	1.0E-113	AU140291.1	EST_HUMAN	AU140291 PLACE2 Homo sapiens cDNA clone NT2RP200807 5'
6072	18264	32583	1.02	1.0E-113	AF016535.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6185	19371	32722	2.57	1.0E-113	11525737	NT	Homo sapiens UDP-N-acetyl-glucose-6-phosphate N-acetylglucosaminyltransferase 8 (GalNAc-1B) (GALNT8), mRNA
6285	19458	32809	0.8	1.0E-113	9861249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TP), member 4 (ABCB4), transcript variant B, mRNA
6285	19458	32810	0.8	1.0E-113	9861249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TP), member 4 (ABCB4), transcript variant B, mRNA
6448	19613	32878	0.88	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
6448	19613	32877	0.88	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7474	20549	34021	0.63	1.0E-113	BE262181.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508362 5'
7474	20549	34022	0.63	1.0E-113	BE262181.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508362 5'
8093	22172	35717	0.5	1.0E-113	8822819	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
8296	22372	35921	2.91	1.0E-113	BE392542.1	EST_HUMAN	601287709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
8296	22372	35922	2.91	1.0E-113	BE392542.1	EST_HUMAN	601287709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
8601	22656		0.62	1.0E-113	BE77287.1	EST_HUMAN	RC1-FT0134-280600-021-402 FT0134 Homo sapiens cDNA
10036	23074	36674	1.27	1.0E-113	11423387	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
10256	23291	36888	1.01	1.0E-113	5453597	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10256	23291	36889	1.01	1.0E-113	5453597	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10842	23876	37485	0.47	1.0E-113	AW60617.1	EST_HUMAN	U1-H-BN0-ak-b-10-0-U1:ri NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077322 5'
11385	24446	38107	1.89	1.0E-113	AW300519.1	EST_HUMAN	U1-H-BN0-ak-b-10-0-U1:ri NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077322 5'
11386	24457	38119	5.42	1.0E-113	AW630291.1	EST_HUMAN	h18f609.y1 NC1 CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869176 5' similar to TR:O60327 O60327
11396	24457	38120	6.42	1.0E-113	AW630291.1	EST_HUMAN	h18f609.y1 NC1 CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869176 5' similar to TR:O60327 O60327
11640	24598	38272	2.81	1.0E-113	BE292398.1	EST_HUMAN	KIAA0594 PROTEIN:
59	13287	28314	0.78	1.0E-114	Y17151.2	NT	601105652F1 NIH_MGC_13 Homo sapiens cDNA clone IMAGE:2988366 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
69	13297	26316	0.75	1.0E-114 Y17151.2	NT	Homo sapiens mRNA for multic drug resistance protein 3 (ABCC3)	
69	13297	26316	0.75	1.0E-114 Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)	
692	13848	28876	7.46	1.0E-114 T70551.1	EST_HUMAN	yt1sc01.01 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:109288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element	
1098	14261	27318	2.54	1.0E-114	8923087 NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA	
1341	14487	27569	4.65	1.0E-114	7857329 NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA	
1673	14825	27809	1.9	1.0E-114	6831094 NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA	
1706	14858	27845	5.08	1.0E-114	6879073 NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA	
2145	15281	28408	2.52	1.0E-114 BE171894.1	EST_HUMAN	WFO-H10559-250200-002-d07 HT0559 Homo sapiens cDNA	
2330	15482	28585	0.99	1.0E-114 AB002374.1	NT	Human mRNA for KIAA0376 gene, partial cds	
2865	13283	29280	0.8	1.0E-114 AB003102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds	
2865	13283	29280	0.8	1.0E-114 AB003102.1	NT	Homo sapiens mRNA for KIAA1270 protein, partial cds	
3201	16376	29386	2.6	1.0E-114 X04086.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13	
3240	16414	29429	1.03	1.0E-114 BF206374.1	EST_HUMAN	60186932F NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4100214 5'	
4124	17278	30275	3.27	1.0E-114 AF14973.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3	
4510	17649	30837	0.7	1.0E-114 J03171.1	NT	Human Interferon-alpha receptor (HuIFN-alpha-Rc) mRNA, complete cds	
5282	18401	31370	1.1	1.0E-114 AW284203.1	EST_HUMAN	U1-H-B12-eno-d-01-Q-UL s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2726424 3'	
6616	18714	31727	1.58	1.0E-114	4509880 NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (Semaphorin) 5A (SEMA5A) mRNA	
5516	18714	31728	1.88	1.0E-114	4509880 NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (Semaphorin) 5A (SEMA5A) mRNA	
5712	18905	32200	0.9	1.0E-114	9257201 NT	Homo sapiens cldtrif, heavy polypeptide-like 1 (CLTCL1), transcript variant 2, mRNA	
7224	20088		0.71	1.0E-114 AB041533.1	NT	Homo sapiens HMOGT-1 mRNA for sperm antigen, complete cds	
7388	20466	33931	1.09	1.0E-114 AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'	
7388	20466	33932	1.09	1.0E-114 AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'	
7434	20511	33983	8.2	1.0E-114 Y18000.1	NT	Homo sapiens NF2 gene	
7434	20511	33984	8.2	1.0E-114 Y18000.1	NT	Homo sapiens NF2 gene	
8075	21157	34978	1.94	1.0E-114	4557600 NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA	
8360	21441	34983	1.85	1.0E-114 AI363139.1	EST_HUMAN	g868d06.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2017163 3'	
8360	21441	34984	1.85	1.0E-114 AI363139.1	EST_HUMAN	g868d06.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2017163 3'	
8888	21977	35518	2.88	1.0E-114 U63041.1	NT	Human neural cell adhesion molecule CD66 mRNA, complete cds	
8966	22045	35689	5.81	1.0E-114 AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds	
8966	22045	35690	5.81	1.0E-114 AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8384	22456	36022	0.87	1.0E-114	BF108132.1	EST_HUMAN	7189g12.x1 Soares_NSF_F8_9V_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3526847 3' similar to TR-O9UH6 Q9UHN6 TRANSMEMBRANE PROTEIN 2.
9614	22669		1.3	1.0E-114	AW327455.1	EST_HUMAN	cd0305.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 5'
9662	21104	34621	2.67	1.0E-114	AF07754.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
9748	22812		1.36	1.0E-114	M13536.1	NT	Human ceruloplasmin mRNA
10343	23378	36939	1.02	1.0E-114	BE670004.1	EST_HUMAN	601449152F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853500 5'
10364	23399	37010	1.11	1.0E-114	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10762	23795	37416	1.18	1.0E-114	BE171884.1	EST_HUMAN	M804HT0559-250200-002-007 HT0559 Homo sapiens cDNA
							bat7g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906086 6' similar to gbX17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gblM20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE).
11027	24106		4.31	1.0E-114	BE302466.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdaBA08 5'
11466	24525	38197	8.11	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdaBA08 5'
11466	24525	38198	8.11	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdaBA08 5'
11842	24831	38522	6.28	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdaBA08 5'
11842	24831	38523	6.28	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdaBA08 5'
12843	26187		4.63	1.0E-114	11418041	NT	Homo sapiens TNF-inducible protein CG12.2 (CG12-1), mRNA
12836	26616	31975	2.75	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
12836	26616	31976	2.75	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
24	13282	26284	3.06	1.0E-115	4758111	NT	Homo sapiens HLA-B associated transcript-1 (DS81E), mRNA
132	13358	26391	1.09	1.0E-115	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220KD) (POLR2A), mRNA
136	13362		18.42	1.0E-115	4557887	NT	Homo sapiens keratin 18 (KRT18), mRNA
303	13519	26552	2.02	1.0E-115	AW804759.1	EST_HUMAN	QV4UM0094-300300-156-508 UM0094 Homo sapiens cDNA
549	13742	26766	1.68	1.0E-115	AI339208.1	EST_HUMAN	q06071.x1 NC1_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1846809 3' similar to TR-O00536 O00536
849	13742	26767	1.68	1.0E-115	AI339208.1	EST_HUMAN	q06071.x1 NC1_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1846809 3' similar to TR-O00536 O00536
809	13988	27041	3	1.0E-115	5174702	NT	TTF4 INTERACTING PEPTIDE 8 ;
809	13988	27042	3	1.0E-115	5174702	NT	TTF4 INTERACTING PEPTIDE 8 ;
811	13990	27044	15.24	1.0E-115	4603784	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
1680	14742	27823	1.15	1.0E-115	AF228180.1	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1), mRNA
1590	14742	27824	1.15	1.0E-115	AF228180.1	NT	Homo sapiens alpha-amylase-like semilabile alpha-amylase mRNA, complete cds
1888	16032	28140	1.31	1.0E-116	U78027.1	NT	Homo sapiens Brn-3 tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2142	16278	28400	1.13	1.0E-116	BE745489.1	EST_HUMAN	60157838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3828832 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2142	15278	28401	1.13	1.0E-115	BE745389.1	EST_HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928932 5'
2150	15286	28411	1.1	1.0E-115	AB007502.1	NT	Homo sapiens KIAA0442 mRNA, partial cds
2374	15505	28631	1.11	1.0E-115	AF231124.1	NT	Homo sapiens testican-1 mRNA, complete cds
2912	18080		1.03	1.0E-115	AW804759.1	EST_HUMAN	QV4JIM0094-300300-153-508 UM0094 Homo sapiens cDNA
3184	16359	29365	2.88	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3184	16359	29368	2.88	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3561	16726	29742	1.8	1.0E-115	AL277892.1	NT	Homo sapiens partial TTN gene for titin
4153	17305	30289	4.2	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0360 protein, partial cds
4521	17690	30847	2.49	1.0E-115		NT	Homo sapiens sir2-like 3 (SIRT3) mRNA
4537	17695	30674	4.28	1.0E-115	6812659	NT	Homo sapiens EphA4 (EPHA4) mRNA
4787	17832	30918	2.86	1.0E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4797	17832	30919	2.86	1.0E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
6028	18165	31132	2.89	1.0E-115	AL163388.2	NT	Homo sapiens chromosome 21 segment HS21C068
6028	18165	31133	2.89	1.0E-115	AL163388.2	NT	Homo sapiens chromosome 21 segment HS21C068
5044	18172	31149	1.01	1.0E-115	Y18215.1	NT	Homo sapiens putative pshHBC pseudogene for hair keratin, exons 1 to 9
5304	18421	31391	1.23	1.0E-115	4504638	NT	Homo sapiens interleukin 1 receptor, type 1 (IL1R1) mRNA
5347	18460	31425	0.92	1.0E-115	AB018311.1	NT	Homo sapiens mRNA for KIAA0769 protein, partial cds
8463	18663	31642	2.8	1.0E-115	AW970365.1	EST_HUMAN	EST362478 MAGE resequences, MAGEK Homo sapiens cDNA
5540	18737	31754	0.97	1.0E-115	BF665387.1	EST_HUMAN	602118346F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4276738 5'
5559	18853	32136	1.74	1.0E-115	11423128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5559	18853	32137	1.74	1.0E-115	11423128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5608	18998	32304	1.15	1.0E-115	AB28789.1	EST_HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:U07807.2
5808	18998	32305	1.15	1.0E-115	AB28789.1	EST_HUMAN	601579838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2519568 3' similar to gb:U07807.2
6391	19560	32919	0.68	1.0E-115	11426786	NT	DYNAMIN-1 (HUMAN);
6391	19560	32920	0.68	1.0E-115	11426786	NT	DYNAMIN-1 (HUMAN);
6525	19890	33084	9.49	1.0E-115	11426038	NT	Homo sapiens sperm surface protein (HSS) mRNA
6525	19890	33084	9.49	1.0E-115	11426038	NT	Homo sapiens sperm surface protein (HSS) mRNA
6658	19817	33204	1.68	1.0E-115	7661883	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC83439), mRNA
6658	19817	33204	1.68	1.0E-115	7661883	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC83439), mRNA
6668	19817	33205	1.68	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product Helicase (KIAA0054), mRNA
6668	19817	33205	1.68	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product Helicase (KIAA0054), mRNA
7074	20127	33543	0.75	1.0E-115	T8674.1	EST_HUMAN	Y88808.t1 Soares fetal liver spleen 1NF.LS Homo sapiens cDNA clone IMAGE:115095 5' similar to
7428	20505	33975	1.24	1.0E-115	AI076598.1	EST_HUMAN	SP-DOG YEAST P15801 DNA POLYMERASE GAMMA ;
7428	20505	33976	1.24	1.0E-115	AI076598.1	EST_HUMAN	0231a08.x1 Soares total fetus_Nb2HFB_bv Homo sapiens cDNA clone IMAGE:1876914 3'
7428	20505	33976	1.24	1.0E-115	AI076598.1	EST_HUMAN	0231a08.x1 Soares total fetus_Nb2HFB_bv Homo sapiens cDNA clone IMAGE:1876914 3'

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Probe Seq ID NO:	Exon Seq ID NO:	ORF Seq ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7246	20329	33775	1	1.0E-118	AL043761.1	EST_HUMAN	DKFZp434O0127.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434O0127.5'
7776	20833	34324	4.7	1.0E-118	11431050	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
7790	20846	34339	0.72	1.0E-118	L48690.1	NT	Homo sapiens very long chain acyl-CoA dehydrogenase gene, exon 1-20, complete cds
8156	21241	34761	1.85	1.0E-118	BE062895.1	EST_HUMAN	B01469159F.1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872247.5'
8577	21658	35198	7	1.0E-118	BE062895.1	EST_HUMAN	QV0-B10263-090200-097-403 B10263 Homo sapiens cDNA
8577	21658	35198	7	1.0E-118	BE062895.1	EST_HUMAN	QV0-B10263-090200-097-403 B10263 Homo sapiens cDNA
8583	21684	35205	1.1	1.0E-118	AA443024.1	EST_HUMAN	z288d07.t1 Soares_NHMFPL_S1 Homo sapiens cDNA clone IMAGE:811789.5'
8583	21684	35205	1.1	1.0E-118	AA443024.1	EST_HUMAN	z288d07.t1 Soares_NHMFPL_S1 Homo sapiens cDNA clone IMAGE:811789.5'
8873	21952	35488	0.84	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8873	21952	35488	0.84	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8918	21997	35536	1.94	1.0E-118	453732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8918	21997	35536	1.94	1.0E-118	453732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
9236	22313	35855	5.15	1.0E-118	BE263134.1	EST_HUMAN	B01144653F.2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502.5'
9236	22313	35855	5.15	1.0E-118	BE263134.1	EST_HUMAN	B01144653F.2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502.5'
9266	22343	35894	0.55	1.0E-118	AL048474.2	EST_HUMAN	DKFZp586K1824.1 586 (synonym: huko) Homo sapiens cDNA clone DKFZp586K1824
9792	22832	36411	1.07	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
10541	23576	37184	1.23	1.0E-118	BE736213.1	EST_HUMAN	601307146F.1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603.5'
10541	23576	37184	1.23	1.0E-118	BE736213.1	EST_HUMAN	601307146F.1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603.5'
10586	23621	37228	1.75	1.0E-118	BF185407.1	EST_HUMAN	7n1760B.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3504785.3' similar to SW:ZP3A_HUMAN
10752	23785	37399	0.59	1.0E-118	AW28351.1	EST_HUMAN	P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR ;
10752	23785	37399	0.59	1.0E-118	AW28351.1	EST_HUMAN	U4-BV06-alc-a-07-0JUL1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2728772.3'
11555	24610	38290	3.75	1.0E-118	AA31507.1	EST_HUMAN	EST186814 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light chain 1, cytoplasmic
11555	24610	38290	3.75	1.0E-118	AA31507.1	EST_HUMAN	EST186814 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to dynein, light chain 1, cytoplasmic
11855	24843	38539	2.92	1.0E-118	BE080876.1	EST_HUMAN	601489514F.1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563.5'
11855	24843	38539	2.92	1.0E-118	BE080876.1	EST_HUMAN	601489514F.1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563.5'
11855	24843	38540	2.92	1.0E-118	BE080876.1	EST_HUMAN	601489514F.1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563.5'
12071	25052	38761	1.81	1.0E-118	BE218235.1	EST_HUMAN	h36a06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175474.3' similar to TR:Q9Z2H4
776	13856	27007	2.46	1.0E-118	AF10492.1	NT	Q9Z2H4 G PROTEIN-COUPLED RECEPTOR LGR4 ;
1062	16029	27284	0.83	1.0E-118	7703607	NT	Homo sapiens chloride channel CLCA4 (CLCA) mRNA, complete cds
1897	15129	28232	2.98	1.0E-118	AB023147.1	NT	Homo sapiens CGI-105 protein (LOC81011), mRNA
3171	16346	28353	1.01	1.0E-118	8922205	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3171	16346	28353	1.01	1.0E-118	8922205	NT	Homo sapiens mRNA for KIAA0930 protein, partial cds
3312	18485		2.17	1.0E-118	AA916760.1	EST_HUMAN	on10b05.ct1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1556241.3' similar to WFP:EO4F6.2
4063	17219	30227	1.22	1.0E-118	4504110	NT	CE01214 ;
4063	17219	30227	1.22	1.0E-118	4504110	NT	on10b05.ct1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1556241.3' similar to WFP:EO4F6.2
9453	18533	31632	3.86	1.0E-118	AU133389.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
9453	18533	31632	3.86	1.0E-118	AU133389.1	EST_HUMAN	AU1333399 NTZRP4 Homo sapiens cDNA clone NTZRP4001891.5'



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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6466	18686	31645	15.48	1.0E-119	M8914.1	NT	Human neurofibromin (NF1) gene, complete cds
6470	18670	31650	3.29	1.0E-119	BE69121.1	EST_HUMAN	RC1-NN0073-250800-018-g06 NN0073 Homo sapiens cDNA
6550	18747	31782	1.61	1.0E-119	AV693731.1	EST_HUMAN	AV693731 GK/G Homo sapiens cDNA clone GKCDH03 5'
6707	18900	32194	0.86	1.0E-119	AL134903.1	EST_HUMAN	DKFZp762M0710.t1 762 (synonym: hme2) Homo sapiens cDNA clone DKFZp762M0710 5'
6707	18900	32195	0.86	1.0E-119	AL134903.1	EST_HUMAN	DKFZp762M0710.t1 762 (synonym: hme2) Homo sapiens cDNA clone DKFZp762M0710 5'
6255	19429	32775	6.7	1.0E-119	AI150703.1	EST_HUMAN	qb77609.x1 Soares fetal heart NbhH19W Homo sapiens cDNA clone IMAGE:1708128 3' similar to SW:K1C1 MOUSE P02535 KERATIN TYPE I CYTOSKELETAL 10 ;
6414	19583	32944	0.71	1.0E-119	AF315683.1	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6461	19628	32989	1.22	1.0E-119	AA76732.1	EST_HUMAN	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6589	19760	33133	2.39	1.0E-119	X06282.1	NT	hm23110.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157451 3'
6801	19781	33149	4.01	1.0E-119	AV974193.1	EST_HUMAN	Human c-fes/fps proto-oncogene
7368	20840	34116	1.09	1.0E-119	BE796714.1	EST_HUMAN	EST388236 MAGE sequences, MAGEM Homo sapiens cDNA
8862	21941	35476	0.83	1.0E-119	BE515150.1	EST_HUMAN	601592005f1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946081 5'
8967	22896	36592	0.46	1.0E-119	11F45921	EST_HUMAN	801280564f1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622528 5'
10111	23149	36750	0.86	1.0E-119	11036543	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5) mRNA
10311	23346	36952	0.61	1.0E-119	AI149796.1	EST_HUMAN	Homo sapiens KIAA0477 gene product (KIAA0477) mRNA
10452	23487	37095	2.29	1.0E-119	AA465124.1	EST_HUMAN	q143a11.x1 Soares blastis NIH Homo sapiens cDNA clone IMAGE:1752764 3' similar to TR:Q13458
10722	23765	37361	1.13	1.0E-119	AJ297701.1	NT	aa32105.t1 NCI_CGAP_G031 Homo sapiens cDNA clone IMAGE:814977 5'
10765	23789	37420	0.77	1.0E-119	11425837	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
10789	23789	37421	0.77	1.0E-119	11425837	NT	Homo sapiens hypothetical protein FLJ10208 (FLJ10208) mRNA
10844	23877	37497	0.59	1.0E-119	BE561967.1	EST_HUMAN	801347190f1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687887 5'
10849	23882	37502	0.73	1.0E-119	AB032281.1	NT	Homo sapiens Scd mRNA for stearoyl-CoA desaturase, complete cds
11308	24373	38015	1.58	1.0E-119	AJ287701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
11308	24373	38016	1.58	1.0E-119	AJ287701.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
11478	24538		6.82	1.0E-119	BE599571.1	EST_HUMAN	80216602f1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5'
12460	26098		6.48	1.0E-119	AV847919.1	EST_HUMAN	RC3-C10212-24089-011-f03 C10212 Homo sapiens cDNA
12845	25982		3.03	1.0E-119	X89211.1	NT	H sapiens DNA for endogenous retroviral like element
247	13468	28500	0.68	1.0E-120	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
312	13628	28561	0.97	1.0E-120	AF248340.1	NT	Homo sapiens synaptobrevin 1 (SVN1) mRNA
1066	14232	27280	2.74	1.0E-120	AF248340.1	NT	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
1066	14232	27281	2.74	1.0E-120	AF248340.1	NT	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
1456	14609	27689	3.26	1.0E-120	NA4873.1	EST_HUMAN	iy40g12.t1 Soares melanocyte 2NbhHM Homo sapiens cDNA clone IMAGE:273766 5'

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1831	14783	27869	11.18	1.0E-120	AF167706.1	NT	Homo sapiens cyclin-like repeat-containing protein S52 precursor, mRNA, complete cds
1848	14985	28098	8.58	1.0E-120	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2174	16309	28437	1.83	1.0E-120	AB011389.1	NT	Homo sapiens gene for Af-8, complete cds
2174	15308	28438	1.83	1.0E-120	AB011389.1	NT	Homo sapiens gene for Af-8, complete cds
3382	13628	26561	1.61	1.0E-120	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
4477	17617	30598	2.05	1.0E-120	AF053480.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4477	17617	30599	2.05	1.0E-120	AF053480.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4784	17919	30906	3.11	1.0E-120	AF093483.1	NT	Homo sapiens stannocalcin (STC) gene, partial cds
4784	17919	30907	3.11	1.0E-120	AF093483.1	NT	Homo sapiens stannocalcin (STC) gene, partial cds
6853	18043	32349	16.08	1.0E-120	BF586222.1	EST_HUMAN	602183984F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
6853	18043	32350	16.08	1.0E-120	BF586222.1	EST_HUMAN	602183984F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
7748	20806	34295	1.84	1.0E-120	D84619.1	NT	Human TBXA31 gene for thromboxane synthase, exon 7
8078	21180	34677	1.38	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8078	21180	34678	1.38	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8527	21608	35147	2.31	1.0E-120	BF337589.1	EST_HUMAN	6020355362F1 NCI_CGAP_Brl64 Homo sapiens cDNA clone IMAGE:4183333 5'
8599	21680	35218	0.9	1.0E-120	AE003057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8599	21680	35219	0.9	1.0E-120	AE003057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8603	21684	35221	1.94	1.0E-120	AE007984.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8603	21684	35222	1.94	1.0E-120	AE007984.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8647	21727	35264	1.31	1.0E-120	AB007984.1	NT	Homo sapiens mRNA for KIAA0465 protein, partial cds
8701	22750	36319	4.87	1.0E-120	BE302102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3825544 5'
8701	22750	36320	4.87	1.0E-120	BE302102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3825544 5'
8948	22885	36578	3.54	1.0E-120	BF306341.1	EST_HUMAN	601868966F1 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:3826544 5'
8948	22885	36579	3.54	1.0E-120	BF306341.1	EST_HUMAN	601868966F1 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:3826544 5'
9978	23018	36812	1.02	1.0E-120	AU138203.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10088	23134	36816	0.55	1.0E-120	AB004151.1	EST_HUMAN	CM-B1043-080289-076 BT043 Homo sapiens cDNA
10281	23318	36816	3.4	1.0E-120	AB028900.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
11391	24452	38115	8.66	1.0E-120	BE286387.1	EST_HUMAN	601167277F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532015 5'
11625	24705	38397	2.12	1.0E-120	BE887019.1	EST_HUMAN	601443135F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3847281 5'
11625	24705	38398	2.12	1.0E-120	BE887019.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
12687	26436	32049	1.42	1.0E-120	Y18000.1	NT	Homo sapiens calcineurin binding protein 1 (KIAA0393), mRNA
75	13311	26337	0.62	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
389	13595	26831	1.35	1.0E-121	AU134983.1	EST_HUMAN	AU134983 PLACE1 Homo sapiens cDNA clone PLACE1000889 5'
742	16020	26964	1.31	1.0E-121	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2023	16164	28269	1	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2023	16164	28270	1	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2169	13304	28431	1.22	1.0E-121	L76031.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds
2643	15766	28880	1.07	1.0E-121	BF344378.1	EST_HUMAN	802014759F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4190286 5'
2643	16766	28881	1.07	1.0E-121	BF344378.1	EST_HUMAN	802014759F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4190286 5'
3150	16325	28336	6.8	1.0E-121	Y19203.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3150	16325	28337	5.8	1.0E-121	Y19203.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3626	16780	28807	1.23	1.0E-121	AB037768.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3626	16780	28808	1.23	1.0E-121	AB037768.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3768	16829	28934	8.25	1.0E-121	AF155166.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
4450	17690	30671	1.76	1.0E-121	AL683294.1	EST_HUMAN	q657b01.x1 NCI_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2005417 3'
5091	18219	31189	3.42	1.0E-121	X91937.1	NT	H. sapiens ECE-1 gene (exon 17)
5382	18584	31453	0.84	1.0E-121	BE222260.1	EST_HUMAN	hU0908.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166119 3'
5678	18873	32167	0.73	1.0E-121	BE271424.1	EST_HUMAN	601140485F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049820 5'
6757	18913	33308	0.64	1.0E-121	M81463.1	NT	Human glucose transporter (GLUT4) gene, complete cds
7028	20164	31483	0.98	1.0E-121	AJ271736.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 2/2
7102	18529	31483	0.79	1.0E-121	AW898086.1	EST_HUMAN	RC3-NN0066-270400-011-102 NN0066 Homo sapiens cDNA
8123	21203	34725	1.07	1.0E-121	11436217	NT	RC3-NN0066-270400-011-102 NN0066 Homo sapiens cDNA
8127	21209	34729	2.51	1.0E-121	D84122.1	NT	Homo sapiens gamma-aminobutyrate acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
8127	21209	34730	2.51	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
10062	23100	36702	1.02	1.0E-121	AW563858.1	EST_HUMAN	la05605.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:075457 075457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA. ;
10062	23100	36703	1.02	1.0E-121	AW563858.1	EST_HUMAN	la05605.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:075457 075457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA. ;
11015	24094	37733	3.45	1.0E-121	11427788	NT	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA
11023	24102	37740	1.94	1.0E-121	AF064200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele, complete cds
11211	24280	37819	5.74	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
11243	24312	37850	1.83	1.0E-121	N59824.1	EST_HUMAN	yv74c01.s1 Scars fetal liver spleen TNF1S Homo sapiens cDNA clone IMAGE:248448 3'
278	13486	28526	2.64	1.0E-122	11528176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
346	13557	26585	2.33	1.0E-122	AF114189.1	NT	Homo sapiens Intersectin short isoform (ITSN), mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit/Accession No.	Top Hit Database Source	Top Hit Descriptor
368	13577	26610	2.66	1.0E-122	J1526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
805	14080	27146	3.34	1.0E-122	AF114498.1	NT	Homo sapiens intercalin short isoform (ITSN), mRNA, complete cds
1247	14406	27468	5.19	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1728	14878	27693	18.7	1.0E-122	AF167705.1	NT	Homo sapiens cysteine-rich repeat-containing protein S92 precursor, mRNA, complete cds
1750	14889	27695	1.61	1.0E-122	J1418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1750	14889	27696	1.61	1.0E-122	J1418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1657	15003	28110	6.92	1.0E-122	BE906024.1	EST_HUMAN	601487032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898358 5'
2560	15685	28810	7.43	1.0E-122	BF316170.1	EST_HUMAN	601866173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2560	15685	28811	7.43	1.0E-122	BF316170.1	EST_HUMAN	601866173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2501	16080	29086	4.87	1.0E-122	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
4971	18100	31076	3.81	1.0E-122	4502169	NT	Homo sapiens amyloid beta (A4) precursor protein (presenilin-2, Alzheimer disease) (APP), mRNA
5104	18232	32164	1.41	1.0E-122	AF504048.1	EST_HUMAN	U1-HF-BN0-ali-a-03-0-JL17 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079948 5'
6881	18976	32164	1.2	1.0E-122	BE236039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
6886	18875	32164	6.8	1.0E-122	BE236039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
7363	20442	33804	0.64	1.0E-122	AA888671.1	EST_HUMAN	ak46903.s1 Soares, Jastis, NHT Homo sapiens cDNA clone IMAGE:1409398 3'
8998	22076	35614	0.6	1.0E-122	AJ278901.1	NT	Homo sapiens mRNA for doublesex and mab-3 related transcription factor 1 (DMRT1)
9228	22306	35849	1.17	1.0E-122	J1424216	NT	Homo sapiens telial giant larvae (Drosophila) homolog 2 (LGL2), mRNA
9524	22589	36159	0.96	1.0E-122	AB59618.1	EST_HUMAN	q32b07.x1 NCI_CGAP_Brn3 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.1
9524	22589	36160	0.96	1.0E-122	AB59618.1	EST_HUMAN	q32b07.x1 NCI_CGAP_Brn3 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW:MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.1
10338	23373	36983	0.64	1.0E-122	AL117234.1	NT	Novel human gene mapping to chromosome X, isoform of dhl (proto-oncogene)
11233	24302	37939	2.12	1.0E-122	AB565934.1	EST_HUMAN	EST1367804 MAGE resequences, MAGE Homo sapiens cDNA
11687	24744	38436	1.83	1.0E-122	AB024088.1	NT	Homo sapiens gene for B120, exon 10
1231	25178		5.28	1.0E-122	J1418187	NT	Homo sapiens phosphonamutase 1 (PMM1), mRNA
789	13989	27019	1.53	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
789	13989	27020	1.53	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
1038	14206	27263	6.18	1.0E-123	AL163219.2	NT	Homo sapiens chromosome 21 segment H521C049
1047	14213	27270	3.36	1.0E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (IMMT), mRNA
1267	14424	27491	3.83	1.0E-123	4505618	NT	Homo sapiens phosphatidylinositol-4-phosphate 6-kinase, type II, beta (PIP5K2B), mRNA, and translated products

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1267	14424	27492	3.83	1.0E-123	4606918	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP3K2B) mRNA, and translated products
2035	15176	28286	0.94	1.0E-123	11422478	NT	Homo sapiens similar to sex comb on midleg (Drosophila)-like 2 (H. sapiens) (LOC63782), mRNA
2166	15301	28427	3.21	1.0E-123	M55418.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2166	15301	28428	3.21	1.0E-123	M55418.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2166	15301	28428	3.21	1.0E-123	M55418.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2389	15520		4.21	1.0E-123	7705692	NT	Homo sapiens RAB9-like protein (LOC51209), mRNA
3322	16495	29512	0.71	1.0E-123	6912817	NT	Homo sapiens glutathionyl-peptide cyclotransferase (glutaminyl cyclase) (QPCT), mRNA
5563	18760	31789	1.62	1.0E-123	L34218.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5563	18760	31800	1.62	1.0E-123	L34218.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds
5689	18863	32185	1.76	1.0E-123	BE789748.1	EST_HUMAN	601591108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945433 5'
6599	19759	33146	1.63	1.0E-123	AU118435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
7143	20278	33718	0.91	1.0E-123	H53186.1	EST_HUMAN	yx8d11.1 Soares fetal liver spleen 11NLS Homo sapiens cDNA clone IMAGE:202444 5' similar to SP-YAK1, YEAST P14680 PROTEIN KINASE YAK1:
7156	20280	33733	1.39	1.0E-123	U42224.1	NT	Human growth hormone releasing hormone gene, exon 7
7344	20424	33887	0.71	1.0E-123	U56258.1	NT	Human HBRVONIN-CAM precursor (HBRVONIN-CAM) gene, complete cds
7662	20634	34105	0.83	1.0E-123	11525833	NT	Homo sapiens heparan sulfate (glucosaminyl) 3-O-sulfotransferase 2 (HSST2), mRNA
7620	20875	34374	1.31	1.0E-123	11436439	NT	Homo sapiens 2'-5'-oligoadenylate synthetase 2 (OAS2), mRNA
7629	20884	34386	2.22	1.0E-123	BE283001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509162 5'
7636	20891	34393	0.6	1.0E-123	11437202	NT	Homo sapiens hypophyseal protein FLJ20184 (FLJ20184), mRNA
7676	21026	34536	0.6	1.0E-123	N35941.1	EST_HUMAN	yx8d11.1 Soares melanocyte 2nbhm Homo sapiens cDNA clone IMAGE:268617 5' similar to PIR.S48611
7676	21026	34536	0.6	1.0E-123	N35941.1	EST_HUMAN	S48611 protein kinase PKA - Phycomyces blakesleeanus:
7676	21026	34536	0.6	1.0E-123	N35941.1	EST_HUMAN	yx8d11.1 Soares melanocyte 2nbhm Homo sapiens cDNA clone IMAGE:268617 5' similar to PIR.S48611
8100	21182	34701	0.79	1.0E-123	AU131891.1	EST_HUMAN	S48611 protein kinase PKA - Phycomyces blakesleeanus:
8100	21182	34702	0.79	1.0E-123	AU131891.1	EST_HUMAN	AU131891 NT2RP3 Homo sapiens cDNA clone NT2RP3003409 5'
8732	21812		0.7	1.0E-123	AW371924.1	EST_HUMAN	AU131891 NT2RP3 Homo sapiens cDNA clone NT2RP3003409 5'
8669	22711	36279	2.07	1.0E-123	AB007923.1	NT	RC4-BT0311-251189-012-a07 BT0311 Homo sapiens cDNA
8669	22711	36279	2.07	1.0E-123	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9705	22754	36325	18.77	1.0E-123	U09823.1	NT	Ornithine decarboxylase New Zealand white elongation factor 1 alpha (Rabef2), mRNA, complete cds
12020	25004	38705	4.91	1.0E-123	BF677282.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
12020	25004	38706	4.91	1.0E-123	BF677282.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
12114	26094	38798	2.71	1.0E-123	AW450831.1	EST_HUMAN	UHH-B13-alf-f-10-0-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737291 3'
12114	26094	38798	2.71	1.0E-123	AW450831.1	EST_HUMAN	UHH-B13-alf-f-10-0-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737291 3'

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
278	13497	28627	1.02	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
278	13497	28628	1.02	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
286	13503		1.49	1.0E-124	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
488	13693	26725	2.26	1.0E-124	AL163246.2	NT	Homo sapiens chromosome 21 segment H321C046
709	13891	26926	4	1.0E-124	AA397551.1	EST_HUMAN	Z81b04.r1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
709	13891	26927	4	1.0E-124	AA397551.1	EST_HUMAN	Z81b04.r1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
777	13857	27008	3.72	1.0E-124	AF155654.1	NT	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
831	14009	27065	2.06	1.0E-124	4507500	NT	Human putative ribosomal protein S1 mRNA
827	14102	27165	2.67	1.0E-124	7705446	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1343	14499	27572	0.68	1.0E-124	11419092	NT	Homo sapiens hypothetical protein (HSPC068), mRNA
1377	14532	27605	6.42	1.0E-124	AF274892.1	NT	Homo sapiens ring finger protein (RNF), mRNA
1377	14532	27608	6.42	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1858	15004	28111	4.06	1.0E-124	AF131712.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
2123	15269	28379	2.16	1.0E-124	BE878524.1	EST_HUMAN	Homo sapiens mRNA for nuclear RNA-helicase (nol11 gene)
2528	15853	28777	0.98	1.0E-124	AB024063.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ8/IR1) gene, exon
3678	16744	29761	1.06	1.0E-124	S78694.1	NT	Homo sapiens A TP-sensitive inwardly rectifying K-channel subunit (KCNJ8/IR1) gene, exon
3739	16900	28904	1.24	1.0E-124	S78694.1	NT	Homo sapiens lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and joined CDS)
4006	17183	30170	0.84	1.0E-124	14507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4179	17329	30321	0.69	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4187	17387	30330	0.98	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4866	17899	30983	2.51	1.0E-124	AB024063.1	NT	Homo sapiens gene for B120, exon 11
6050	18178		15.32	1.0E-124	AM18178.1	NT	Human fibronectin gene extra type III repeat (EDII), exon x+1
5205	18326	31286	0.74	1.0E-124	AW663390.1	EST_HUMAN	EST1376463 IMAGE resequencer, MAGH Homo sapiens cDNA
5412	18614	31588	10.49	1.0E-124	8922337	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
6789	18981	32284	1.2	1.0E-124	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
6008	19183	32511	6.89	1.0E-124	BF669135.1	EST_HUMAN	602124644F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281635 5'
6238	19471	32826	0.8	1.0E-124	AV711283.1	EST_HUMAN	AV711283 Cl Homo sapiens cDNA clone CUAADF07 5'
6563	19725	33103	1.12	1.0E-124	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facies related) (USP9X), mRNA
7152	20286	33728	3.15	1.0E-124	Y11717.1	NT	Mmusculus mRNA for hoxa3 gene.
7287	20370	33824	0.94	1.0E-124	BE271256.1	EST_HUMAN	800843771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2866585 5'

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Table 4  
Single Exon Probe Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7287	20370	33825	0.94	1.0E-124	BE271286.1	EST_HUMAN	600943777F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2968585 5'
7726	20789	34278	2.38	1.0E-124	AA63033.1	EST_HUMAN	ncdb8105.s1 Strangene HeLa cell s3 837216 Homo sapiens cDNA clone IMAGE:855897 3'
8453	21534	35064	2.73	1.0E-124	4509654	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
8667	21737	35277	1.24	1.0E-124	AW612106.1	EST_HUMAN	hgb4408.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:085162
8667	21737	35278	1.24	1.0E-124	AW612106.1	EST_HUMAN	hgb4408.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:085162
8933	22438	35998	0.68	1.0E-124	AW99884.1	EST_HUMAN	085162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ;
8863	22438	35997	0.68	1.0E-124	AW99884.1	EST_HUMAN	hgb4408.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:085162
8891	22740	36309	1.72	1.0E-124	AV645633.1	EST_HUMAN	085162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ;
8891	22740	36310	1.72	1.0E-124	AV645633.1	EST_HUMAN	hgb4408.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:085162
8808	22848	36426	7.77	1.0E-124	AW67133.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
8808	22848	36427	7.77	1.0E-124	AW67133.1	EST_HUMAN	AV645633 GLC Homo sapiens cDNA clone GLCACE04 3'
8808	22848	36427	7.77	1.0E-124	AW67133.1	EST_HUMAN	hgb4408.x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2400891 3'
10079	23113	36717	1.46	1.0E-124	AW503755.1	EST_HUMAN	w8302.x1 NCI_CGAP_Kd12 Homo sapiens cDNA clone IMAGE:2400891 3'
11302	24368	39009	1.57	1.0E-124	U94776.1	NT	UHF-BNO-alc-b-04-0.U1.1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:3078848 5'
11817	24688	38356	3.9	1.0E-124	AW683633.1	EST_HUMAN	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17
11761	23947	37676	2.18	1.0E-124	AW446451.1	EST_HUMAN	h05cd08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2900906 3'
11761	23947	37676	2.18	1.0E-124	AW446451.1	EST_HUMAN	h05cd08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2900906 3'
11761	23947	37676	2.18	1.0E-124	AW446451.1	EST_HUMAN	YKRS PROTEIN. ;
12310	13891	28926	4.6	1.0E-124	AA397351.1	EST_HUMAN	YKRS PROTEIN. ;
12310	13891	28926	4.6	1.0E-124	AA397351.1	EST_HUMAN	h18e03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:031662 031662
12310	13891	28926	4.6	1.0E-124	AA397351.1	EST_HUMAN	h18e03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:031662 031662
12310	13891	28926	4.6	1.0E-124	AA397351.1	EST_HUMAN	YKRS PROTEIN. ;
12780	25522	32004	1.99	1.0E-124	AB028016.1	NT	z81b04.11 Strangene scilizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
13080	26038	31680	2.36	1.0E-124	11417892	EST_HUMAN	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
13080	26038	31681	2.36	1.0E-124	11417892	EST_HUMAN	z81b04.11 Strangene scilizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482
328	13543	26239	7.32	1.0E-125	AB028016.1	NT	G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
439	13239	26239	4.69	1.0E-125	BE743922.1	EST_HUMAN	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
661	13847	26874	2.02	1.0E-125	AI10656.1	EST_HUMAN	Homo sapiens mRNA for KIAA1172 protein, partial cds
661	13847	26874	2.02	1.0E-125	AI10656.1	EST_HUMAN	60157781F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926985 5'
746	13927	26988	2.42	1.0E-125	AF284750.1	NT	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
883	14059	27124	1.45	1.0E-125	AA042813.1	EST_HUMAN	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
883	14059	27124	1.45	1.0E-125	AA042813.1	EST_HUMAN	Homo sapiens ALR-like protein mRNA, partial cds
883	14059	27124	1.45	1.0E-125	AA042813.1	EST_HUMAN	zK5307.s1 Soares_pregnant_uterus_NbHFU Homo sapiens cDNA clone IMAGE:48540 3' similar to
883	14059	27124	1.45	1.0E-125	AA042813.1	EST_HUMAN	gb:265857_cds1 OLFATORY RECEPTOR-LIKE PROTEIN HGMPOYE (HUMAN)

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1023	14194	27252	1.54	1.0E-128	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1177	14340	27394	1.73	1.0E-128	U90288.1	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
1707	16045	27946	1.44	1.0E-128	U90288.1	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
1854	15000	28108	5.91	1.0E-128	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
1854	15000	28107	5.91	1.0E-128	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
2433	16561	28687	4.81	1.0E-128	AA011278.1	EST_HUMAN	z01g081.1 Soares, fetal liver, spleen, TNF.LS, S1 Homo sapiens cDNA clone IMAGE:428588 5'
2573	16698	28820	0.96	1.0E-128	AA042813.1	EST_HUMAN	zK53c07.s1 Soares, pregnant uterus, NbhPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gpX68857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN).
2681	16783	28898	2.34	1.0E-128	U90288.1	NT	Homo sapiens inhibin, alpha (INH4) mRNA
2681	15783	28899	2.34	1.0E-128	U90288.1	NT	Homo sapiens inhibin, alpha (INH4) mRNA
3681	17119	30123	1.33	1.0E-128	AA042813.1	EST_HUMAN	zK53c07.s1 Soares, pregnant uterus, NbhPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gpX68857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMPO7E (HUMAN).
4672	17807	30796	1.82	1.0E-128	U90288.1	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4739	17874	30887	0.86	1.0E-128	BE315412.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5677	19067	32376	0.65	1.0E-128	BF683645.1	EST_HUMAN	602139874F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300770 5'
5694	19178	32501	1.39	1.0E-128	U90288.1	EST_HUMAN	Homo sapiens KIAA0986 protein (KIAA0986), mRNA
6013	19197	32514	1.2	1.0E-128	BE175169.1	EST_HUMAN	QV24HT0577.010500-185-506 HT0577 Homo sapiens cDNA
6054	19238	32581	3.63	1.0E-128	BE892860.1	EST_HUMAN	601433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5'
6096	19277	32806	0.85	1.0E-128	AA078900.1	EST_HUMAN	U67c07.x1 NC1_OGAP_Gas4 Homo sapiens cDNA clone IMAGE:2256108 3' similar to WP-C45G9.2
6412	19561	32942	0.72	1.0E-128	BE736055.1	EST_HUMAN	CE01954.1
6711	19869	33258	3.71	1.0E-128	BE662526.1	EST_HUMAN	601305670F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640097 5'
6711	19869	33260	3.71	1.0E-128	BE662526.1	EST_HUMAN	601305626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3693790 5'
7207	20072	33483	4.06	1.0E-128	X03427.1	NT	601335829F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689780 5'
7207	20072	33484	4.08	1.0E-128	X03427.1	NT	Homo sapiens IGF-II gene, exon 5
7700	20785	34249	1.56	1.0E-128	BE278923.1	EST_HUMAN	Homo sapiens IGF-II gene, exon 5
7933	20883	34491	0.59	1.0E-128	U90288.1	NT	601189076F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505603 5'
8743	21822	35357	1.49	1.0E-128	U90288.1	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8743	21822	35358	1.49	1.0E-128	U90288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
8918	22394	35945	4.16	1.0E-128	BE181840.1	EST_HUMAN	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
8918	22394	35946	4.15	1.0E-128	BE181840.1	EST_HUMAN	QV14HT0638-070500-181-312 HT0638 Homo sapiens cDNA
8918	22394	35946	4.15	1.0E-128	BE181840.1	EST_HUMAN	QV14HT0638-070500-181-312 HT0638 Homo sapiens cDNA



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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9881	22723	36283	1.06	1.0E-126	AI666893.1	EST_HUMAN	hs2503.x1 NC1 CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2171981 3' similar to TR:Q14089 Q14089
10670	23704	37313	0.72	1.0E-126	BE794576.1	EST_HUMAN	HYPOTHETICAL PROTEIN:
10712	23745	37351	1.06	1.0E-126	AB002298.1	NT	601590346F1 NIH MGCC 7 Homo sapiens cDNA clone IMAGE:3944531 5'
10821	24004	37639	3.03	1.0E-125	AF043458.1	NT	Human mRNA for KIAA0300 gene, partial cds
11091	24165	37802	1.34	1.0E-126	AF043458.1	NT	Homo sapiens IREL gene, exon 5
11357	24418	38076	2.42	1.0E-125	AL040655.1	EST_HUMAN	Homo sapiens glycine receptor 1 (skelatal) (RYR1), mRNA
11401	24462	38126	3.35	1.0E-126	AB014367.1	NT	DKFZp434N2414, t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N2414 5'
11538	24594	38303	1.63	1.0E-126	R01450.1	EST_HUMAN	Homo sapiens mRNA for KIAA0667 protein, partial cds
11568	24623	38309	2.13	1.0E-125	AF028029.1	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
11755	24630	38375	5.32	1.0E-126	AF028029.1	NT	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
11686	24685	38375	2.27	1.0E-125	AW812839.1	EST_HUMAN	RC3-ST0186-250200-018-c11 ST0186 Homo sapiens cDNA
11783	24783	38479	4.71	1.0E-126	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
11793	24783	38480	4.71	1.0E-125	BE074267.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
785	13974	27027	2.16	1.0E-126	476807	NT	Homo sapiens CDC-like kinase (CLK) mRNA
768	13977	27030	1.74	1.0E-126	M61638.1	NT	Human laminin B1 chain gene, exon 20
942	14116	27175	1.63	1.0E-126	X68735.1	NT	H. sapiens gene for alpha1-antitrypsin, exon 3
2663	15765	28900	4.66	1.0E-126	6382078	NT	Homo sapiens RAN binding protein 2 (RANBP2), mRNA
3140	16316	29329	8.12	1.0E-126	AA160709.1	EST_HUMAN	z072c03.t1 Streptococcus pneumoniae (#837203) Homo sapiens cDNA clone IMAGE:592420 5'
3140	16316	29330	8.12	1.0E-126	AA160709.1	EST_HUMAN	z072c03.t1 Streptococcus pneumoniae (#837203) Homo sapiens cDNA clone IMAGE:592420 5'
3719	16860	29885	0.87	1.0E-126	X63941.1	NT	H. sapiens DNA for liver cytochrome b5 pseudogene
3745	16906	29910	2.52	1.0E-126	7657039	NT	Homo sapiens death receptor 6 (DR6), mRNA
4908	18038	31026	1.06	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4908	18038	31027	1.06	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4959	18086	31092	1.81	1.0E-126	N34073.1	EST_HUMAN	yr76c06.t1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:287850 5'
5620	19010	32216	0.68	1.0E-126	T68998.1	EST_HUMAN	y652b12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:65627 3'
6362	19532	32891	2.91	1.0E-126	AA480075.1	EST_HUMAN	z666c3.t1 Soares fetal liver Nb2HF8_gw Homo sapiens cDNA clone IMAGE:796444 5' similar to
6419	19588	32951	4.33	1.0E-126	AB040958.1	NT	TR:G1145880 G1145880 TITIN:
6419	19588	32952	4.33	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7669	20735	34212	0.9	1.0E-126	AF26737.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7669	20735	34213	0.9	1.0E-126	AF26737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8062	21144	34682	0.73	1.0E-126	AB037715.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
8062	21144	34683	0.73	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8177	21259	34781	2.42	1.0E-128	X16608.1	NT	Human mRNA for ankyrin (variant 2.1)
8377	21458	34982	0.8	1.0E-128	AA483368.1	EST_HUMAN	ne74b12.s1 NCI CGAP_Elv1 Homo sapiens cDNA clone IMAGE:509989 similar to SW:TS68_HUMAN
10000	23038	38629	0.57	1.0E-128	4806424	NT	P88066 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR;
11089	24172	37807	2.01	1.0E-128	BF883176.1	EST_HUMAN	Homo sapiens neuro-oncological ventral antigen 1 (NOVA1), splice variant 1, mRNA
11808	24786	38494	2.2	1.0E-128	BE281680.1	EST_HUMAN	602139138F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4288240 5'
12823	18500	31536	6.48	1.0E-128	BE743922.1	EST_HUMAN	601149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502129 5'
176	13400	28429	2.82	1.0E-127	AB024597.1	NT	601577861F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928685 5'
176	13400	28430	2.92	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
177	13400	28428	2.75	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
177	13400	28430	2.75	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
284	13502	28535	2.14	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
284	13502	28536	2.14	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
804	14078	27145	1.17	1.0E-127	AF114488.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
839	14113	27174	4.81	1.0E-127	U72821.2	NT	Homo sapiens intersein short isoform (ITSN) mRNA, complete cds
1726	14876	27867	2.22	1.0E-127	4827053	NT	Homo sapiens lost on transfection LOT1 mRNA, complete cds
2127	15263	28382	1.97	1.0E-127	5803085	NT	Homo sapiens tubiquitin specific protease 8 (USP8) mRNA
2127	15263	28383	1.97	1.0E-127	5803085	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2127	15263	28383	1.97	1.0E-127	5803085	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2273	15406	28535	17.46	1.0E-127	4806620	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2418	16547	28676	3.12	1.0E-127	AF245305.1	NT	Homo sapiens adipoan mRNA, complete cds
2874	16784	28911	21.48	1.0E-127	X12881.1	NT	Human mRNA for cytokeratin 18
3781	16942	28948	0.61	1.0E-127	AF114488.1	NT	Homo sapiens intersein short isoform (ITSN) mRNA, complete cds
3913	17072	30070	0.7	1.0E-127	AW161297.1	EST_HUMAN	aud0608.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TRC15170 Q15170 TRANSCRIPTION FACTOR S-L-RELATED PROTEIN ;contains element MER22 repetitive element ;
4232	17379	30368	0.59	1.0E-127	AF135188.1	NT	Homo sapiens delayed rectifier potassium channel subunit Isk mRNA, complete cds
4368	17511	30491	24.83	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4368	17511	30492	24.83	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4618	17765	30737	0.83	1.0E-127	AF262287.1	NT	Homo sapiens cytochrome P450 reductase metalbinding protein P450RA12 mRNA, complete cds
4725	17860	30842	6.74	1.0E-127	4506384	NT	Homo sapiens RAD1 (S_pombe) homolog (RAD1) mRNA, and translated products
4765	17890		2.66	1.0E-127	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C008

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4795	17930	30916	4.36	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
5824	18014	32320	1.57	1.0E-127	W03547.1	EST_HUMAN	z01a10.1 Scores melanocyte 2NkHM Homo sapiens cDNA clone IMAGE:291258 5' similar to SW:PIPB_RAT P10898 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1;
6864	18044	32351	0.91	1.0E-127	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
5923	18110	32423	4.18	1.0E-127	X85764.1	NT	H. sapiens NOS2 gene, exon 6
6291	19464	32816	2.23	1.0E-127	X84060.1	NT	H. sapiens TCF11 gene, exon 3-6
6451	18618	32881	5.73	1.0E-127	4504778	NT	Homo sapiens integrin, beta 8 (ITGB8) mRNA
6797	18952	33352	1.09	1.0E-127	11421595	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA
7208	20073	33485	0.81	1.0E-127	4826977	NT	Homo sapiens reelin (RELN) mRNA
7864	21014	34525	1.31	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7864	21014	34526	1.31	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7973	21023	34536	0.83	1.0E-127	BF671356.1	EST_HUMAN	602161232F1 NIH_MGC_8: Homo sapiens cDNA clone IMAGE:4292575 5'
8088	22167	35713	0.81	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8088	22167	35714	0.81	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9840	22880	38462	3.73	1.0E-127	AF274853.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9840	22880	38463	3.73	1.0E-127	AF274853.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10077	23116	38718	0.86	1.0E-127	A128932.1	EST_HUMAN	qmi4h09.x1 NC1_CGAP_LUS Homo sapiens cDNA clone IMAGE:1890449 3'
10551	23588	37184	0.89	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
11426	24487	38190	5.64	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70KD protein 98 (mortalin-2) (H. sapiens) (LOC63184), mRNA
11426	24487	38151	5.64	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70KD protein 98 (mortalin-2) (H. sapiens) (LOC63184), mRNA
11927	24913	38914	1.65	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918917 5'
11927	24913	38915	1.65	1.0E-127	BE895415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918917 5'
12539	13400	26429	3.03	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12539	13400	26430	3.03	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12763	25507	32037	1.74	1.0E-127	AB011359.1	NT	Homo sapiens gene for A-F-6, complete cds
13170	25044		1.64	1.0E-127	AB011359.1	NT	Homo sapiens gene for A-F-6, complete cds
472	13667	26700	1.66	1.0E-128	BE386917.1	EST_HUMAN	601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618922 5'
1179	14342	27393	0.96	1.0E-126	4758081	NT	Homo sapiens chondritin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1179	14342	27397	0.96	1.0E-126	4758081	NT	Homo sapiens chondritin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2132	15288	28387	18.07	1.0E-128	U02623.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2132	15288	28388	18.07	1.0E-128	U02623.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4395	17536	30518	2.32	1.0E-129	AW755264.1	EST_HUMAN	CMV45 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMV45
6216	18991	32739	3.77	1.0E-129	AJ006345.1	NT	Cardiomyopathy associated gene 5
6654	19813	33201	0.61	1.0E-129	BE888934.1	EST_HUMAN	Homo sapiens KVLQT1 gene
7277	23860	33814	3.89	1.0E-129	AJ006345.1	NT	601513891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915350 5'
7340	20420	33882	4.03	1.0E-129	AJ006345.1	NT	Homo sapiens KVLQT1 gene
7697	20762	34245	1.04	1.0E-129	AF041056.1	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63694), mRNA
7697	20762	34246	1.04	1.0E-129	AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
8513	21594	36920	3.57	1.0E-129	AB014534.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
10284	23319	36921	1.03	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10284	23319	36921	1.03	1.0E-129	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
10730	23763	37370	0.52	1.0E-129	AI189117.1	EST_HUMAN	MITOGEN INDUCIBLE GENE MIC-2:
10730	23763	37371	0.62	1.0E-129	AI189117.1	EST_HUMAN	q40d08.x1 NC1 CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1858959 3' similar to TRC14940 Q14940
11497	24555	38230	3.32	1.0E-129	AA825526.1	EST_HUMAN	MITOGEN INDUCIBLE GENE MIC-2:
11678	20420	33882	5.01	1.0E-129	11420850	NT	MITOGEN INDUCIBLE GENE MIC-2:
12387	25273		4.28	1.0E-129	H83155.1	EST_HUMAN	q40d08.x1 NC1 CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1858959 3' similar to TRC14940 Q14940
12817	25544		1.97	1.0E-129	AL120739.1	EST_HUMAN	MITOGEN INDUCIBLE GENE MIC-2:
78	13314	26341	1.01	1.0E-130	1705530	NT	at7207.t1 Soaree, NihMFU, S1 Homo sapiens cDNA clone IMAGE:1047589 5'
1197	14359	27418	0.64	1.0E-130	AB037836.1	NT	DKF2p762K171.t1 762 (synonym: hme12) Homo sapiens cDNA clone DKF2p762K171 5'
1700	14852	27939	22.97	1.0E-130	BE275182.1	EST_HUMAN	SPB49150 B49150 HP-25-HIBERNATION-RELATED PROTEIN - TAMILAS ASIATICUS=ASIAN:
1700	14852	27940	22.97	1.0E-130	BE275182.1	EST_HUMAN	SPB49150 B49150 HP-25-HIBERNATION-RELATED PROTEIN - TAMILAS ASIATICUS=ASIAN:
2040	15181		2.63	1.0E-130	X04092.1	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63694), mRNA
2830	15944		7.23	1.0E-130	AJ010230.1	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63694), mRNA
2943	16120	29132	1.36	1.0E-130	BE684219.1	EST_HUMAN	Human gene for caldesmon (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
2943	16120	29133	1.36	1.0E-130	BE684219.1	EST_HUMAN	Human gene for caldesmon (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
3668	16831	28942	1.03	1.0E-130	AF240698.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
3864	16120	29132	6.31	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens retinal dehydrogenase homolog isoform 1 (RDH) mRNA, complete cds
3864	16120	29133	6.31	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens retinal dehydrogenase homolog isoform 1 (RDH) mRNA, complete cds
3964	16120	29133	6.31	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_33 Homo sapiens cDNA clone IMAGE:3685466 5'
4047	17203	30213	1.8	1.0E-130	AW60380.1	EST_HUMAN	601343016F1 NIH_MGC_33 Homo sapiens cDNA clone IMAGE:3685466 5'
4184	17334	30326	0.91	1.0E-130	M97710.1	NT	UHF-BND-4lyg-08-Q11.t1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
4650	17706	30782	8.77	1.0E-130	AW84393.1	EST_HUMAN	Human T-cell receptor (V alpha 22.1, J alpha RPA14265-variant, C alpha 1) mRNA
							GM4-CNO045-180200-511-02 CNO045 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5208	18329	31300	1.49	1.0E-130	AW363299.1	EST_HUMAN	RC0-CT0318-201189-031-a11 CT0318 Homo sapiens cDNA
5208	18329	31301	1.49	1.0E-130	AW363299.1	EST_HUMAN	RC0-CT0318-201189-031-a11 CT0318 Homo sapiens cDNA
6960	20188	33612	1.03	1.0E-130	AW843975.1	EST_HUMAN	CN0-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6960	20188	33613	1.03	1.0E-130	AW843975.1	EST_HUMAN	CN0-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6976	20203	33630	0.85	1.0E-130	11428448	NT	Homo sapiens estrogen-responsive B box protein [EBBP], mRNA
7404	20482	33949	1.86	1.0E-130	11418777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7506	20580	34052	0.83	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9), mRNA, complete cds
7606	20590	34053	0.63	1.0E-130	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9), mRNA, complete cds
8861	21860		0.53	1.0E-130	AF008561.1	NT	Homo sapiens aurifer-related kinase 1 (ARK1), mRNA, complete cds
8018	22098	35638	2.06	1.0E-130	AW966242.1	EST_HUMAN	EST198812 IMAGE ressequenced, IMAGE Homo sapiens cDNA
8415	22489	36054	1.82	1.0E-130	AB037756.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
10137	23175		0.63	1.0E-130	AW103454.1	EST_HUMAN	xd86808.X1 NC1 CGAP_OV23 Homo sapiens cDNA clone IMAGE:259587.4 3'
4	13243	26243	2.52	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
4	13243	26244	2.52	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
8	13243	26244	2.52	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
8	13246	26248	1.14	0.0E+00	4885126	NT	Homo sapiens chondroitin suppressor 1 (CHES1), mRNA
16	13254	26254	3.34	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
16	13254	26255	3.34	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
23	13261	26262	3.17	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
23	13261	26263	3.17	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
27	13265	26267	8	0.0E+00	AF141349.1	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
35	13273	26277	0.62	0.0E+00	5802897	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
37	13276	26280	0.89	0.0E+00	M69300.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
41	13279	26285	4.6	0.0E+00	6857825	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
58	13286	26312	1.77	0.0E+00	Y171512	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
58	13286	26313	1.77	0.0E+00	Y171512	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
60	13288	26317	1.45	0.0E+00	D78804.1	EST_HUMAN	HUM516H088 Human placenta polyA+ (TFUW82) Homo sapiens cDNA clone GEN-516H08 5'
60	13288	26318	1.45	0.0E+00	D78804.1	EST_HUMAN	HUM516H088 Human placenta polyA+ (TFUW82) Homo sapiens cDNA clone GEN-516H08 5'
61	13289	26319	9.53	0.0E+00	L16583.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds
63	13301	26322	16.36	0.0E+00	AW069334.1	EST_HUMAN	cd48e07.X1 Jila bone marrow stroma Homo sapiens cDNA clone HBMSG_cd48e07 3'
63	13301	26323	16.36	0.0E+00	AW069334.1	EST_HUMAN	cd48e07.X1 Jila bone marrow stroma Homo sapiens cDNA clone HBMSG_cd48e07 3'
67	13304	26327	2.48	0.0E+00	M60876.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
68	13306	26339	23.72	0.0E+00	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
77	13313	26339	2.1	0.0E+00	U758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
77	13313	26340	2.1	0.0E+00	U758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
80	13313	26339	1.06	0.0E+00	U758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
80	13313	26340	1.06	0.0E+00	U758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
83	13318	26346	0.62	0.0E+00	AA63770.1	EST_HUMAN	SW:TMOD_HUMAN P28289 TROPOMODULIN. ;
84	13319	26347	16.99	0.0E+00	4501850	NT	Homo sapiens anion chloride binding protein 1 (anion chloride binding protein 1) (ABP1), nuclear gene
85	13320	26347	12.3	0.0E+00	4504444	NT	encoding mitochondrial protein, mRNA
84	13329	26356	23.92	0.0E+00	5010088	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRP A1) mRNA
87	13332	26356	40.86	0.0E+00	U89277.1	NT	Homo sapiens actin, beta (ACTB) mRNA
103	13339	26366	2.4	0.0E+00	A114743.1	EST_HUMAN	Human polyomavirus 1 homolog (HPV1) mRNA, partial cds
104	13340	26367	0.6	0.0E+00	AB037794.1	NT	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
110	13343	26371	0.68	0.0E+00	X91213.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
118	13350	26377	0.68	0.0E+00	A162370.1	EST_HUMAN	H sapiens nct1 gene (exon 2)
118	13350	26377	1.68	0.0E+00	A162370.1	EST_HUMAN	ts38b05.x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:2230833 3' similar to TR:Q89551 Q89551
120	13350	26378	1.92	0.0E+00	N36040.1	EST_HUMAN	MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
120	13350	26379	1.92	0.0E+00	N36040.1	EST_HUMAN	Y01109.1 Soares melanocyte 2N5H1M Homo sapiens cDNA clone IMAGE:270017 5'
123	13353	26384	1.63	0.0E+00	4505458	NT	Y01109.1 Soares melanocyte 2N5H1M Homo sapiens cDNA clone IMAGE:270017 5'
133	13359	26392	3.65	0.0E+00	4505938	NT	Homo sapiens neurofilin 2 (NRP2) mRNA
133	13359	26393	3.65	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220K) (POLR2A) mRNA
141	13369	26647	1.9	0.0E+00	4503880	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220K) (POLR2A) mRNA
143	13367	26400	0.7	0.0E+00	T56945.1	EST_HUMAN	Homo sapiens IgG Fc binding protein (FCGAMMA)BP mRNA
143	13367	26401	0.7	0.0E+00	T56945.1	EST_HUMAN	YAB3G04.12 Stratagens fetal spleen (8837205) Homo sapiens cDNA clone IMAGE:38310 5'
157	13382	28416	12.8	0.0E+00	4504444	NT	YAB3G04.12 Stratagens fetal spleen (8837205) Homo sapiens cDNA clone IMAGE:38310 5'
161	13386	28416	2.08	0.0E+00	4504444	EST_HUMAN	YAB3G04.12 Stratagens fetal spleen (8837205) Homo sapiens cDNA clone IMAGE:38310 5'
163	13388	28419	96.39	0.0E+00	AF111186.2	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRP A1) mRNA
166	13383	28420	1.03	0.0E+00	BE28973.1	EST_HUMAN	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRP A1) mRNA
169	13383	28420	0.79	0.0E+00	BE28973.1	EST_HUMAN	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRP A1) mRNA

### Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
170	13394	26421	2.4	0.0E+00	W73973.1	EST_HUMAN	z662605.t1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:346201 5' similar to gb:X169282.cdnt1 ZINC FINGER PROTEIN CLONE 647 (HUMAN);
171	13395	26422	0.76	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
171	13395	26423	0.79	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-d04 HT0457 Homo sapiens cDNA
172	13396	26424	4.73	0.0E+00	AF244089.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
176	13399	26427	26.75	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
176	13399	26428	26.75	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
185	13407	26435	6.76	0.0E+00	BE018970.1	EST_HUMAN	CE22831.1; bz24612.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP.Y57A10A.Z
185	13407	26436	6.75	0.0E+00	BE018970.1	EST_HUMAN	CE22831.1; bz24612.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP.Y57A10A.Z
180	13412	26439	2.4	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
180	13412	26440	2.4	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
181	13413	26441	1.66	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
191	13413	26442	1.66	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
189	13422	26453	57.89	0.0E+00	D50659.1	NT	Human gamma-cytoplasmic actin (ACTG9) pseudogene
204	13427	26458	3.13	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen set4-3 mRNA, complete cds
204	13427	26459	3.13	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen set4-3 mRNA, complete cds
206	13429	26461	7.71	0.0E+00	AF16714.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
206	13429	26462	7.71	0.0E+00	AF16714.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
216	16007	26469	12	0.0E+00	AI587308.1	EST_HUMAN	RP408.X1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03181 PROFILIN I (HUMAN);
216	16007	26470	12	0.0E+00	AI587308.1	EST_HUMAN	RP408.X1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03181 PROFILIN I (HUMAN);
218	13440	26472	1.93	0.0E+00	AF165638.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
221	13443		11.48	0.0E+00	4506832	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
222	13444		6.53	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
228	13450	26478	1.48	0.0E+00	AB016264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
228	13450	26478	1.34	0.0E+00	AB016264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
230	13451	26479	2.02	0.0E+00	6674444	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
237	13459	26483	0.89	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia BAYOR-HGSC project=TCBAP1E4466
237	13459	26484	0.89	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia BAYOR-HGSC project=TCBAP1E4466



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
237	13459	26485	0.89	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4468 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP 4468
245	13467	26496	1.17	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
245	13467	26497	1.17	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
246	13469	26501	7.54	0.0E+00	5453805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
250	13471		3.79	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C01
257	13476	26507	4.65	0.0E+00	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
259	13478	26510	1.22	0.0E+00	X69772.1	NT	H. sapiens mRNA for Interferon alpha/beta receptor (long form)
267	13486		5.95	0.0E+00	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
260	13498	26529	1.37	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
260	13498	26530	1.37	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
282	13500	26532	1.9	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC61260), mRNA
283	13510		0.96	0.0E+00	D83327.1	NT	Homo sapiens DCCR1 mRNA, partial cds
284	13511	26545	1.2	0.0E+00	D83327.1	NT	Homo sapiens DCCR1 mRNA, partial cds
284	13511	26546	1.2	0.0E+00	D83327.1	NT	Homo sapiens DCCR1 mRNA, partial cds
286	13512		1.41	0.0E+00	AW845293.1	EST_HUMAN	IL2-CT0031-181199-020-803 CT0031 Homo sapiens cDNA
304	13520	26553	5.65	0.0E+00	4557028	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
304	13520	26554	5.65	0.0E+00	4557028	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
315	13531	26564	6.16	0.0E+00	AB028542.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
316	13532	26565	4.28	0.0E+00	AB028542.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
317	16010		8.13	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
318	13533		1.42	0.0E+00	AA48002.1	EST_HUMAN	z718c03.t1 Soerae NIH/MPU S1 Homo sapiens cDNA clone IMAGE:763994 5'
319	13534	26566	19.56	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
320	13534	26566	24.65	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
324	13538	26570	1.59	0.0E+00	AF114438.1	NT	Homo sapiens intercedin short isoform (ITSN) mRNA, complete cds
337	13550	26579	1.15	0.0E+00	OT14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
337	13550	26580	1.15	0.0E+00	OT14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
338	13551	26581	4.14	0.0E+00	7667213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
339	13551	26581	1.82	0.0E+00	7667213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
344	13595	26593	4.38	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (Drosophila homolog); translocated to, 4 (MLL4) mRNA
355	13568	26594	0.74	0.0E+00	4505266	NT	Homo sapiens moesin (MSN), mRNA
358	13569	26598	4.68	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
361	13572	26603	0.98	0.0E+00	U11600.1	NT	Human zinc finger protein Zfp31 (Zf31) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
366	13576	26607	2.75	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
366	13576	26608	2.75	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
367	16011	26609	2.53	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
369	13578	26611	1.01	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
372	13581	26616	1.99	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA) mRNA
373	13582	26616	2	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
374	13582	26616	1.43	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
376	13584	26618	0.66	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
387	13593	26629	3.37	0.0E+00	AU134633.1	EST_HUMAN	AU134633 PLACE1 Homo sapiens cDNA, clone PLACE1000899 5'
388	13635	26673	7.56	0.0E+00	AB028912.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
389	13636	26674	1.09	0.0E+00	A1863014.1	EST_HUMAN	g81h05.x1 NC1 CGAP_Brc25 Homo sapiens cDNA, clone IMAGE:2018457 3' similar to gp.X5+189
404	13601	26636	1.32	0.0E+00	AW754180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (HUMAN);
407	13603	26639	2.24	0.0E+00	4503680	NT	RC2-CT0820-300100-016-008 CT0320 Homo sapiens cDNA
408	13604	26640	2.34	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FCGAMMA)BP) mRNA
408	13604	26641	2.34	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FCGAMMA)BP) mRNA
409	13605	26642	2.18	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FCGAMMA)BP) mRNA
410	13606	26643	1.42	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FCGAMMA)BP) mRNA
410	13606	26644	1.42	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FCGAMMA)BP) mRNA
411	13607	26645	1.98	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FCGAMMA)BP) mRNA
412	13608	26646	2.55	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FCGAMMA)BP) mRNA
413	13609	26647	2.14	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FCGAMMA)BP) mRNA
414	13610	26648	0.96	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
414	13610	26649	0.86	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
415	13610	26648	1.07	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
415	13610	26649	1.07	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
419	13614		18.46	0.0E+00	4506608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
433	13223	26223	1.46	0.0E+00	R17795.1	EST_HUMAN	XP056021 Scars Infant brain 11N18 Homo sapiens cDNA, clone IMAGE:31852 5'
441	13637	26675	1.39	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase,
442	13638		3.85	0.0E+00	4508728	NT	phosphoribosylglycinamide synthetase (GART) mRNA
443	13639	26678	2.82	0.0E+00	AB028942.1	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
444	13640	26677	17.7	0.0E+00	4507162	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
444	13640	26678	17.7	0.0E+00	4507162	NT	Homo sapiens SON DNA binding protein (SON) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
445	13641	26670	4.23	0.0E+00	AF169607.1	NT	Male myotubular myopathy (SMN) protein (SMN) mRNA, complete cds
457	13652		1.46	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
459	13654	26692	4.44	0.0E+00	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
464	13658		0.76	0.0E+00	BE26447.1	EST_HUMAN	60111520F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'
480	13676	26706	3.38	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
480	13676	26707	3.38	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
486	13680	26715	21.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
486	13680	26716	21.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
486	13691	26722	4.1	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
497	13692	26723	5.9	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
497	13692	26724	5.9	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
500	13700	26729	4.25	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
508	13702	26731	1.81	0.0E+00	AU132898.1	EST_HUMAN	AU132898 NT2P4 Homo sapiens cDNA clone NT2P4-400837 5'
616	13710	26737	1.66	0.0E+00	BE395144.1	EST_HUMAN	60127485F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'
517	16014	26738	1.7	0.0E+00	AW838625.1	EST_HUMAN	PMO-DT0065-130400-002-c06 DT0068 Homo sapiens cDNA
520	13713	26740	1.82	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
521	13714	26741	0.95	0.0E+00	8923955	NT	Homo sapiens PCS26 protein (PCS26) mRNA
526	13718		1.9	0.0E+00	BF373403.1	EST_HUMAN	IL2-FT0159-070800-120-F07 FT0159 Homo sapiens cDNA
532	13725	26751	4.43	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
539	16015	26755	1.57	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA
544	13737	26761	1.15	0.0E+00	BF028005.1	EST_HUMAN	60176458F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3986998 5'
550	13743	26763	1.57	0.0E+00	AB040608.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
563	13746	26771	8.39	0.0E+00	8008030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCF81L) mRNA
564	13747	26772	4.53	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
554	13747	26773	4.53	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
568	13749	26775	0.73	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443) mRNA
568	13749	26776	0.63	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443) mRNA
567	13750	26777	0.63	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443) mRNA
562	13754		4.82	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
570	13762	26786	1.39	0.0E+00	AW135324.1	EST_HUMAN	U1H-BT1-gdb-h-04-0-U1H1 NC1_CGAP_Suk3 Homo sapiens cDNA clone IMAGE:2713951 3'
880	13772		6.31	0.0E+00	DT10063.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
899	13789	26810	1.85	0.0E+00	5174742	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene, encoding mitochondrial protein, mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
612	13801		7.14	0.0E+00	J04056.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
615	13904	26824	1.87	0.0E+00	BF104893.1	EST_HUMAN	60182827F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
617	13806	26826	0.95	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
617	13806	26827	0.98	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
618	13806	26828	0.77	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
618	13806	26827	0.77	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
619	13806	26828	0.72	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
619	13806	26827	0.72	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
619	13806	26827	0.72	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
624	13808	26830	0.64	0.0E+00	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
629	13814	26836	1.93	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
629	13814	26837	1.93	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
639	13824	26847	2.19	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
641	13828	26850	0.93	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1368 protein, partial cds
643	13828	26851	1.89	0.0E+00	6606918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
644	13828	26852	2.34	0.0E+00	6606918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
644	13829	26853	2.34	0.0E+00	6606918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
646	13830	26854	0.98	0.0E+00	6606918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
646	13830	26855	0.98	0.0E+00	6606918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
652	13838	26865	1.42	0.0E+00	AA399436.1	EST_HUMAN	z88007.1 Soares, Jasti NIH Homo sapiens cDNA clone IMAGE:728732 5'
656	13842	26869	6.57	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
660	13846	26872	4.28	0.0E+00	W7881.1	EST_HUMAN	z51b04.r1 Soares, Jasti NIH Homo sapiens cDNA clone IMAGE:415567 5' similar to
660	13846	26873	4.28	0.0E+00	W7881.1	EST_HUMAN	z51b04.r1 Soares, Jasti NIH Homo sapiens cDNA clone IMAGE:415567 5' similar to
663	13849		3.68	0.0E+00	4885528	NT	g6:21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
670	13858	26885	2.16	0.0E+00	6006003	NT	g6:21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
672	13858	26888	1.25	0.0E+00	5031624	NT	g6:21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
676	13861	26892	1.88	0.0E+00	U06235.1	NT	g6:21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
678	13865	26895	1.07	0.0E+00	AF108399.1	NT	g6:21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
678	13865	26896	1.07	0.0E+00	AF108399.1	NT	g6:21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
685	13870	26901	5.11	0.0E+00	4826947	NT	g6:21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
685	13870	26902	5.11	0.0E+00	4826947	NT	g6:21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
691	16018		1.8	0.0E+00	X57147.1	NT	g6:21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
700	13893	26916	3.92	0.0E+00	4504424	NT	g6:21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);

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705	13888	26920	4.84	0.0E+00	AB023012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
715	13897	26935	3.83	0.0E+00	7667468	NT	Homo sapiens similar to rat Integrin membrane glycoprotein POM121 (POM121.1), mRNA
727	13808	26949	13.13	0.0E+00	AA614537.1	EST_HUMAN	np49d01, a1 NCL CGAP, Br.1 Homo sapiens cDNA, clone IMAGE:1129633 3' similar to gb:X57352
731	13913	26953	6.4	0.0E+00	M60675.1	NT	INTERFERON-INDUCIBLE PROTEIN 1-9U (HUMAN);
731	13913	26954	6.4	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
741	13923	26963	1.35	0.0E+00	5032182	NT	Human von Willebrand factor gene, exons 23 through 34
747	13928	26969	4.62	0.0E+00	AF264730.1	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
747	13928	26970	4.62	0.0E+00	AF264730.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
749	13930	26973	9.17	0.0E+00	11545800	NT	Homo sapiens ALR-like protein mRNA, partial cds
755	13936	26981	2.26	0.0E+00	BE241577.1	EST_HUMAN	Homo sapiens hypodermal protein FLJ21634 (FLJ21634), mRNA
776	13955	27005	1.19	0.0E+00	AF226390.2	NT	TCAAP1D0779 Pediatric acute myelogenous leukemia cell (FAB M1) Bayor-HQSC project=TCAA Homo sapiens cDNA clone TCAAP0779
778	13955	27006	1.19	0.0E+00	AF226390.2	NT	sapiens cDNA clone TCAAP0779
778	13958	27009	8.82	0.0E+00	J03764.1	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
781	13981	27011	0.66	0.0E+00	J03764.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
782	13982	27012	2.07	0.0E+00	6912749	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
784	16022	27014	2.36	0.0E+00	D30612.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
785	13984	27015	3.55	0.0E+00	BE869735.1	EST_HUMAN	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
790	13985	27021	4.04	0.0E+00	F48915.1	EST_HUMAN	Homo sapiens mRNA for repressor protein, partial cds
791	13970	27022	2.85	0.0E+00	5032088	NT	Homo sapiens mRNA for repressor protein, partial cds
800	13979	27031	1.64	0.0E+00	AB011398.1	NT	Homo sapiens gene for A-F-6, complete cds
803	13983	27035	3.01	0.0E+00	7661865	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
815	13994	27048	1.24	0.0E+00	D80006.1	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
816	13994	27049	1.24	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
820	13999	27053	2.74	0.0E+00	X89772.1	NT	Human mRNA for KIAA0184 gene, partial cds
824	14003	27057	3.25	0.0E+00	AB020717.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
824	14003	27058	3.25	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0970 protein, partial cds
829	14007	27064	13.47	0.0E+00	5174476	NT	Homo sapiens mRNA for KIAA0970 protein, partial cds
830	14008		11.09	0.0E+00	4507500	NT	Homo sapiens pericentrih (PCNT) mRNA
847	14025	27085	1.65	0.0E+00	7667213	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TILM1) mRNA
848	14026	27086	2.46	0.0E+00	7667213	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TILM1) mRNA
860	14028	27088	1.84	0.0E+00	4557686	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
							Homo sapiens potassium voltage-gated channel, tek-related family, member 1 (KCNE1) mRNA

### Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
856	14033	27094	2.19	0.0E+00	AF108630.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
856	14033	27095	2.19	0.0E+00	AF108630.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
857	14034	27096	1.45	0.0E+00	AF108630.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
862	14039	27101	2.85	0.0E+00	U60385.1	NT	Homo sapiens G-kinin protein transduction factor, alpha subunit (GABPA) mRNA
866	14042	27106	1.37	0.0E+00	U60385.1	NT	Homo sapiens G-kinin protein transduction factor, alpha subunit (GABPA) mRNA
866	14042	27107	1.37	0.0E+00	U60385.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TAM1) mRNA
873	14049	27118	2.07	0.0E+00	AF027153.1	NT	Homo sapiens sodium/myosin-III co-receptor (SICR) gene, complete cds
877	14053	27119	5.27	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
878	14054	27120	11.32	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
879	14055	27121	4.03	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
880	14056	27122	3.87	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
884	14060	27125	1.54	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
884	14060	27126	1.54	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
885	14061	27127	1.82	0.0E+00	AA53327.2.1	EST_HUMAN	U60385.1 NCI CGAP P10 Homo sapiens cDNA clone IMAGE:987453
885	14061	27128	1.82	0.0E+00	AA53327.2.1	EST_HUMAN	U60385.1 NCI CGAP P10 Homo sapiens cDNA clone IMAGE:987453
888	14062	27129	8.41	0.0E+00	BF677854.1	EST_HUMAN	60208557/9F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248915.9
890	14066	27130	1.4	0.0E+00	U60385.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
890	14066	27131	1.4	0.0E+00	U60385.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
891	14067	27132	2.54	0.0E+00	U60385.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
891	14067	27133	2.54	0.0E+00	U60385.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
894	14069	27135	0.88	0.0E+00	AF163203.2	NT	Homo sapiens chromosomal 21 segment HS21C003
894	14069	27136	0.88	0.0E+00	AF163203.2	NT	Homo sapiens chromosomal 21 segment HS21C003
921	14096	27160	1.83	0.0E+00	BE089592.1	EST_HUMAN	QV4-BT0703-280400-211-g11 B10703 Homo sapiens cDNA
921	14096	27161	1.83	0.0E+00	BE089592.1	EST_HUMAN	QV4-BT0703-280400-211-g11 B10703 Homo sapiens cDNA
931	14108	27170	2.7	0.0E+00	AF163203.2	NT	Homo sapiens chromosomal 21 segment HS21C003
941	14116	27176	8.08	0.0E+00	AF163203.2	NT	Homo sapiens chromosomal 21 segment HS21C003
943	14115	27176	8.08	0.0E+00	AF163203.2	NT	Homo sapiens chromosomal 21 segment HS21C003
944	14117	27177	1.42	0.0E+00	AF089147.1	NT	Homo sapiens lamellipodium receptor 1 (LAMP1) mRNA
945	14118	27178	0.69	0.0E+00	AF089147.1	NT	Homo sapiens lamellipodium receptor 1 (LAMP1) mRNA
946	14118	27179	0.69	0.0E+00	AF089147.1	NT	Homo sapiens lamellipodium receptor 1 (LAMP1) mRNA
946	14118	27180	0.69	0.0E+00	AF089147.1	NT	Homo sapiens lamellipodium receptor 1 (LAMP1) mRNA
946	14118	27181	0.69	0.0E+00	AF089147.1	NT	Homo sapiens lamellipodium receptor 1 (LAMP1) mRNA
949	14122	27184	0.71	0.0E+00	AF089147.1	NT	Homo sapiens lamellipodium receptor 1 (LAMP1) mRNA

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
873	14146	27206	0.83	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
874	14147	27208	8.11	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
875	14148	27207	0.79	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
876	14149	27208	1.24	0.0E+00	4507430	NT	Human septins thymotropic embryonic factor (TEF), mRNA
878	14149	27209	1.24	0.0E+00	4507430	NT	Human septins thymotropic embryonic factor (TEF), mRNA
879	16027	27216	3.95	0.0E+00	A001848.1	EST_HUMAN	os88603.s1 NCI_OGAP_GC3 Homo septins cDNA clone IMAGE:1613404.3'
884	16027	27217	3.95	0.0E+00	A001848.1	EST_HUMAN	os88603.s1 NCI_OGAP_GC3 Homo septins cDNA clone IMAGE:1613404.3'
886	14168	27219	14.34	0.0E+00	7657268	NT	Homo septins KIAA0929 protein Max2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
897	14168	27229	1.76	0.0E+00	AB030936.1	NT	Homo septins mRNA for PSP24, complete cds
1008	14177	27236	43.62	0.0E+00	BF366974.1	EST_HUMAN	PM2.GN0014-050900-001-f02 GN0014 Homo septins cDNA
1008	14177	27237	43.62	0.0E+00	BF366974.1	EST_HUMAN	PM2.GN0014-050900-001-f02 GN0014 Homo septins cDNA
1008	14177	27238	43.62	0.0E+00	BF366974.1	EST_HUMAN	PM2.GN0014-050900-001-f02 GN0014 Homo septins cDNA
1008	14179	27241	2.02	0.0E+00	X52207.1	NT	Homo septins partial c-fgr gene, exons 2 and 3
1008	14179	27242	2.02	0.0E+00	X52207.1	NT	Homo septins partial c-fgr gene, exons 2 and 3
1017	14188	27249	3.97	0.0E+00	4757889	NT	Homo septins chromodomain protein, Y chromosome-like (CDYL), mRNA
1028	14189	27257	1.07	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1030	14200	27258	5.81	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1031	14200	27258	8.08	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1034	14203		4	0.0E+00	AF168480.1	NT	Homo septins 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1035	14203		28.66	0.0E+00	AF168480.1	NT	Homo septins 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1039	14207	27284	0.96	0.0E+00	AF111170.3	NT	Homo septins 14q32 Jagged2 gene, complete cds; and unknown gene
1040	14207	27284	4.68	0.0E+00	AF111170.3	NT	Homo septins 14q32 Jagged2 gene, complete cds; and unknown gene
1041	14207	27284	1.3	0.0E+00	AF111170.3	NT	Homo septins 14q32 Jagged2 gene, complete cds; and unknown gene
1042	14208	27285	1.18	0.0E+00	AF111170.3	NT	Homo septins 14q32 Jagged2 gene, complete cds; and unknown gene
1045	14211	27288	2.11	0.0E+00	7661685	NT	Homo septins DKFZP586M0122 protein (DKFZP586M0122), mRNA
1048	14218	27272	1.27	0.0E+00	5803114	NT	Homo septins inner membrane protein, mitochondrial (mitofilin) (TIMMT), mRNA
1051	14217		1.39	0.0E+00	AA458610.1	EST_HUMAN	aa88607.s1 Stralagene fetal retina 837202 Homo septins cDNA clone IMAGE:838238.3' similar to SW:PRRS_HUMAN P47210.268 PROTEINASE REGULATORY SUBUNIT 8;
1054	14220	27277	2.43	0.0E+00	N43182.1	EST_HUMAN	(alignment Ser and Pro with BLASTx or p)
1054	14220	27278	2.43	0.0E+00	N43182.1	EST_HUMAN	(alignment Ser and Pro with BLASTx or p)
1056	14221	27279	0.97	0.0E+00	4759249	NT	Homo septins TRAF family member-associated NFKB activator (TANK), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1055	14221	27280	0.97	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1058	14224		3.27	0.0E+00	6922833	NT	Homo sapiens hypothetical protein FLJ11188 (FLJ11188) mRNA
1072	14238	27295	1.51	0.0E+00	4768569	NT	Homo sapiens heat shock 70kD protein 88 (mortalin-2) (HSPA8B) mRNA
1090	14255	27310	1.51	0.0E+00	4926672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1090	14255	27311	1.51	0.0E+00	4826672	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1094	14259	27315	2.74	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695) mRNA
1094	14259	27316	2.74	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695) mRNA
1095	14260	27317	13.57	0.0E+00	AIJ246922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1097	14262		0.92	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080) mRNA
1098	14264	27321	2.81	0.0E+00	6174384	NT	Homo sapiens alkylation repair, alkB homolog (ABH1) mRNA
1106	14271	27330	2.04	0.0E+00	4759117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1120	14285	27340	1.81	0.0E+00	BE005203.1	EST_HUMAN	MRG-BN016-200300-003-008 BN0115 Homo sapiens cDNA
1143	14308	27364	3.82	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9) mRNA
1143	14308	27365	3.82	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9) mRNA
1155	14319	27373	0.82	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1155	14319	27374	0.82	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1156	14320	27375	9.35	0.0E+00	4506712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1158	14322	27377	1.2	0.0E+00	8823299	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309) mRNA
1161	14325	27380	3.95	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM1, complete cds
1163	14327	27381	19.6	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM1, complete cds
1164	14328	27382	4.52	0.0E+00	7657498	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1) mRNA
1164	14328	27383	4.62	0.0E+00	7657498	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1) mRNA
1168	14331	27386	1.44	0.0E+00	7706600	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729) mRNA
1169	14332	27387	0.71	0.0E+00	X65823.1	NT	H. sapiens ART4 gene
1169	14332	27388	0.71	0.0E+00	X65823.1	NT	H. sapiens ART4 gene
1170	14333	27389	1.15	0.0E+00	AI147650.1	EST_HUMAN	qB22610.x1 Scores: pregnant uterus, NBHPU Homo sapiens cDNA clone IMAGE:1897011.3'
1172	14335	27391	1.82	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1181	14344	27400	1.22	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1181	14344	27401	1.22	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1182	14345	27402	1.32	0.0E+00	6988944	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1185	14357	27416	2.19	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1185	14357	27416	2.19	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1198	14360	27419	1.09	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1205	14367	27428	8.64	0.0E+00	4667887	NT	Homo sapiens keratin 18 (KRT18) mRNA



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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1440	14593	27666	1.03	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis cysd gene
1449	14602	27680	13.57	0.0E+00	6042206	NT	RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1457	14610	27680	0.97	0.0E+00	4505648	NT	Homo sapiens protein convertase subtilisin/kexin type 2 (PCSK2), mRNA
1457	14610	27681	0.97	0.0E+00	4505648	NT	Homo sapiens protein convertase subtilisin/kexin type 2 (PCSK2), mRNA
1459	14612	27684	1.99	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1459	14612	27685	1.99	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1462	14615	27697	29.09	0.0E+00	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1471	14625	27709	4.53	0.0E+00	AF038280.1	NT	Homo sapiens elphat1-6/ucsf/transferase (elphat1-6/ucsf) gene, exon 7
1490	14643	27724	4.2	0.0E+00	AF038280.1	NT	Novel human gene on chromosome 1
1491	14644	27725	1.37	0.0E+00	AL137764.1	NT	Novel human gene mapping to chromosome 1
1495	14648	27730	1.73	0.0E+00	D87077.1	NT	Novel human gene mapping to chromosome 1
1498	14651	27733	8.24	0.0E+00	8912457	NT	Human mRNA for KIAA0240 gene, partial cds
1500	14653	27735	2.28	0.0E+00	7661865	NT	Homo sapiens calicheurin binding protein 1 (KIAA0330), mRNA
1500	14653	27736	2.28	0.0E+00	7661865	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1501	14654	27736	3.74	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1507	14660	27742	6.62	0.0E+00	M60678.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1507	14660	27743	6.62	0.0E+00	M60678.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1541	14683	27772	2.61	0.0E+00	7706434	NT	Homo sapiens hHOC for homolog of Drosophila headcase (LOC1098), mRNA
1555	14708	27788	2.66	0.0E+00	AA48112.1	EST_HUMAN	Homo sapiens hHOC for homolog of Drosophila headcase (LOC1098), mRNA
1562	14715	27792	27.8	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1562	14715	27793	27.8	0.0E+00	AF023860.1	NT	Cercopithecus aethiops cyclophilin A mRNA, complete cds
1564	14717	27786	1.53	0.0E+00	AW978097.1	EST_HUMAN	EST388208 MAGE repeat sequences, MAGN Homo sapiens cDNA
1564	14717	27797	1.55	0.0E+00	AW978097.1	EST_HUMAN	EST388208 MAGE repeat sequences, MAGN Homo sapiens cDNA
1565	14718	27788	1.03	0.0E+00	D10884.1	NT	Bovine mRNA for neurocalcin
1567	14720		3.2	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44), and FTR3 (FTR3) genes, complete cds
1568	14721	27801	28.69	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB), mRNA
1568	14721	27802	28.69	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB), mRNA
1570	14723	27804	3.83	0.0E+00	7662405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1571	14724		9.78	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1576	14729	27810	64.77	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1578	14731	27811	0.87	0.0E+00	4507720	NT	Homo sapiens titin (TTN), mRNA
1578	14731	27812	0.97	0.0E+00	4507720	NT	Homo sapiens titin (TTN), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1579	16042		32.23	0.0E+00	4506654	NT	Human sapiens ribosomal protein L5 (RPL5) mRNA
1580	14732	27813	27.68	0.0E+00	M414198.1	NT	Human laminin receptor (245 epitope) mRNA, 6' end
1592	14746	27828	1.43	0.0E+00	4507720	NT	Human sapiens titin (TTN) mRNA
1592	14745	27829	1.43	0.0E+00	4507720	NT	Human sapiens titin (TTN) mRNA
1594	14747	27830	13.85	0.0E+00	4503098	NT	Human sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4) mRNA
1602	14755		3.25	0.0E+00	D003331	NT	human c-yes-2 gene
1611	14764	27844	11.38	0.0E+00	Z83738.1	NT	H.sapiens FH2B1e gene
1612	14765	27845	2.55	0.0E+00	5921460	NT	Human sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1612	14765	27846	2.55	0.0E+00	5921460	NT	Human sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1613	14768	27847	11.09	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1613	14769	27848	11.09	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1616	16043	27851	2.1	0.0E+00	AB040955.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1618	14770	27852	1.88	0.0E+00	AF167476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (PDEV3) mRNA, complete cds
1620	14772	27856	6.83	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1620	14772	27856	6.83	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1622	14774	27857	56.88	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1622	14774	27858	56.88	0.0E+00	5729876	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1624	14776	27860	1.53	0.0E+00	M81803.1	NT	Human sodium channel mRNA
1639	14781	27876	6.29	0.0E+00	H269731.1	EST_HUMAN	yo76c05.s1 Source: adult brain N244H8657 Homo sapiens cDNA clone IMAGE:183948 3'
1648	14801	27887	1.87	0.0E+00	AB040829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1648	14801	27888	1.87	0.0E+00	AB040829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1658	14820	27903	1.66	0.0E+00	AW444637.1	EST_HUMAN	UI-H-B13-ajw-c-04-0-UL1.s1 NCI CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733294 3'
1658	14850	27936	2.12	0.0E+00	BE144364.1	EST_HUMAN	WFO-HT0166-197189-004-b11 HT0168 Homo sapiens cDNA
1698	14860	27937	2.12	0.0E+00	BE144364.1	EST_HUMAN	WFO-HT0166-197189-004-b11 HT0168 Homo sapiens cDNA
1702	14894	27941	1.3	0.0E+00	AF168104.1	EST_HUMAN	wg81b07.x1 Soares, NSF_P8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371477 3' similar to TR:Q62788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN. ;
1703	14855	27942	1.71	0.0E+00	4758513	NT	Human sapiens hematopoietic-derived zinc finger protein (HD-ZNF1) mRNA
1704	14856	27943	2.8	0.0E+00	AF05177.1	NT	Human sapiens T-cell receptor gamma V1 gene region
1708	14859	27947	2.1	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1708	14869	27948	2.1	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1710	14861	27950	64.4	0.0E+00	4557687	NT	Homo sapiens keratin 18 (KRT18) mRNA
1711	14862	27951	2.42	0.0E+00	7657065	NT	Homo sapiens wels avian erythroblastosis virus E26 oncogene related (ERG) mRNA
1714	14865	27954	1.08	0.0E+00	BE222374.1	EST_HUMAN	hut1405.x1 NCI CGAP_Luz4 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1714	14895	27955	1.08	0.0E+00	BE222374.1	EST_HUMAN	hnt1005.x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3168281 3' similar to TR:095147 095147
1716	14956	27957	3.2	0.0E+00	4357610	NT	WKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ; Homo sapiens gamma-aminobutyric acid (GABA) A receptor, gamma 2 (GABRG2) mRNA
1719	14859	27960	4.3	0.0E+00	H30132.1	EST_HUMAN	yo56e08.t1 Soeres breast 3NBH8st Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099
1719	14859	27961	4.3	0.0E+00	H30132.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN); yo56e08.t1 Soeres breast 3NBH8st Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099
1721	14871	27963	0.87	0.0E+00	A1149880.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN); gr4309.x1 Soeres Testis_NHT Homo sapiens cDNA clone IMAGE:1752809 3'
1722	14872	27964	10.28	0.0E+00	Z80780.1	NT	H. sapiens H2Bln gene
1725	14873	27976	21.3	0.0E+00	5031748	NT	H. sapiens H2Bln gene
1734	14883	27976	6.13	0.0E+00	8922841	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17) mRNA
1737	14883	27979	1.63	0.0E+00	5453855	NT	Homo sapiens FOXJ2 forkhead factor (LOC658410) mRNA
1741	14890	27983	1.95	0.0E+00	M75980.1	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1741	14890	27984	1.95	0.0E+00	M75980.1	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1744	14893	27986	1.11	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1747	14896	27990	2.54	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1747	14896	27991	2.54	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1751	14900	27997	8.57	0.0E+00	AB026542.1	NT	Human hepatocyte growth factor gene, exon 15
1753	14902		2.64	0.0E+00	S94400.1	NT	Human hepatocyte growth factor gene, exon 15
1762	14911	28006	5.29	0.0E+00	4557538	NT	Human hepatocyte growth factor gene, exon 15
1784	14933	28027	3.33	0.0E+00	AF273811.1	NT	Human hepatocyte growth factor gene, exon 15
1826	16047		41.98	0.0E+00	4506718	NT	Human hepatocyte growth factor gene, exon 15
1830	14978	28073	3.2	0.0E+00	4557556	NT	Human hepatocyte growth factor gene, exon 15
1830	14978	28074	3.2	0.0E+00	4557556	NT	Human hepatocyte growth factor gene, exon 15
1833	14980	28078	2.47	0.0E+00	U63963.1	NT	Human hepatocyte growth factor gene, exon 15
1837	16048	28083	7.66	0.0E+00	4606332	NT	Human hepatocyte growth factor gene, exon 15
1839	14985	28085	1.7	0.0E+00	AA113030.1	EST_HUMAN	Human hepatocyte growth factor gene, exon 15
1850	14996	28099	24.06	0.0E+00	U14967.1	NT	Human hepatocyte growth factor gene, exon 15
1852	14996	28102	9	0.0E+00	AB002331.1	NT	Human hepatocyte growth factor gene, exon 15
1853	14999	28103	24.99	0.0E+00	4502284	NT	Human hepatocyte growth factor gene, exon 15
1853	14999	28104	24.99	0.0E+00	4502284	NT	Human hepatocyte growth factor gene, exon 15

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1833	14938	28105	24.89	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1870	15015	28124	3.11	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1870	15015	28125	3.11	0.0E+00	4604628	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1881	15025	28131	7.19	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1) mRNA
1881	15025	28132	7.19	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1) mRNA
1882	15039	28143	1.84	0.0E+00	AB032878.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1892	15039	28144	1.84	0.0E+00	AB032878.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1895	15039	28149	3.59	0.0E+00	4828783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1895	15039	28147	3.59	0.0E+00	4828783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1896	15039	28148	7.35	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1896	15039	28149	7.35	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1899	15042	28152	2.3	0.0E+00	AW207280.1	EST_HUMAN	UH-B1-efn-f-07-0-JLst NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722333.3'
1899	15042	28153	2.3	0.0E+00	AW207280.1	EST_HUMAN	UH-B1-efn-f-07-0-JLst NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722333.3'
1924	15067	28171	3.22	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239.5'
1924	15067	28172	3.22	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239.5'
1943	15086	28187	1.04	0.0E+00	BE006292.1	EST_HUMAN	RC2-BN0126-200300-012-b04 BN0126 Homo sapiens cDNA
1972	15115	28215	1.62	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220) mRNA
1972	15115	28216	1.62	0.0E+00	7657390	NT	Homo sapiens nuclear protein (NP220) mRNA
1973	15118	28218	3.14	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1973	15118	28219	3.14	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1981	15124	28228	1.29	0.0E+00	AB037788.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1985	15128	28230	1.64	0.0E+00	AF167476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1986	15051	28231	67.92	0.0E+00	MB9478.1	NT	Human transglutaminase mRNA, complete cds
1986	15051	28231	67.92	0.0E+00	MB9478.1	NT	Human transglutaminase mRNA, complete cds
1991	15133	28238	3.19	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3) mRNA
1991	15133	28239	3.19	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3) mRNA
1994	15135	28241	2.41	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6) mRNA
1996	15137		6.39	0.0E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2001	15142		5.28	0.0E+00	MS9632.1	NT	Human topoisomerase I pseudogene 1
2003	16062	28248	1.84	0.0E+00	6901805	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2005	15145	28250	1.3	0.0E+00	BE018036.1	EST_HUMAN	Bb73f1.1 y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3048045 5'
2011	15151	28255	1.69	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
2011	15151	28256	1.69	0.0E+00	4809282	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
2024	15155		1.04	0.0E+00	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C052
2026	15167	28272	1.41	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB) mRNA
2026	15167	28273	1.41	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB) mRNA
2027	15168	28274	12.98	0.0E+00	4826838	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
2027	15168	28275	12.98	0.0E+00	4826838	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
2037	15178	28288	2.11	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
2037	15178	28289	2.11	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0780 protein, partial cds
2043	15184	28283	1.93	0.0E+00	M33782.1	NT	Human TIEB protein mRNA, partial cds
2043	15184	28284	1.93	0.0E+00	M33782.1	NT	Human TIEB protein mRNA, partial cds
2045	15186	28285	3.24	0.0E+00	AW193024.1	EST_HUMAN	X89b01.x1 NC1 CGAP_Part Homo sapiens cDNA clone IMAGE:2879913 3'
2045	15186	28286	3.24	0.0E+00	AW193024.1	EST_HUMAN	X89b01.x1 NC1 CGAP_Part Homo sapiens cDNA clone IMAGE:2879913 3'
2046	15187	28297	9.68	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330) mRNA
2046	15187	28298	9.68	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330) mRNA
2048	15189	28300	1.53	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2049	15190	28301	1.09	0.0E+00	Z47558.1	NT	H. sapiens genes for semenogelin I and semenogelin II
2049	15190	28302	1.09	0.0E+00	Z47558.1	NT	H. sapiens genes for semenogelin I and semenogelin II
2056	15197	28311	5.04	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
2078	15218	28337	1.85	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2078	15218	28338	1.85	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
2109	15247	28369	1.63	0.0E+00	8394548	NT	Homo sapiens chromosome 21 open reading frame 7 (YGB1) mRNA
2112	15260	28370	0.88	0.0E+00	7708742	NT	Homo sapiens TP53TG3A (TP53TG3A) mRNA
2117	15265	28374	35.36	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2117	15265	28375	35.36	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2119	15257	28376	1.02	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2121	15258	28378	67.63	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'
2122	14612	27694	0.87	0.0E+00	7705665	NT	Homo sapiens KIAA1114 protein (KIAA1114) mRNA
2122	14612	27695	0.97	0.0E+00	7705665	NT	Homo sapiens KIAA1114 protein (KIAA1114) mRNA
2124	15260	28380	2.59	0.0E+00	AA077589.1	EST_HUMAN	7822E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7822E10
2124	15260	28381	2.69	0.0E+00	AA077589.1	EST_HUMAN	7822E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7822E10
2126	15262		3.79	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L7) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit/Accession No.	Top Hit/ Database Source	Top Hit Descriptor
2128	15284		1.48	0.0E+00	4585863	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2129	15285	28384	2.9	0.0E+00	Z42399.1	EST_HUMAN	HSC01C021 normalized infant brain cDNA Homo sapiens cDNA clone c-01C02
2131	15267		2.38	0.0E+00	A1244247.1	EST_HUMAN	q956f08.x1 NC1_CGAP_U12 Homo sapiens cDNA clone IMAGE:1888871, 3' similar to contains Alu repetitive element.
2136	15272	28393	4.37	0.0E+00	BE877225.1	EST_HUMAN	601485146F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3987747 5'
2138	15274	28395	2.25	0.0E+00	BF315325.1	EST_HUMAN	601802804F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2138	15274	28396	2.25	0.0E+00	BF315325.1	EST_HUMAN	601802804F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4135320 5'
2144	15280	28404	3.6	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2144	15280	28405	3.6	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-d10 CT0413 Homo sapiens cDNA
2152	15288	28414	3.43	0.0E+00	L00820.1	NT	Human plasma membrane calcium ATPase isoform 2 (AP12B2) mRNA, complete cds
2152	15288	28415	3.43	0.0E+00	L00820.1	NT	Human plasma membrane calcium ATPase isoform 2 (AP12B2) mRNA, complete cds
2153	15289	28416	1.11	0.0E+00	AJ287709.1	NT	Homo sapiens mRNA for CDC2L6 protein kinase, (CDC2L6 gene), isoform 1
2158	15284	28420	1.16	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2162	15298	28423	1.84	0.0E+00	BE500995.1	EST_HUMAN	734502.x1 NC1_CGAP_G08 Homo sapiens cDNA clone IMAGE:3220610 3' similar to SW:DTD_HUMAN P50443 SULFATE TRANSPORTER.
2182	15317		3.17	0.0E+00	BE767984.1	EST_HUMAN	QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA
2183	15318		1.26	0.0E+00	AF078933.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLR31) gene, exon 6 and complete cds
2185	15320	28446	4.64	0.0E+00	BF027532.1	EST_HUMAN	601672056F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2186	15321	28447	1.5	0.0E+00	BE072624.1	EST_HUMAN	PJM0-BT0547-210300-004-F04 BT0547 Homo sapiens cDNA
2189	15323	28448	1.29	0.0E+00	AF240736.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2180	15325	28450	3.41	0.0E+00	AW752708.1	EST_HUMAN	IL3-CT0218-271099-022-G10 CT0219 Homo sapiens cDNA
2192	15327	28452	6.48	0.0E+00	A1804840.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2192	15327	28453	6.48	0.0E+00	A1804840.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2225	15359		1.08	0.0E+00		NT	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNM3L), mRNA
2249	15382		1.52	0.0E+00	L14781.1	NT	Human DNA-binding protein mRNA, 3' end
2259	15392	28518	1.26	0.0E+00	BE274698.1	EST_HUMAN	601122338F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346888 5'
2281	15394	28521	0.94	0.0E+00	D87635.1	NT	Human mRNA for KIAA0244 gene, partial cds
2282	15395	28522	23.12	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2282	15395	28523	23.12	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2284	15397	28525	2.57	0.0E+00	AA931891.1	EST_HUMAN	cc32801.s1 NC1_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1567898 5'
2288	15401	28529	24.38	0.0E+00	BF344434.1	EST_HUMAN	802014829F1 NC1_CGAP_Brm84 Homo sapiens cDNA clone IMAGE:4150734 5'
2289	15402	28530	40.14	0.0E+00	BE748899.1	EST_HUMAN	601672186F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'

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Probe SEQ ID	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source
2272	16405	28593	5.56	0.0E+00	BFS7897.1	EST_HUMAN
2272	19405	28594	6.56	0.0E+00	BFS7897.1	EST_HUMAN
2276	16059	28599	4.06	0.0E+00	BFS13617.1	EST_HUMAN
2276	16411	28542	3.13	0.0E+00	BE018750.1	EST_HUMAN
2281	16413	28544	1.68	0.0E+00	AAG42813.1	EST_HUMAN
2281	16413	28545	1.68	0.0E+00	AAG42813.1	EST_HUMAN
2289	16421	28553	3.06	0.0E+00	AL163204.2	NT
2289	16421	28554	3.06	0.0E+00	AL163204.2	NT
2280	16422	28555	3.72	0.0E+00	7662401	NT
2280	16422	28556	3.72	0.0E+00	7662401	NT
2295	16427	28561	2.34	0.0E+00	U36384.1	NT
2295	16427	28561	1.02	0.0E+00	AA282281.1	EST_HUMAN
2298	16445	28579	7.92	0.0E+00	4557568	NT
2313	16452	28584	2.63	0.0E+00	7662401	NT
2320	16459	28592	3.44	0.0E+00	BE896281.1	EST_HUMAN
2327	16483	28596	1.51	0.0E+00	BE896563.1	EST_HUMAN
2331	16483	28597	1.51	0.0E+00	BE896563.1	EST_HUMAN
2331	16483	28597	1.51	0.0E+00	BE896563.1	EST_HUMAN
2333	16484	28599	1.83	0.0E+00	AB037784.1	NT
2333	16484	28599	1.83	0.0E+00	AB037784.1	NT
2337	16506	28632	4.36	0.0E+00	11565748	NT
2337	16506	28633	4.36	0.0E+00	11565748	NT
2376	16507	28634	2.67	0.0E+00	AA078404.1	EST_HUMAN
2378	16509	28636	2.95	0.0E+00	AAA28001.1	EST_HUMAN
2378	16509	28637	2.86	0.0E+00	AAA28001.1	EST_HUMAN
2380	16511	28639	1.82	0.0E+00	BF347038.1	EST_HUMAN
2385	16516	28645	1.33	0.0E+00	AB020171.1	NT
2385	16516	28646	1.33	0.0E+00	AB020171.1	NT
2386	16517	28647	2.34	0.0E+00	6325468	NT
2393	16524	28653	2.36	0.0E+00	BE67895.1	EST_HUMAN
2396	16527	28655	5.46	0.0E+00	AF044571.1	NT
2397	16528	28656	2.6	0.0E+00	AI625542.1	EST_HUMAN



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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2389	15530	28657	1.5	0.0E+00	AB011309.1	NT	Homo sapiens gene for Af-4, complete cds
2402	15533	28659	2.22	0.0E+00	7662401	NT	Homo sapiens KIA00952 protein (KIA00952), mRNA
2402	15533	28660	2.22	0.0E+00	7662401	NT	Homo sapiens KIA00952 protein (KIA00952), mRNA
2405	15536	28663	3.83	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2405	15536	28664	3.83	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2424	15553	28679	3.04	0.0E+00	5174678	NT	Homo sapiens signal regulatory protein, beta, 1 (SRP-BETA-1), mRNA
2428	15556	28683	3.66	0.0E+00	AU131142.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002064 5'
2429	15557	28684	9.82	0.0E+00	7662017	NT	Homo sapiens KIA00244 protein (KIA00244), mRNA
2430	15559	28685	3.96	0.0E+00	4768487	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2431	15559	28686	1.39	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2432	15560		7.14	0.0E+00	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 6 (CYP3A6) gene, partial cds
2434	15562	28688	10.61	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2434	15562	28689	10.61	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2434	15562	28690	10.61	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2452	15580		1.03	0.0E+00	BE814424.1	EST_HUMAN	MRO-BN0070-090600-029-d12 BN0070 Homo sapiens cDNA
2485	15612	28735	1.14	0.0E+00	AU119692.1	EST_HUMAN	AU119692 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5'
2487	15614		4.63	0.0E+00	AU042033.1	EST_HUMAN	006b02.x1 Scars_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1650863 3' similar to TR:008662
2489	15616	28737	0.94	0.0E+00	8923620	NT	008662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE
2492	15619		1.35	0.0E+00	BE89503.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20693 (FLJ20693), mRNA
2503	15630		2.22	0.0E+00	AB005622.1	EST_HUMAN	AB005622 HELA MGC_72 Homo sapiens cDNA clone IMAGE:3918168 5'
2505	15632	28752	6.05	0.0E+00	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2510	15636	28756	1.89	0.0E+00	D85606.1	NT	Homo sapiens gene for cholesteryl ester transfer protein, complete cds
2510	15636	28757	1.89	0.0E+00	D85606.1	NT	Homo sapiens gene for cholesteryl ester transfer protein, complete cds
2520	15646	28769	2.42	0.0E+00	AF106275.1	NT	Homo sapiens intronless type-A receptor, complete cds
2524	15649	28773	0.96	0.0E+00	BF343274.1	EST_HUMAN	602018058F1 NCI CGAP Bm67 Homo sapiens cDNA clone IMAGE:4153670 5'
2530	15653	28780	3.64	0.0E+00	5729177	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2538	15663	28786	1.02	0.0E+00	U13666.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2538	15663	28787	1.02	0.0E+00	U13666.1	NT	Human G protein-coupled receptor (GPR1) gene, complete cds
2539	15694	28788	28.11	0.0E+00	BF569144.1	EST_HUMAN	60218458F1 NCI MGC_42 Homo sapiens cDNA clone IMAGE:4300393 3'
2547	15672	28786	4.16	0.0E+00	AW46922.1	EST_HUMAN	ha04n04.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2650	15576	28768	3.03	0.0E+00	AW501010.1	EST_HUMAN	U1-HF-BP0-p-als-c-07-0-U1.1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2575	15700		2.02	0.0E+00	AW813833.1	EST_HUMAN	RC3-ST0197-300300-016-c04-ST0197 Homo sapiens cDNA
2578	15704	28824	7.28	0.0E+00	BE795542.1	EST_HUMAN	601592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2579	15135	28241	1.12	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
2680	15705	28825	1.44	0.0E+00	BF509482.1	EST_HUMAN	U1-H-B14-a02-b-08-0-U1.1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3086535 3'
2583	15708	28827	2.21	0.0E+00	Z32894.2	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR $\alpha$ ) mRNA
2585	15710		5.17	0.0E+00	5453871	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR $\alpha$ ) mRNA
2587	15712	28830	1.07	0.0E+00	BE910378.1	EST_HUMAN	601503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5'
2588	15713	28831	2.39	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2589	15714	28832	3.09	0.0E+00	UG9239.1	NT	Homo sapiens Sec62 (Sec62) mRNA, complete cds
2595	15720	28838	1.66	0.0E+00	BE888460.1	EST_HUMAN	60150821F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908866 5'
2596	15722	28842	13.07	0.0E+00	BE875311.1	EST_HUMAN	60148924F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2598	15722	28843	13.07	0.0E+00	BE875511.1	EST_HUMAN	60148924F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
2599	15723	28844	1.12	0.0E+00	AF245505.1	NT	Homo sapiens edlinen mRNA, complete cds
2616	15740	28852	1.83	0.0E+00	BE638921.1	EST_HUMAN	601064738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2623	15746	28860	3.66	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2623	15746	28861	3.66	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2624	15747	28862	1.25	0.0E+00	BE282896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 5'
2624	15747	28863	1.25	0.0E+00	BE282896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987955 5'
							7427N12.X1 NCI CGAP_G06 Homo sapiens cDNA clone IMAGE:3 similar to TR:CO0246 O00246
							HYPOTHETICAL 9.3 KD PROTEIN:
2625	15748	28864	1.04	0.0E+00	BF223011.1	EST_HUMAN	
2628	15751	28868	8.3	0.0E+00	AF245505.1	NT	Homo sapiens edlinen mRNA, complete cds
2664	15000	28901	2.18	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2664	15000	28902	2.18	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2666	15766		2.35	0.0E+00	BF613835.1	EST_HUMAN	U1-H-BW1-amp-f-12-0-U1.1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070631 3'
2675	15765	28912	32.6	0.0E+00	BF204131.1	EST_HUMAN	601868073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2676	15765	28913	32.6	0.0E+00	BF204131.1	EST_HUMAN	601868073F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111411 5'
2678	15768	28915	2.15	0.0E+00	AB037842.1	NT	Homo sapiens mRNA for KIAA1321 protein, partial cds
							Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28KD (TAF21)
2679	15769	28916	2.52	0.0E+00	5032150	NT	mRNA
2681	15801	28918	8.53	0.0E+00	AB037856.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
2682	15802	28919	1.16	0.0E+00	BE785446.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2682	15802	28920	1.16	0.0E+00	BE785446.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944304 5'
2690	15810		2.75	0.0E+00	BE782172.1	EST_HUMAN	601584930F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2700	15819	28835	2.62	0.0E+00	4504866	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2710	15828		1.16	0.0E+00	U78027.1	NT	
2711	15829	28942	5.97	0.0E+00	AF178227.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2715	15833	28943	1.07	0.0E+00	AB011108.1	NT	Homo sapiens guanylate cyclase activating protein 2 (GUCA1B) gene, exon 1
2718	15836	28946	0.98	0.0E+00	AU133385.1	EST_HUMAN	Homo sapiens mRNA for KIAA0536 protein, partial cds
2721	15839	28948	1.16	0.0E+00	AU130403.1	EST_HUMAN	AU133386 NT2RP4 Homo sapiens cDNA clone NT2RP4001964 5'
2721	15839	28950	1.16	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2724	15842	28953	1.69	0.0E+00	AW887015.1	EST_HUMAN	RC1-OT0086-220300-011-407 OT0086 Homo sapiens cDNA
2727	15845	28956	4.83	0.0E+00	BE383163.1	EST_HUMAN	B01298714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628923 5'
2728	15846		2.8	0.0E+00	BE383163.1	EST_HUMAN	B01278373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610287 5'
2763	15878	28987	1	0.0E+00	AB037732.1	NT	Homo sapiens mRNA for KIAA1311 protein, partial cds
2785	15901		11.89	0.0E+00	AA318723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2789	15906	29013	4.04	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2791	15907	29015	3.72	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2792	15908	29016	2.32	0.0E+00	AB051828.1	NT	Homo sapiens hCG28K mRNA for GTP-binding protein like 1, complete cds
2797	15912	29020	11.38	0.0E+00	BE788376.1	EST_HUMAN	B01591891F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3845983 5'
2800	16072	29024	17.3	0.0E+00	BE583433.1	EST_HUMAN	B01335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3889684 5'
2801	15915		3.28	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTB8YE09 5'
2803	15917	29027	2.18	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2803	15917	29028	2.18	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2804	15918	29029	2.21	0.0E+00	AF290185.1	NT	Homo sapiens hyperextension-related calcium-regulated gene mRNA, complete cds
2806	15919		47.74	0.0E+00	AV651058.1	EST_HUMAN	AV651068 GIC Homo sapiens cDNA clone GIC00107 3'
2808	15920	29030	5.84	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2808	15920	29031	5.84	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2810	15924	29036	1.15	0.0E+00	4757863	NT	Homo sapiens cerebellar degeneration-related protein (34KD) (CDR1) mRNA
2813	15927	29039	21.96	0.0E+00	BE747193.1	EST_HUMAN	Homo sapiens cerebellar degeneration-related protein (34KD) (CDR1) mRNA
2814	15928	29040	1.05	0.0E+00	N44974.1	EST_HUMAN	Y35810.1 Soares melanocyte 2N3HM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR-A45773
2816	15930	29042	1.15	0.0E+00	BE176836.1	EST_HUMAN	RC4-H10587-170300-012-d11 HT0587 Homo sapiens cDNA
2827	15941		1.13	0.0E+00	AL163291.2	NT	Homo sapiens chromosome 21 segment HS21C001
2828	15942	29052	3.19	0.0E+00	BF514110.1	EST_HUMAN	U1-H-BW1-amiw-e-07-0-U1.s1 NC1 CGAP Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2835	15949		1.97	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2841	15955	29062	1.08	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2841	15955	29063	1.08	0.0E+00	7705276	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2842	15956	29064	6.05	0.0E+00	BF077634.1	EST_HUMAN	602085579F1 NIH_MGC_33 Homo sapiens cDNA clone IMAGE:424915 5'
2848	15962	28072	1.33	0.0E+00	7427622	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR1), mRNA
2852	15966	28075	17.21	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2852	15966	28076	17.21	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2854	15968		14.75	0.0E+00	AI070163.1	EST_HUMAN	au55404.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:251663 5' similar to SW-610A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A.
2857	15971	29081	2.14	0.0E+00	BF630691.1	EST_HUMAN	602071957F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4214678 5'
2858	15972	29082	71.97	0.0E+00	BE072768.1	EST_HUMAN	601450912F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3854842 5'
2860	15974	29083	2.42	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2860	15974	29084	2.42	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2861	15975	29085	64.06	0.0E+00	BE300344.1	EST_HUMAN	600844794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860806 5'
2861	15975	29086	64.06	0.0E+00	BE300344.1	EST_HUMAN	600844794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2860806 5'
2867	13415	26444	5.26	0.0E+00	S768301.1	NT	glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3088 nt]
2870	15982		1.64	0.0E+00	AB033281.1	NT	Homo sapiens BTROP2 mRNA for F-box end W/D-repeats protein isoform C, complete cds
2876	13933	26978	1.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2876	13933	26979	1.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2890	14230	27287	2.04	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (diarrhoea-inducible), polypeptide 1 (glucanase 3, primary infantile) (CYP1B1) mRNA
2890	14230	27288	2.04	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (diarrhoea-inducible), polypeptide 1 (glucanase 3, primary infantile) (CYP1B1) mRNA
2897	16076	29094	3.73	0.0E+00	X65980.1	NT	H. sapiens serine hydroxymethyltransferase pseudogene
2898	16077		1.28	0.0E+00	AF068624.1	NT	Homo sapiens 5-aminolevulinic acid synthase 2 (ALAS2) gene, complete cds
2900	16079		1.91	0.0E+00	AB040860.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2907	16085	29088	4.25	0.0E+00	AL160201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2911	16089	29102	6.5	0.0E+00	M60902.1	NT	Human AHNK nucleoprotein mRNA, 5' end
2914	16092	29104	0.93	0.0E+00	BE154604.1	EST_HUMAN	PM0-H10343-281288-003-602 HT0343 Homo sapiens cDNA
2914	16092	29105	0.93	0.0E+00	BE154604.1	EST_HUMAN	PM0-H10343-281288-003-602 HT0343 Homo sapiens cDNA
2916	16094		2.05	0.0E+00	X73428.1	NT	H. sapiens lds gene for HLH type transcription factor
2918	16096		2.6	0.0E+00	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21C068
2919	16097	29108	1.3	0.0E+00	7018594	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2919	16097	29108	1.3	0.0E+00	7018594	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA

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Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2919	16097	29110	1.3	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2921	16099	29111	16.94	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
2926	16103	29117	30.49	0.0E+00	D50657.1	NT	Homo sapiens gamma-globulin mRNA, complete cds
2926	16103	29118	30.49	0.0E+00	D50657.1	NT	Homo sapiens gamma-globulin mRNA, complete cds
2929	16106	29121	3.42	0.0E+00	AF162303.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2930	16107		6.12	0.0E+00	Y10659.1	NT	H. sapiens mRNA for nuclear DNA helicase II
2931	16108		1.13	0.0E+00	AF162303.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1), mRNA, complete cds
2932	16109	29122	74.83	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2932	16109	29123	74.83	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2944	16121	29134	2.54	0.0E+00	4507280	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2947	16124	29138	1.19	0.0E+00	AL047839.1	EST_HUMAN	DKEZp586G0821_1 586 (synonym: huta1) Homo sapiens cDNA clone DKFZp586G0821
2948	16125	29139	0.98	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product, Helicase (KIAA0054), mRNA
2948	16125	29140	0.96	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product, Helicase (KIAA0054), mRNA
2949	16126		2.44	0.0E+00	4503088	NT	Homo sapiens chondroin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2952	16129	29142	5.16	0.0E+00	BE081893.1	EST_HUMAN	QV2-BT0636-130400-138-H03 BT0636 Homo sapiens cDNA
2952	16129	29143	5.16	0.0E+00	BE081893.1	EST_HUMAN	QV2-BT0636-130400-138-H03 BT0636 Homo sapiens cDNA
2958	16135	29151	0.77	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2958	16135	29152	0.77	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2961	16138	29156	2.3	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2961	16138	29157	2.3	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2962	16139	29158	1.3	0.0E+00	AA215579.1	EST_HUMAN	z86b11.s1 NCI_QGAP_GCB1 Homo sapiens cDNA clone IMAGE:383517 3' similar to contains Aliu repetitive element.
2969	16145		3.99	0.0E+00	Y18210.1	NT	Homo sapiens h-hb gene for hair keratin, exons 1 to 9
2972	16148	29167	1.05	0.0E+00	4788279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2974	16150	29170	25.86	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2975	16151	29171	1.15	0.0E+00	AI561002.1	EST_HUMAN	U18407.X1 NCI_QGAP_Bm28 Homo sapiens cDNA clone IMAGE:2167881 3' similar to TR-O16247
2975	16151	29172	1.15	0.0E+00	AI561002.1	EST_HUMAN	U18407.X1 NCI_QGAP_Bm28 Homo sapiens cDNA clone IMAGE:2167881 3' similar to TR-O16247
2977	16153	29174	1.18	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
2978	16154	29175	1.04	0.0E+00	AF152388.1	NT	Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2984	16170	29187	3.4	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2984	16170	29188	3.4	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2985	16171	29189	6.2	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds

## Table 4

Probe SEQ ID NO.	Exam SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2895	16171	28190	6.2	0.0E+00	ABO40941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2898	16174	28193	3.31	0.0E+00	U7651903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2896	16174	28194	3.31	0.0E+00	U7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2899	16175	28195	4.53	0.0E+00	S174574	NT	Homo sapiens myeloid lymphoid or mixed-lineage leukemia (t(11;16)(q24;q32)) translocated to 4, (MLLT4) mRNA
2899	16175	28195	4.53	0.0E+00	S174574	NT	Homo sapiens myeloid lymphoid or mixed-lineage leukemia (t(11;16)(q24;q32)) translocated to 4, (MLLT4) mRNA
2899	16175	28195	4.53	0.0E+00	S174574	NT	Homo sapiens myeloid lymphoid or mixed-lineage leukemia (t(11;16)(q24;q32)) translocated to 4, (MLLT4) mRNA
2899	16175	28195	4.53	0.0E+00	S174574	NT	Homo sapiens myeloid lymphoid or mixed-lineage leukemia (t(11;16)(q24;q32)) translocated to 4, (MLLT4) mRNA
3003	16178	28199	1.28	0.0E+00	Bf110702.1	EST_HUMAN	Tn40d03 x1 NC1 CGAP L124 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:QVNLN1
3003	16178	28199	1.28	0.0E+00	Bf110702.1	EST_HUMAN	Tn40d03 x1 NC1 CGAP L124 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:QVNLN1
3003	16178	28200	1.28	0.0E+00	Bf110702.1	EST_HUMAN	Tn40d03 x1 NC1 CGAP L124 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:QVNLN1
3011	16187	28211	3.91	0.0E+00	A4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
3011	16187	28212	3.91	0.0E+00	A4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
3019	16106	28218	1.51	0.0E+00	A758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3022	16198	28221	0.98	0.0E+00	AB030304.1	NT	Homo sapiens mRNA for KIAA1208 protein, partial cds
3024	16200	28223	9.6	0.0E+00	A1106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
3038	16214	28242	1.44	0.0E+00	A1148865.1	EST_HUMAN	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
3045	16221	28242	0.71	0.0E+00	A1148865.1	EST_HUMAN	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
3045	16221	28243	0.71	0.0E+00	A1148865.1	EST_HUMAN	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
3046	16222	28244	0.82	0.0E+00	A1148865.1	EST_HUMAN	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
3047	16223	28245	2.81	0.0E+00	AB004894.1	NT	Homo sapiens neuropilin-2 (NP2) gene, complete cds, alternatively spliced
3057	16233	28252	1.85	0.0E+00	Z7892273	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
3058	16234	28253	1.82	0.0E+00	Z7892273	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
3059	16235	28254	2.4	0.0E+00	Z7892273	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
3059	16235	28255	2.4	0.0E+00	Z7892273	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
3067	16243	28263	1.17	0.0E+00	A1144383.1	NT	Homo sapiens intercalin short isoform (ITSN) mRNA, complete cds
3067	16243	28264	1.17	0.0E+00	A1144383.1	NT	Homo sapiens intercalin short isoform (ITSN) mRNA, complete cds
3081	16267	28285	0.61	0.0E+00	A1163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3083	16269	28286	1.29	0.0E+00	M74099.1	NT	Human displacement protein (COAT) mRNA
3102	16276	28292	0.68	0.0E+00	A4505082	NT	Homo sapiens semaphorin I (SEMG1) mRNA
3109	16285	28303	3.53	0.0E+00	A1165953.1	NT	Homo sapiens membrane-bound aminopeptidase P (NBPEP2) gene, complete cds
3112	16288	28304	4.9	0.0E+00	A1165953.1	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3112	16288	28304	4.9	0.0E+00	A1165953.1	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
3114	16290		7.27	0.0E+00	AL359403.1	NT	Isoderm 2 of a novel human mRNA from chromosome 22	
3119	16295	29309	1.88	0.0E+00	AF017433.1	NT	Homo septins putative transcription factor CRE3 (CRE3) mRNA, partial cds	
							Homo septins transcription factor (GHM) enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds; and L-type calcium channel $\alpha_2$	
3122	16298		2.21	0.0E+00	AF199779.1	NT		
3124	16300	29313	3.78	0.0E+00	4504664	NT	Homo septins interleukin 2 receptor, beta (IL2RB) mRNA	
3145	16321	29333	3.23	0.0E+00	X03529.1	NT	Human germine gene 16.1 for Ig lambda L-chain C region (IgLC16.1)	
3151	16326		1.92	0.0E+00	AF199355.1	NT	Homo septins F-box protein FBL5 (FBL5) mRNA, complete cds	
3155	16330	29340	1.76	0.0E+00	AF064589.1	NT	Homo septins melanoma-associated antigen (MAGE-C1) gene, complete cds	
3175	16350	29356	4.71	0.0E+00	AF265208.1	NT	Homo septins SWI-SNF complex protein p270 mRNA, partial cds	
3176	16351	29357	10.17	0.0E+00	AF149773.1	NT	Homo septins NOD1 protein (NOD1) gene, exons 1, 2, and 3	
3181	16356	29361	3.92	0.0E+00	7662139	NT	Homo septins KIAA0469 gene product (KIAA0469) mRNA	
3182	16367	29362	1.29	0.0E+00	AF042075.1	NT	Homo septins diffractory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds	
3187	16362	29368	1.19	0.0E+00	AW188148.1	EST_HUMAN	ye8207.x1 Scores, NFL_T_GBC_S1 Homo septins cDNA clone IMAGE:2664733 3' similar to SW:RNP_HYDHY P00877 RIBONUCLEASE PANCREATIC ;	
3210	16384	29395	3.81	0.0E+00		4828783	NT	Homo septins potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3219	16383	29404	20.63	0.0E+00	L20941.1	NT	Human ferritin heavy chain mRNA, complete cds	
3222	16386	29407	1.06	0.0E+00	AB011121.1	NT	Homo septins mRNA for KIAA0549 protein, partial cds	
3222	16386	29408	1.05	0.0E+00	AB011121.1	NT	Homo septins mRNA for KIAA0549 protein, partial cds	
3229	16403	29415	26.81	0.0E+00	T94870.1	EST_HUMAN	ye3203.e1 Stragene lung (#937210) Homo septins cDNA clone IMAGE:118453 3' similar to SP:S29539	
3244	16418	29433	0.93	0.0E+00	BF243336.1	EST_HUMAN	S29539 BASIC PROTEIN, 23K - ;	
3246	16419	29434	1.22	0.0E+00	AB088036.1	EST_HUMAN	601878507.F1 NIH_MGC_55 Homo septins cDNA clone IMAGE:4107433 5'	
3250	16424	29441	5.38	0.0E+00	X69822.1	NT	wu12h10.x1 NCI_CGAP_P128 Homo septins cDNA clone IMAGE:2616903 3'	
3250	16424	29442	5.36	0.0E+00	X69822.1	NT	H. septins mRNA for gamma-glutamyltransferase	
3262	16426	29444	1.01	0.0E+00	AI065950.1	EST_HUMAN	H. septins mRNA for gamma-glutamyltransferase	
3262	16436	29455	1.39	0.0E+00		4758827	NT	tu88g69.x1 NCI_CGAP_P128 Homo septins cDNA clone IMAGE:2253376 3' similar to SW:RASD_DICD1
3262	16436	29456	1.39	0.0E+00		4758827	NT	P03987 RAS-LIKE PROTEIN RASD ;
3270	16444	29464	9.58	0.0E+00		4604658	NT	Homo septins neuron III (NFYN3) mRNA
3288	16462	29482	4.54	0.0E+00	M28693.1	NT	Homo septins interleukin 1 receptor, type I (IL1R1) mRNA	
							Homo septins nuclear phosphoprotein B23 (NPM1) mRNA, complete cds	
							Homo septins solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA	
3292	16466	29485	1.92	0.0E+00		4602098	NT	

### Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3289	16472	29463	0.78	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rb) (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3288	16472	29464	0.78	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3300	16474	29465	29.49	0.0E+00	AA774783.1	EST_HUMAN	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3308	16482	29503	8.38	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3308	16482	29504	8.38	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3320	16493	29610	3.04	0.0E+00	4557580	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3328	16498	29617	1.01	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3334	16507		10.18	0.0E+00	M65180.1	NT	Homo sapiens 43 processed pseudogene
3335	16508	29524	0.85	0.0E+00	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21B1, complement component C2 (C2) genes, >
3338	16511	29527	4.05	0.0E+00	AF05084.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLCGR1) mRNA, complete cds
3348	16464	29535	1.34	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AAAP1) mRNA
3348	16464	29536	1.34	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AAAP1) mRNA
3363	16535	29549	3.56	0.0E+00	AF265708.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3364	16536	29550	1.95	0.0E+00	8822882	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3377	16540	29583	0.42	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3388	16558	29573	0.72	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3401	16571	29588	3.14	0.0E+00	AI688294.1	EST_HUMAN	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3404	16574	29589	8.94	0.0E+00	AW851400.1	EST_HUMAN	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3412	16581	29596	2.41	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3412	16581	29597	2.41	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3413	16582	29598	1.03	0.0E+00	7657213	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3413	16582	29599	1.03	0.0E+00	7657213	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3416	16585	29601	1.29	0.0E+00	4502582	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3416	16585	29602	1.29	0.0E+00	4502582	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3419	16588	29604	11.92	0.0E+00	AF111163.1	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3421	16590	29606	1.02	0.0E+00	AB040490.1	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3428	16596	29612	0.79	0.0E+00	BE778399.1	EST_HUMAN	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3441	16609	29627	0.67	0.0E+00	AI683569.1	EST_HUMAN	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3483	16651	29687	10	0.0E+00	AU123684.1	EST_HUMAN	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3492	16659	29671	1.16	0.0E+00	7708239	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3493	16680	29672	1.26	0.0E+00	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1-a Isoform (CACNA1I) mRNA, complete cds
3498	16685		0.94	0.0E+00	AF1897015.1	EST_HUMAN	MIR1-SN0033-100400-001-c08 SN0033 Homo sapiens cDNA
3511	16677	29687	2.02	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3511	16677	29688	2.02	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3512	16678	29689	0.82	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3514	16680	29690	2.35	0.0E+00	5803067	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3523	16807	28015	3.08	0.0E+00	AF110703.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3528	16693	28703	2.46	0.0E+00	7697038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3532	16697	28706	5.5	0.0E+00	K02380.1	NT	Bacteriophage P1 replication region including repA, repA, and parB genes and incA, incB, and incC incompatibility determinant
3535	16700	28711	1.38	0.0E+00	7427222	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
3538	16703	28714	1.83	0.0E+00	4557746	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET) mRNA
3544	16709	28719	4.17	0.0E+00	A1835153.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634
3544	16709	28720	4.17	0.0E+00	A1835153.1	EST_HUMAN	wp14d10.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634
3548	16713	28725	1.91	0.0E+00	AL278120.1	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3555	16720	28734	5.38	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3555	16720	28735	5.38	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3560	16725	28741	1.41	0.0E+00	M141231.1	NT	Human endogenous retrovirus HERV-K10
3568	16731	28747	5.78	0.0E+00	UA3293.1	NT	Human MDS1A (AML1/MDS1 fusion) mRNA, partial cds
3574	16739	28755	2.57	0.0E+00	AF045432.1	NT	Homo sapiens cell-line K562 transcriptional regulatory protein p54 mRNA, complete cds
3574	16739	28756	2.57	0.0E+00	AF045432.1	NT	Homo sapiens cell-line K562 transcriptional regulatory protein p54 mRNA, complete cds
3582	16747	28768	1.18	0.0E+00	AF231822.1	NT	Homo sapiens chromosome 21 unknown mRNA
3584	16758	28773	3.29	0.0E+00	BE304791.1	EST_HUMAN	601143833.F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3594	16758	28774	3.29	0.0E+00	BE304791.1	EST_HUMAN	601143833.F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3597	16761	28777	1.04	0.0E+00	4626785	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNK2) mRNA
3600	16764	28780	0.8	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3603	16767	28782	0.89	0.0E+00	A1894007.1	EST_HUMAN	1635g12.x1 Soares NIHMPU.S1 Homo sapiens cDNA clone IMAGE:2086742 3' similar to TR:O00498
3621	16785	28801	0.6	0.0E+00	AB032879.1	NT	000498 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN:
3621	16785	28802	0.6	0.0E+00	AB032879.1	NT	Homo sapiens mRNA for KIAA1153 protein, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3623	16787	29803	0.68	0.0E+00	AA456202.1	EST_HUMAN	29803.17 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:811927 5'
3623	16787	29804	0.68	0.0E+00	AA456202.1	EST_HUMAN	29804.17 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:811927 5'
3630	16784	29811	1.45	0.0E+00	AV701869.1	EST_HUMAN	AV701869 ADB Homo sapiens cDNA clone ADBDAH06 5'
3631	16795	29812	4.48	0.0E+00	4306984	NT	Homo sapiens semaphorin II (SEMG2) mRNA
3633	16797		1.17	0.0E+00	AF073898.1	NT	Homo sapiens homologue yeast-4.2 protein mRNA, complete cds
3642	16806	29820	1.34	0.0E+00	AL133264.1	NT	Novel human gene mapping to chromosome X
3644	16807	29821	1.16	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3666	16828	29837	0.67	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3666	16828	29838	0.67	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3667	16830	29841	1.06	0.0E+00	6325463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA
3672	16835		4.28	0.0E+00	AV1852217.1	EST_HUMAN	QVO-CT0225-230300-169-e01 CT0225 Homo sapiens cDNA
3679	16842		1.28	0.0E+00	AF118948.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLC1C) gene, partial cds
3680	16843	29850	7.66	0.0E+00	BF676393.1	EST_HUMAN	002004593F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248606 5'
3704	16866	29868	0.69	0.0E+00	BF672054.1	EST_HUMAN	602152496F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283645 5'
3704	16866	29869	0.69	0.0E+00	BF672054.1	EST_HUMAN	602152496F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283645 5'
3705	16868		0.69	0.0E+00	4828867	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2) mRNA
3707	16868	29871	0.76	0.0E+00	AV1864693.1	EST_HUMAN	h184g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3707	16868	29872	0.76	0.0E+00	AV1864693.1	EST_HUMAN	h184g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3711	16872	29876	0.89	0.0E+00	4828763	NT	Homo sapiens heparan sulfatase (glucosaminidase) 3-O-sulfotransferase 1 (HS3ST1) mRNA
3713	16874	29879	0.83	0.0E+00	7662319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
3720	16881	29885	0.74	0.0E+00	4567762	NT	Homo sapiens midline 1 (OpitzBBB syndrome) (MID1) mRNA
3720	16881	29887	0.74	0.0E+00	4567762	NT	Homo sapiens midline 1 (OpitzBBB syndrome) (MID1) mRNA
3737	16898	29901	2.36	0.0E+00	087327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3741	16902		6.28	0.0E+00	7668481	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
3757	16918	29920	3.98	0.0E+00	AB026532.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3761	16922	29923	5.16	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3761	16922	29924	5.16	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3767	16928	29932	32.49	0.0E+00	AA1862743.1	EST_HUMAN	h184g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3767	16928	29933	32.49	0.0E+00	AA1862743.1	EST_HUMAN	h184g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979024 3'
3770	16931	29935	1.95	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3770	16931	29936	1.95	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3771	16932	29937	0.99	0.0E+00	AB002351.1	NT	Human mRNA for KIAA0333 gene, partial cds
3771	16932	29938	0.99	0.0E+00	AB002351.1	NT	Human mRNA for KIAA0333 gene, partial cds
3774	16935	29941	2.4	0.0E+00	AW/851714.1	EST_HUMAN	MR2-CT0222-281099-005-605 CT0222 Homo sapiens cDNA
3776	16937	29943	2.37	0.0E+00	5729028	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3778	16938	29945	1.15	0.0E+00	AB018389.1	NT	Homo sapiens mRNA for KIAA0796 protein, partial cds
3780	16941	29947	0.74	0.0E+00	C14897	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3782	16943	29949	1.02	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3782	16943	29950	1.02	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3794	16956	29959	5.42	0.0E+00	AW/288134.1	EST_HUMAN	UH-BWD-8fs-e-12-0-ULst NCI CGAP Sub6 Homo sapiens cDNA clone IMAGE:27330223
3794	16956	29960	5.42	0.0E+00	AW/288134.1	EST_HUMAN	UH-BWD-8fs-e-12-0-ULst NCI CGAP Sub6 Homo sapiens cDNA clone IMAGE:27330223
3823	16963	29965	1.04	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen $\alpha 1$ chain, exon 6
3824	16984	29987	1.17	0.0E+00	AA463639.1	EST_HUMAN	aad9g01.r1 Soares_NHHMP_S1 Homo sapiens cDNA clone IMAGE:812465 5' similar to SW:KR84_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4, [1]
3831	16991	29993	3.23	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3841	17000	30003	0.83	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3855	17015	30015	5.72	0.0E+00	7662183	NT	Homo sapiens KIAA0568 gene product (KIAA0568), mRNA
3869	17019	30018	18.03	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
3869	17025	30023	1.52	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3869	17025	30024	1.52	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3869	17028	30027	8.94	0.0E+00	4505594	NT	Homo sapiens plasminogen activator inhibitor, type II (arginine-serpin) (PAI2), mRNA
3922	17081	30077	1.96	0.0E+00	AF146712.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
3924	17083		0.73	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3), gene, complete cds
3925	17084	30079	2.36	0.0E+00	AF179733.1	NT	Part troglodytes clectary receptor (PTR208), gene, partial cds
3928	17087	30083	2.36	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3928	17087	30084	2.36	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3929	17088	30085	1.74	0.0E+00	AF020091.1	NT	Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, partial cds
3935	17084	30092	1.05	0.0E+00	AF127831.1	NT	Gonilla gonilla olfactory receptor (GGOT1), gene, partial cds
3935	17094	30093	1.05	0.0E+00	AF127831.1	NT	Gonilla gonilla olfactory receptor (GGOT1), gene, partial cds
3936	17095	30094	1.29	0.0E+00	AF137769.1	EST_HUMAN	66210.x1 Soares_NF_T_G9C_S1 Homo sapiens cDNA clone IMAGE:20913073
3937	17098		1	0.0E+00	AF162408.1	NT	Homo sapiens proteasubunit beta 3 (PCDH-beta3), mRNA, complete cds
3938	17097	30095	2.6	0.0E+00	4768189	NT	Homo sapiens desmoplakin (DPL, DP11) (DSP), mRNA
3940	17099	30096	15.6	0.0E+00	S78865.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6BIR1), gene, complete cds
3942	17101	30098	2.14	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA

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3943	17102	30089	1.78	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3946	17105	30101	1.62	0.0E+00	AF088601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3948	17105	30102	1.62	0.0E+00	AF088601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3951	17109	30107	1.02	0.0E+00	AB001523.1	NT	Homo sapiens gene for TMEH1 and PWP2, complete and partial cds
3951	17109	30108	1.02	0.0E+00	AB001523.1	NT	Homo sapiens gene for TMEH1 and PWP2, complete and partial cds
3952	17110	30109	0.9	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
3957	17115	30117	6.86	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3957	17115	30118	6.86	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3959	17117	30121	4.85	0.0E+00	U08412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3960	17118	30122	1.12	0.0E+00	AF114486.1	NT	Homo sapiens intersein short isoform (ITSN) mRNA, complete cds
3963	17121	30124	1.23	0.0E+00	4826763	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNE1) mRNA
3968	17124	30127	1.44	0.0E+00	AF012615.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3967	17125	30128	2.87	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRP128), mRNA
3968	17127	30130	0.77	0.0E+00	AF099117.1	NT	Homo sapiens amphiphysin gene, partial cds
3978	17138	30140	3.22	0.0E+00	AB84727.1	EST_HUMAN	wk01701.X1 NC1_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411085 3' similar to TR.O43340
3980	17137	30141	1.03	0.0E+00	AL163248.2	NT	O43340 R28830_2, conlins element PTR7 repetitive element:
3983	17140	30145	18.17	0.0E+00	4508742	NT	Homo sapiens chromosome 21 segment HS21C048
3988	17145	30161	1.33	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein S8 (RPS8), mRNA
3994	17151	30168	1.8	0.0E+00	6005887	NT	DKFZ434N0413_J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZ434N0413 5'
3994	17151	30169	1.9	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3996	17163	30181	3.94	0.0E+00	4504138	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3997	17164	30184	2.28	0.0E+00	4505078	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
4001	17168	30184	0.97	0.0E+00	AF148412.1	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
4013	17170	30178	2.65	0.0E+00	4508758	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
4017	17174	30182	1.9	0.0E+00	4586642	NT	Homo sapiens tyrosine kinase receptor 3 (RYR3) mRNA
4026	17182	30191	5.14	0.0E+00	BF956295.1	EST_HUMAN	Homo sapiens zinc finger protein (KIAA0412) mRNA
4028	17184	30193	1.37	0.0E+00	AW888221.1	EST_HUMAN	RC3-H10860-170800-011-412 HT10860 Homo sapiens cDNA
4028	17184	30194	1.37	0.0E+00	AW888221.1	EST_HUMAN	MXRAS Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1086726 similar to MXRAS
4035	17191	30201	3.05	0.0E+00	AF128533.1	NT	Matrix remodeling associated gene 5
4038	17194	30204	1.14	0.0E+00	UB8281.1	NT	MXRAS Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1086726 similar to MXRAS

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4038	17194	30206	1.14	0.0E+00	U88281.1	NT	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
4042	17198	30209	3.47	0.0E+00	BE378502.1	EST_HUMAN	601226866f1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5'
4043	17199	30210	1.2	0.0E+00	BE313146.1	EST_HUMAN	801153727f1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3509743 5'
4061	17207	30217	1.28	0.0E+00	AW580740.1	EST_HUMAN	PM3-LT0031-100700-003-109 LT0031 Homo sapiens cDNA
4062	17208	30218	1.03	0.0E+00	53602215	NT	Homo sapiens iduronate-2-sulfatase (Hunter syndrome) (IDS), transcript variant 1, mRNA
4077	17233	30238	0.8	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4077	17233	30239	0.8	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4077	17233	30240	0.8	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4084	17239	30244	9.31	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4084	17239	30245	9.31	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4083	17248		3.51	0.0E+00	M23910.1	NT	Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
4095	17260		7.25	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
4104	17268	30268	2.93	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4112	17268	30268	2.13	0.0E+00	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
4127	17281		111.8	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4134	17287		0.89	0.0E+00	AB657076.1	EST_HUMAN	455g08.x1 NCI_GCAP_G08 Homo sapiens cDNA clone IMAGE:2244734 3' similar to TR:080309 060309 KIAA0563 PROTEIN.
4137	17288	30284	1.91	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569) mRNA
4138	17288	30286	2.85	0.0E+00	U09396.1	NT	Human zinc finger protein ZNF133
4157	17308	30304	6	0.0E+00	AB015610.1	NT	Chloroceryx aethiops mRNA for ribosomal protein S4X, complete cds
4166	17316		3.22	0.0E+00	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor RNA-associated antigenic protein (RNA48 gene)
4177	17327	30318	1.58	0.0E+00	AL163293.2	NT	Homo sapiens chromosome 21 segment HS21C003
4178	17328	30319	2.68	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rape-2 (rape gene)
4178	17328	30320	2.68	0.0E+00	AJ277276.1	NT	Homo sapiens mRNA for rape-2 (rape gene)
4185	17335	30327	8.33	0.0E+00	6032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4185	17335	30328	8.33	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4184	17344	30337	0.84	0.0E+00		NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylmethanimidazole synthetase (GAR1) mRNA
4202	17351	30343	6.02	0.0E+00	4865306	NT	Homo sapiens G protein-coupled receptor 21 (GPR21) mRNA
4203	17352	30344	11.98	0.0E+00	AB000623.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4206	17355	30345	1.26	0.0E+00	4788807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
4207	17356	30346	7.08	0.0E+00	114718207	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (INPDI1) mRNA
4208	17357	30347	4.33	0.0E+00	AL069857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes

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4209	17358		0.88	0.0E+00 AA018975.1	EST_HUMAN	z55609.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:362920 5' similar to contains Alu repetitive element.	
4218	17367	30356	5.32	0.0E+00 AF165327.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds	
4227	14319	27373	0.7	0.0E+00	4828947 NT	Homo sapiens protein kinase X-linked (PRKX) mRNA	
4227	14319	27374	0.7	0.0E+00	4828947 NT	Homo sapiens protein kinase X-linked (PRKX) mRNA	
4234	17381	30369	1.32	0.0E+00	4503854 NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA) mRNA	
4234	17381	30370	1.32	0.0E+00	4503854 NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA) mRNA	
4236	16785	28812	0.84	0.0E+00	4506884 NT	Homo sapiens serinepinin II (SEMG2) mRNA	
4238	17384	30372	0.91	0.0E+00	8922391 NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	
4238	17384	30373	0.91	0.0E+00	8922391 NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA	
4244	17390	30377	0.85	0.0E+00 AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds	
4242	17398	30386	5.57	0.0E+00 AB982597.1	EST_HUMAN	wu04004.x1 NC1_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2515975 3'	
4252	17398	30387	5.57	0.0E+00 AB982597.1	EST_HUMAN	wu04004.x1 NC1_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2515975 3'	
4255	17400	30389	1	0.0E+00 BE184856.1	EST_HUMAN	MR1-H10707-100500-001-b02 HT0707 Homo sapiens cDNA	
4255	17400	30390	1	0.0E+00 BE184856.1	EST_HUMAN	MR1-H10707-100500-001-b02 HT0707 Homo sapiens cDNA	
4259	17404		5.89	0.0E+00 BE274217.1	EST_HUMAN	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967690 5'	
4266	17410	30396	2.07	0.0E+00	5729725 NT	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA	
4272	17417		5.76	0.0E+00 AW675899.1	EST_HUMAN	ba5104.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900095 3' similar to SW:TH12_BOVIN Q85108 MITOCHONDRIAL THIOREDOXIN PRECURSOR;	
4277	17422	30410	1.12	0.0E+00 AW403788.1	EST_HUMAN	UI-HF-BMO-bdx-c-020-UI.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5'	
4278	17423	30411	1.65	0.0E+00	8922468 NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA	
4278	17423	30412	1.55	0.0E+00	8922468 NT	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA	
4287	17432		2.35	0.0E+00	5174632 NT	Homo sapiens polyovisic kidney disease (polyovisic) and REJ (epim receptor for egg jelly, sea urchin homolog)-like (PKDREL) mRNA	
4300	17443	30429	1.07	0.0E+00 AB037739.1	NT	Homo sapiens mRNA for KIAA1318 protein, partial cds	
4308	17452	30438	11.47	0.0E+00 AA401438.1	EST_HUMAN	zue6807.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element;	
4309	17492	30439	11.47	0.0E+00 AA401438.1	EST_HUMAN	zue6807.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element;	
4312	17455	30443	1.2	0.0E+00 AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds	
4338	17481	30481	8.09	0.0E+00	4758199 NT	Homo sapiens desmoplakin (DPL, DP11) (DSP) mRNA	
4338	17481	30482	8.09	0.0E+00	4758199 NT	Homo sapiens desmoplakin (DPL, DP11) (DSP) mRNA	
4345	17488		0.86	0.0E+00 AL163303.2	NT	Homo sapiens chromosome 21 segment H521C103	
4388	17531	30512	5.01	0.0E+00 J02610.1	NT	Human apolipoprotein B-100 mRNA, complete cds	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4402	17545	30629	0.81	0.0E+00	AW936689.1	EST_HUMAN	PM2-DT0023-080300-004-a08 DT0023 Homo sapiens cDNA
4406	16698	28612	0.65	0.0E+00	BE779039.1	EST_HUMAN	601464085F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3968246 5'
4410	17552	30537	5	0.0E+00	AF174590.1	NT	Homo sapiens F-box protein Fb4 (FBL4) mRNA, partial cds
4419	17680	30644	0.71	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4419	17680	30545	0.71	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
							q02306.x1 Soares placenta, 8bweeks, 2bHP8409W Homo sapiens cDNA clone IMAGE:1724579 3'
							similar to contig MER20.b2 MER20 repetitive element:
4420	17561		2.25	0.0E+00	AI189844.1	EST_HUMAN	Human CBF3A3 (Cbf3a3) gene, partial cds
4424	17564		4.58	0.0E+00	U14520.1	NT	Human CBF3A3 (Cbf3a3) gene, partial cds
4428	17568	30550	0.96	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (vltorax (Drosophila) homolog); translocated to, 4 (VLT4) mRNA
4446	17585	30585	0.72	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4446	17585	30586	0.72	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4451	17591	30572	1.08	0.0E+00	U10391.1	NT	Human G2 protein mRNA, partial cds
4451	17591	30573	1.08	0.0E+00	U10391.1	NT	Human G2 protein mRNA, partial cds
4460	17600	30578	10.33	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4480	17620		1.06	0.0E+00	AF163047.2	NT	Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds
							Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4480	17630	30611	3.62	0.0E+00	L14561.1	NT	Homo sapiens H2B/h gene
4484	17634	30616	6.28	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4484	17634	30617	6.28	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
4500	17640	30623	1.59	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4500	17640	30624	1.59	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4505	17644	30630	10.05	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4505	17644	30631	10.05	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4517	17656	30645	14.1	0.0E+00	4865126	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4518	17657	30646	1.16	0.0E+00	AJ271736.1	NT	Homo sapiens Xq pseudocautosomal region, segment 212
4519	17668		1.24	0.0E+00	AI163207.2	NT	Homo sapiens chromosome 21 segment H521C007
4522	17661	30648	1.2	0.0E+00	AB037701.1	NT	Homo sapiens myosin regulatory light chain interacting protein (MLIR), mRNA
4553	17691	30671	1.9	0.0E+00	7019456	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4564	17702		6.61	0.0E+00	AF185933.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4570	17708	30687	2.78	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4570	17708	30688	2.78	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4574	17711	30684	0.69	0.0E+00	W26179.1	EST_HUMAN	2467 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4574	17711	30685	0.69	0.0E+00	W26179.1	EST_HUMAN	2467 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4591	17728		2.29	0.0E+00	AF200859.1	NT	Homo sapiens HPST gene, Intron 5
4610	17747	30726	0.65	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA-C08-HAP-F1 Homo sapiens cDNA clone b4HB3MA-C08-HAP-F205 5'
4610	17747	30727	0.65	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA-C08-HAP-F1 Homo sapiens cDNA clone b4HB3MA-C08-HAP-F205 5'
4613	17750		0.89	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
4623	17760	30742	27.37	0.0E+00	AW084964.1	EST_HUMAN	xc88a08.x1 NC1 CGAP_Esc2 Homo sapiens cDNA clone IMAGE:2589446 3' similar to SW:AHNK_HUMAN
4625	18470		2.97	0.0E+00	8051619	NT	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4627	17763	30745	1.48	0.0E+00	AF016050.1	NT	Homo sapiens vascular endothelial cell growth factor 165 receptor/neuropilin (VEGF165) mRNA, complete cds
4631	17767		8.47	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4633	17769	30750	0.87	0.0E+00	AW381670.1	EST_HUMAN	PM1-HT0305-101189-002-d03 HT0305 Homo sapiens cDNA
4640	17776	30757	1.3	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4640	17776	30758	1.3	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4642	17778	30760	1.06	0.0E+00	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4643	17779	30761	2.07	0.0E+00	AF108840.1	NT	Homo sapiens serine-threonine protein kinase (MINB) mRNA, complete cds
4651	17787	30770	1.02	0.0E+00	S78684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K <sup>+</sup> -channel subunit (KCNJ6/IRK1) gene, exon
4652	17788	30771	1.2	0.0E+00	AF111163.1	NT	Homo sapiens p75N (MEFV) gene, complete cds
4652	17788	30772	1.2	0.0E+00	AF111163.1	NT	Homo sapiens p75N (MEFV) gene, complete cds
4661	18471	30783	3.18	0.0E+00	6005973	NT	Homo sapiens zinc finger protein 195 (ZNF195) mRNA
4666	17801	30788	20.19	0.0E+00	AF208161.1	NT	Homo sapiens synuclein precursor, mRNA, complete cds
4671	17806	30786	2.17	0.0E+00	AF152317.1	NT	Homo sapiens procathepsin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4674	17809	30789	2.17	0.0E+00	5484175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4685	17820	30808	59.87	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4693	17828	30814	0.73	0.0E+00	4506016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated product
4697	17832	30817	1.84	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4702	17837	30823	1.03	0.0E+00	4502558	NT	Homo sapiens calcineurin-modulin-dependent protein kinase IV (CAMK4) mRNA
4707	17842		3.18	0.0E+00	U35485.1	NT	Homo sapiens iduronate sulphate sulphatase (IDS) gene, complete cds
4708	17844	30826	15.03	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4708	17844	30827	15.03	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4724	17859	30841	2.87	0.0E+00	AF143314.1	NT	Homo sapiens PTEF (PTEF) gene, exons 3 through 5
4727	17862	30844	11.67	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G1c protein (G1c gene located in the class III region of the major histocompatibility complex)



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4727	17892	30845	11.57	0.0E+00	AA245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4748	17881		1.68	0.0E+00	AA174072.1	EST_HUMAN	zfp18g08.s1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3'
4749	17884		1.88	0.0E+00	7657410	NT	Homo sapiens odc (odd Oz/ten-in, Drosophila) homolog 1 (ODZ1), mRNA
4761	17886		3.31	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4752	17887	30888	1.33	0.0E+00	AF164110.1	NT	Homo sapiens cyclophilin-related protein (NKTR) gene, complete cds
4753	17888	30869	4.83	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4754	17889		1.95	0.0E+00	AB037521.1	NT	Homo sapiens gene for naturalistic protein, partial cds
4756	17891	30870	0.68	0.0E+00	AF168638.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4761	17896	30876	1.06	0.0E+00	AL162331.1	NT	Novel human gene mapping to chromosome 1
4764	17898	30879	31.32	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4764	17899	30880	31.32	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4765	17900	30881	1.42	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4765	17900	30882	1.42	0.0E+00	AF153819.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4766	17901	30883	2.62	0.0E+00	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4776	17911	30895	0.88	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4776	17911	30896	0.88	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4781	17918	30902	17.22	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4787	17922	30910	1.88	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0835-180400-142-hc5 BT0835 Homo sapiens cDNA
4788	17923	30911	1.37	0.0E+00	AA418246.1	EST_HUMAN	z96807.st Soares, Nht-MPU, S1 Homo sapiens cDNA clone IMAGE:767605 3'
4794	17929		1.9	0.0E+00	AF086841.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4799	17934	30921	1.3	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4799	17934	30922	1.3	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4800	17935	30923	2.72	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4800	17936	30924	2.72	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4801	17936	30925	3.06	0.0E+00	M74096.1	NT	Human displacement protein (CCAA1) mRNA
4804	17939	30927	2.08	0.0E+00	6453912	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4804	17939	30928	2.08	0.0E+00	6453912	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4806	13367	28400	2.83	0.0E+00	T569451.1	EST_HUMAN	Y83304.12 Stratiogene fetal spleen (8937205) Homo sapiens cDNA clone IMAGE:88310 5'
4806	13367	28401	2.83	0.0E+00	T569451.1	EST_HUMAN	Y83304.12 Stratiogene fetal spleen (8937205) Homo sapiens cDNA clone IMAGE:88310 5'
4810	17943		1.18	0.0E+00	BE278730.1	EST_HUMAN	601158835F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505521 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4814	17947	30932	1.13	0.0E+00	BE390C50.1	EST_HUMAN	601285246F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607087 5'
4830	17963	30951	0.95	0.0E+00	6728817	NT	Homo sapiens ecotropic viral integration site 2B (EV12B), mRNA
4830	17963	30952	0.95	0.0E+00	6728817	NT	Homo sapiens ecotropic viral integration site 2B (EV12B), mRNA
4835	17968	30956	50.79	0.0E+00	M80902.1	NT	Human AHNK nucleoprotein mRNA, 6' end
4838	17971	30959	3.07	0.0E+00	M69187.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4838	17971	30960	3.07	0.0E+00	M69187.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4842	17975	30965	2.07	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NCTR) gene, complete cds
4844	17977	30967	1.05	0.0E+00	7662478	NT	Homo sapiens KIAA1084 protein (KIAA1084), mRNA
4846	17978	30968	1.73	0.0E+00	7662181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4851	17984	30972	1.15	0.0E+00	U07563.1	NT	Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exon 2-10, complete cds
4858	17989	30977	1.29	0.0E+00	AL09657.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4872	18005	30987	0.74	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4872	18005	30988	0.74	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4882	18012	30986	1.25	0.0E+00	AF026801.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-28
4886	18016	31000	0.82	0.0E+00	7019320	NT	Homo sapiens proteinX0008 (AD013), mRNA
4886	18016	31001	0.82	0.0E+00	7019320	NT	Homo sapiens proteinX0008 (AD013), mRNA
4907	18037	31025	1.29	0.0E+00	AW444637.1	EST_HUMAN	U14-B13-giw-c-04-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733284 3'
4911	18041	31031	1.18	0.0E+00	AF303134.1	NT	Homo sapiens aldolase dehydrogenase 12 (ALDH12) mRNA, complete cds
4913	18043		2.01	0.0E+00	AF083242.1	NT	Homo sapiens HSPC024-iso mRNA, complete cds
4924	18054		1.33	0.0E+00	M63189.1	NT	Human cornelin 43 processed pseudogene
4925	18055		0.64	0.0E+00	AW330253.1	EST_HUMAN	x289003.X1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871371 3'
4966	18095		2.87	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1) gene, complete cds
4967	18098	31072	1.95	0.0E+00	4505384	NT	Homo sapiens nidogen (nidogen) (NID) mRNA
4970	18099	31075	1.09	0.0E+00	X67206.1	NT	M.1asciulantis mRNA for metalloproteinase-like, disintegrin-like protein, IVa
4972	18101	31077	0.99	0.0E+00	AF084478.1	NT	Homo sapiens Williams-Buren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
4973	18102	31078	1.04	0.0E+00	AF097416.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4974	18103	31079	4.54	0.0E+00	4503766	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4976	18105	31081	9.88	0.0E+00	4885048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4977	18106	31082	1	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4982	18111	31083	3.41	0.0E+00	8923080	NT	Homo sapiens hypothelial protein FLJ20073 (FLJ20073), mRNA
4985	18114	31091	1.35	0.0E+00	M94081.1	NT	Human Tor-C-delta gene, exons 1-4; Tor-V-delta gene, exons 1-2; Tor-cell receptor alpha (Tor-alpha) gene, J1-181 segments; and Tor-C-alpha gene, exons 1-4

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4985	18114	31092	1.35	0.0E+00	M94081.1	NT	Human Tor-C-delta gene, exons 1-4; Tor-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1- let1 segments; and Tor-C-alpha gene, exons 1-4
4987	18116	31094	1.3	0.0E+00	X94628.1	NT	H. sapiens MeCP-2 gene
4987	18116	31095	1.3	0.0E+00	X94628.1	NT	H. sapiens MeCP-2 gene
4980	18118	31098	1.46	0.0E+00	M5582.1	NT	Human collagenase type IV (CLG4) gene, exon 2
4991	18120	31099	2.55	0.0E+00	AL163260.2	NT	Human sapiens chromosome 21 segment HS21C080
5000	18126	31104	1.08	0.0E+00	5032150	NT	Human sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kd (TAF2)
5007	18136	31110	1.19	0.0E+00	X92841.1	NT	H. sapiens MICA gene
5009	18138	31112	1.32	0.0E+00	4585642	NT	Human sapiens zinc finger protein (KIA0412) mRNA
5010	18138	31113	1.39	0.0E+00	AB014533.1	NT	Human sapiens mRNA for KIA0633 protein, partial cds
5011	18140	31114	2.74	0.0E+00	6677649	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zik1) mRNA
5012	18141	31116	1.02	0.0E+00	5174580	NT	Human sapiens meningioma expressed antigen 8 (colled-coll proline-rich) (MGEA8), mRNA
5013	18142	31116	0.94	0.0E+00	BE007935.1	EST	Human sapiens meningioma expressed antigen 8 (colled-coll proline-rich) (MGEA8), mRNA
5013	18142	31117	0.94	0.0E+00	BE007935.1	EST	Human sapiens meningioma expressed antigen 8 (colled-coll proline-rich) (MGEA8), mRNA
5014	18143	31118	4.26	0.0E+00	4758198	NT	Human sapiens desmoplakin (DPI, DP11) (DSP) mRNA
5016	18145	31120	1.79	0.0E+00	5174580	NT	Human sapiens meningioma expressed antigen 8 (colled-coll proline-rich) (MGEA8), mRNA
5016	18145	31121	1.79	0.0E+00	5174580	NT	Human sapiens meningioma expressed antigen 8 (colled-coll proline-rich) (MGEA8), mRNA
5017	18146	31122	0.98	0.0E+00	7705546	NT	Human sapiens zinc-finger DNA-binding protein (HUNHOX1), mRNA
5020	18148	31127	11.02	0.0E+00	AF055086.1	NT	Human sapiens MHC class 1 region
5022	18161		2.46	0.0E+00	4505508	NT	Human sapiens opicid receptor, delta 1 (OPRD1) mRNA
5023	18162	31130	2.77	0.0E+00	AF091711.1	NT	Human sapiens splice variant AKAP350 mRNA, partial cds
5036	18164	31140	1.56	0.0E+00	4503684	NT	Human sapiens fatty acid synthase (fatty acid synthase), partial cds
5040	18168		1.17	0.0E+00	AL163235.2	NT	Human sapiens chromosome 21 segment HS21C085
5042	18170	31145	1.14	0.0E+00	D16050.1	NT	Human sapiens chromosome 21 segment HS21C085
5042	18170	31146	1.14	0.0E+00	D16050.1	NT	Human sapiens chromosome 21 segment HS21C085
5043	18171	31147	7.67	0.0E+00	AB006825.1	NT	Human sapiens chromosome 21 segment HS21C085
5043	18171	31148	7.67	0.0E+00	AB006825.1	NT	Human sapiens chromosome 21 segment HS21C085
5049	18177	31154	1.39	0.0E+00	4504082	NT	Human sapiens chromosome 21 segment HS21C085
5049	18177	31155	1.39	0.0E+00	4504082	NT	Human sapiens chromosome 21 segment HS21C085
5073	18195	31173	0.71	0.0E+00	7662319	NT	Human sapiens chromosome 21 segment HS21C085
5082	18210	31182	1.15	0.0E+00	8922926	NT	Human sapiens chromosome 21 segment HS21C085

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5087	18215		7.68	0.0E+00	U14967.1	NT	Human ribosomal protein L21 mRNA, complete cds
5097	18225	31187	1.25	0.0E+00	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
5099	18227		2.97	0.0E+00	BE408863.1	EST_HUMAN	801303729F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 6'
5102	18230	31201	4.85	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP) mRNA
5110	18238	31205	1.43	0.0E+00	AB028568.1	NT	Homo sapiens mRNA for KIAA1043 protein, partial cds
5121	18247	31212	2.32	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5121	18247	31213	2.32	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5135	18259	31225	0.72	0.0E+00	AA601246.1	EST_HUMAN	not4g09.st NCI_CGAP_Fhet1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TRIE239140
5135	18259	31226	0.72	0.0E+00	AA601246.1	EST_HUMAN	not4g09.st NCI_CGAP_Fhet1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TRIE239140
5135	18259	31227	0.72	0.0E+00	AA601246.1	EST_HUMAN	not4g09.st NCI_CGAP_Fhet1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TRIE239140
5139	18262	31229	2.09	0.0E+00	UB2871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LIP
5139	18262	31230	2.09	0.0E+00	UB2871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LIP
5148	18270	28472	0.72	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5148	18270		1.09	0.0E+00	4758225	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5160	18282	31247	0.64	0.0E+00	U53586.1	NT	Homo sapiens MHC class 1 region
5167	18289		1.89	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C006
5170	18292		18.98	0.0E+00	D50857.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
5182	18304	31268	0.92	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
5186	18318	31287	3.55	0.0E+00	X62989.1	NT	Bacillus amyloqueliculus sacB gene for levansucrase (EC 2.4.1.10)
5197	18319	31288	0.61	0.0E+00	X72791.1	NT	Human endogenous retrovirus mRNA for gag protein
5213	18334	31305	1.82	0.0E+00	AF240636.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5213	18334	31306	1.82	0.0E+00	AF240636.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5214	18335	31307	1.18	0.0E+00	5454153	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
5232	18354	31322	0.82	0.0E+00	6902055	NT	Homo sapiens ring finger protein (RNF), mRNA
5234	18356	31323	4.58	0.0E+00	M10805.1	NT	Human cellular fibronectin mRNA
5234	18356	31324	4.58	0.0E+00	M10805.1	NT	Human cellular fibronectin mRNA
5236	18358	31327	0.8	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6250	18371	31338	0.65	0.0E+00	6902091	NT	Homo sapiens solute carrier family 5 (inositol transporters), member 3 (SLC5A3), mRNA
6253	18373	31339	1.91	0.0E+00	AF124250.1	NT	Homo sapiens SH-2-containing protein Nsp2 mRNA, complete cds
6266	18385	31351	1.2	0.0E+00	8923822	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA
6266	18385	31352	1.2	0.0E+00	8923822	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 16 (KCNJ16), mRNA
6267	18386	31353	0.69	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
6267	18386	31354	0.69	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
6274	18393	31362	1.89	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C079
6278	18397	31364	1.03	0.0E+00	AA425183.1	EST_HUMAN	ZW44112.1 Soares fetal_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:772843 5'
6278	18397	31365	1.03	0.0E+00	AA425183.1	EST_HUMAN	ZW44112.1 Soares fetal_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:772843 5'
6290	18408	31375	0.93	0.0E+00	7667442	NT	Homo sapiens procalcitonin 11 (PCH11), mRNA
6294	18412	31378	1.47	0.0E+00	AF165632.1	NT	Homo sapiens core1 UDP-galactose-4-epimerase-epimerase (GALT1) mRNA, complete cds
6297	18472	31382	1.84	0.0E+00	AF167336.1	NT	Homo sapiens interleukin 1 receptor accessory protein (IL1RAP) gene, exon 4
6300	18417	31386	0.94	0.0E+00	S69002.1	NT	AML1-EV1-1-AML1-EV1-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5838 nt]
6301	18418	31387	1.93	0.0E+00	AF008638.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
6301	18418	31388	1.93	0.0E+00	AF008638.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
6303	18420	31390	24.35	0.0E+00	5360213	NT	Homo sapiens glypican 3 (GPC3) mRNA
6306	18423	31393	1.07	0.0E+00	7667203	NT	Homo sapiens acidic 82 kDa protein mRNA (HSU15652), mRNA
6318	18435	31405	0.79	0.0E+00	X76060.1	NT	H. sapiens mRNA for YRRM2
6321	18426	28444	0.85	0.0E+00	AI895950.1	EST_HUMAN	U03809.X1 NC1_CGAP_P128 Homo sapiens cDNA clone IMAGE:2253376 3' similar to SW-RASD_DICD1
6328	18441	31410	0.96	0.0E+00	AF245703.1	NT	P03967 RAS-LIKE PROTEIN RASD
6328	18441	31411	0.96	0.0E+00	AF245703.1	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
6333	18446	31414	0.96	0.0E+00	AL163208.2	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
6338	18451	31419	110.8	0.0E+00	AF008061.1	NT	Homo sapiens chromosome 21 segment HS21C006
6340	18453	31421	1.06	0.0E+00	AV726832	EST_HUMAN	AV726832 HTC Homo sapiens cDNA clone HTGCEN03 5'
6344	18457	31423	1.29	0.0E+00	6174632	NT	Homo sapiens polyoma kidney disease (polykyn) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
6346	18459	31424	1.18	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
6366	18462		2.46	0.0E+00	AF093093.1	NT	Homo sapiens acylase (ACD2) gene, nuclear gene encoding mitochondrial protein, exon 15
6366	18466	31436	2.17	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
6366	18469	31437	2.17	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
6368	18590	31592	1.21	0.0E+00	AI894804.1	EST_HUMAN	wp06608.x1 NC1_CGAP_K112 Homo sapiens cDNA clone IMAGE:2464094 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6391	18693	31565	1.2	0.0E+00	9256579	NT	Homo sapiens protocadherin alpha 13 (PCDH13), mRNA
6406	18608	31580	3.52	0.0E+00	BE931080.1	EST_HUMAN	RC3-GN0078-310800-013-b03 GN0076 Homo sapiens cDNA
5410	18612	31584	3.5	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5410	18612	31585	3.5	0.0E+00	AF182034.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
6418	18619	31584	8.57	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
6418	18619	31585	8.57	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5499	18688	31714	6.41	0.0E+00	BE876498.1	EST_HUMAN	7710606.x1 NC1_CGAP_CLL.1 Homo sapiens cDNA clone IMAGE:3294250.3'
6500	18699	31715	1.7	0.0E+00	BE220753.1	EST_HUMAN	h89a02.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3165194.3' similar to SW:Y054_HUMAN
5501	18700	31716	1.57	0.0E+00	BE794412.1	EST_HUMAN	P42694 HYPOTHETICAL PROTEIN KIAA0054.:
5501	18700	31717	1.57	0.0E+00	BE794412.1	EST_HUMAN	601569422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3843804.5'
							801569422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3843804.5'
6502	18701	31718	0.72	0.0E+00	AI189142.1	EST_HUMAN	q046d4.x1 Source: placenta, 8dweeks, 2NbpP8c6W Homo sapiens cDNA clone IMAGE:1722702.3' similar to SW:T2D3_DROKIE P49846 TRANSCRIPTION INITIATION FACTOR TFIIID 85 KD SUBUNIT;
6506	18705	31721	6.23	0.0E+00	ME28908.1	NT	Homo sapiens eosinophil peroxidase (EPP) gene, exon 7
6510	18709	31724	1.3	0.0E+00	AI791383.1	EST_HUMAN	0168609.y5 NC1_CGAP_Kd5 Homo sapiens cDNA clone IMAGE:1472152.5' similar to gb:U18512 IG
6520	25806	31732	4.62	0.0E+00	11421038	NT	HEAVY CHAIN PRECURSOR V1 REGION (HUMAN);
6530	18727		4	0.0E+00	BE685682.1	EST_HUMAN	602118928F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4276254.5'
5531	18728	31743	0.78	0.0E+00	AU134406.1	EST_HUMAN	AU134406 OVARC1 Homo sapiens cDNA clone OVARC1001894.5'
5531	18728	31744	0.78	0.0E+00	AU134406.1	EST_HUMAN	AU134406 OVARC1 Homo sapiens cDNA clone OVARC1001894.5'
6537	18734	31761	0.61	0.0E+00	BE538857.1	EST_HUMAN	601061459F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447839.5'
6540	18743	31777	1.63	0.0E+00	BE282784.1	EST_HUMAN	801105891F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988310.5'
5551	18748	31783	1.65	0.0E+00	BE528328.1	EST_HUMAN	602071372F1 NC1_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214272.5'
6551	18748	31784	1.65	0.0E+00	BE528328.1	EST_HUMAN	802071372F1 NC1_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214272.5'
5570	20121	33535	1.71	0.0E+00		NT	Homo sapiens Bicom syndrome (BLM) mRNA
6573	18769	31811	1.29	0.0E+00	AB007035.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
6573	18769	31812	1.29	0.0E+00	AB007035.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
5577	18772	31816	8.85	0.0E+00	AF26737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5577	18772	31817	8.85	0.0E+00	AF25737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5590	18785	31831	1.34	0.0E+00	D26535.1	NT	Human gene for dihydrodipomide succinyltransferase, complete cds (exon 1-15)
5590	18785	31832	1.34	0.0E+00	D26535.1	NT	Human gene for dihydrodipomide succinyltransferase, complete cds (exon 1-15)
5606	18801	31867	2.01	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
6612	18808	31873	0.79	0.0E+00	Z38133.1	NT	H. sapiens mRNA for myosin

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5630	18824	31898	0.73	0.0E+00	D61664.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#65535) Homo sapiens cDNA clone GEN-418D05 5'
5630	18824	31899	0.73	0.0E+00	D61664.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#65535) Homo sapiens cDNA clone GEN-418D05 5'
5633	18827	31803	2.92	0.0E+00	BF52893.1	EST_HUMAN	602042322F1 NCI CGAP Bim67 Homo sapiens cDNA clone IMAGE:4179988 5'
5633	18827	31804	2.92	0.0E+00	BF52893.1	EST_HUMAN	602042322F1 NCI CGAP Bim67 Homo sapiens cDNA clone IMAGE:4179988 5'
5638	18832	31808	2.62	0.0E+00	BF31338.1	EST_HUMAN	601897658F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126815 5'
5649	18843	32124	4.23	0.0E+00	11434392	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G) mRNA
5664	18858	32141	0.59	0.0E+00	A1928131.1	EST_HUMAN	w05b02.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:075054
5664	18858	32142	0.59	0.0E+00	A1928131.1	EST_HUMAN	w05b02.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:075054
5664	18858	32142	0.59	0.0E+00	A1928131.1	EST_HUMAN	w05b02.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2463051 3' similar to TR:075054
5692	18876	32165	1.3	0.0E+00	BE260777.1	EST_HUMAN	601150252F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502909 5'
5691	18885	32180	3.99	0.0E+00	AW867316.1	EST_HUMAN	MFR-SN0037-030400-001-h07 SN0037 Homo sapiens cDNA
5705	18898	32191	2.49	0.0E+00	BE29289.1	EST_HUMAN	601106281F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5705	18898	32191	2.49	0.0E+00	BE29289.1	EST_HUMAN	601106281F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987903 5'
5725	18918	32212	1.7	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1) mRNA
5725	18918	32213	1.7	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1) mRNA
5733	18926	32221	4.16	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5733	18926	32222	4.16	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5740	18933	32232	2.64	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5740	18933	32233	2.64	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5769	18961	32262	1	0.0E+00	A1198515.1	EST_HUMAN	qf84g10.x1 Soares, placenta, B2NH8P80W Homo sapiens cDNA clone IMAGE:1757730 3'
5773	18965	32268	7.56	0.0E+00	M85719.1	EST_HUMAN	similar to SW-CADC, HUMAN P55289 BRAIN-CADHERIN PRECURSOR;
5780	18972	32277	4.52	0.0E+00	AW405472.1	EST_HUMAN	EST02238 Fetal brain, Striatum (cat836209) Homo sapiens cDNA clone IMAGE:3067658 5'
5783	18984	32287	1.12	0.0E+00	Z26269.1	NT	HL-septins isoform 1 gene for L-type calcium channel, exon 14 and 15
5804	18994	32288	1.85	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-405 CT0263 Homo sapiens cDNA
5804	18994	32288	1.85	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-405 CT0263 Homo sapiens cDNA
5804	18994	32289	1.85	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091299-007-405 CT0263 Homo sapiens cDNA
5807	18997	32302	0.59	0.0E+00	AB033566.1	NT	Homo sapiens mRNA for neurxin II, complete cds
5807	18997	32303	0.59	0.0E+00	AB033566.1	NT	Homo sapiens mRNA for neurxin II, complete cds
5809	18999	32308	1.97	0.0E+00	U39251.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 13
5840	19030	32336	1.02	0.0E+00	AB048861.1	NT	Homo sapiens mRNA for KIAA1641 protein, partial cds

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5889	18088	32400	1.48	0.0E+00	AJ008345.1	NT	Homo sapiens KVLQ11 gene
5899	18089	32401	1.49	0.0E+00	AJ008345.1	NT	Homo sapiens KVLQ11 gene
5908	19085	32410	1.23	0.0E+00	AI207613.1	EST_HUMAN	HA2981 Human fetal liver cDNA library Homo sapiens cDNA
5928	19114	32427	4.63	0.0E+00	11416801	NT	Homo sapiens protocadherin beta 2 (PCDH2), mRNA
5933	19118	32430	1.18	0.0E+00	BE791173.1	EST_HUMAN	601584032F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3838551 5'
5942	19126	32441	1.1	0.0E+00	8998943	NT	Homo sapiens emilioride-sensitive calton channel 1, neuronal (degenerin) (ACCN1), mRNA
5943	19128	32442	7.24	0.0E+00	BE660082.1	EST_HUMAN	601345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677843 5'
5944	19130	32443	2.46	0.0E+00	10048478	NT	Mus musculus aczonin (Acz), mRNA
5945	19131	32444	3.06	0.0E+00	U86991.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5945	19131	32445	3.06	0.0E+00	U86991.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5965	19161	32466	2.98	0.0E+00	BF338835.1	EST_HUMAN	602036272F1 NCI_CGAP_Brl64 Homo sapiens cDNA clone IMAGE:4184321 5'
5968	19154	32469	0.92	0.0E+00	AF142621.1	NT	Homo sapiens calcium channel gamma 5 subunit (CACNG5) gene, exon 4 and complete cds
5969	19165	32470	3.07	0.0E+00	BE273983.1	EST_HUMAN	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347483 5'
5979	19164	32484	1.12	0.0E+00	BE603096.1	EST_HUMAN	h283d11 x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214591 3' similar to TR:Q62084 PHOSPHOLIPASE C NEIGHBORING
5984	19169	32491	2.09	0.0E+00	BF569805.1	EST_HUMAN	602185852F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4310076 5'
5989	19174	32495	0.99	0.0E+00	AA484642.1	EST_HUMAN	z988d06 st Seares_NHIMPu_s1 Homo sapiens cDNA clone IMAGE:811893 3'
6021	19204	32524	2.15	0.0E+00	AF21729.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6023	19206	32526	4.69	0.0E+00	BE828144.1	EST_HUMAN	RC5-E10027-210800-022-G10 ET0027 Homo sapiens cDNA
6028	19211	32531	1.19	0.0E+00	BE68638.1	EST_HUMAN	601645287F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3830453 5'
6044	19227	32550	0.98	0.0E+00	BE673888.1	EST_HUMAN	7472a11 x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278540 3' similar to SW:DAX1_HUMAN
6044	19227	32551	0.98	0.0E+00	BE673888.1	EST_HUMAN	P51843 ORPHAN NUCLEAR RECEPTOR DAX-1 (1);
6048	19231	32555	0.8	0.0E+00	AW276780.1	EST_HUMAN	7472a11 x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278540 3' similar to SW:DAX1_HUMAN
6059	19240	32565	0.96	0.0E+00	BF031742.1	EST_HUMAN	P51843 ORPHAN NUCLEAR RECEPTOR DAX-1 (1);
6058	19240	32586	0.98	0.0E+00	BF031742.1	EST_HUMAN	7472a11 x1 NCI_CGAP_OX58 Homo sapiens cDNA clone IMAGE:2745245 3' similar to TR:P78335 P78335
6070	19252	32581	0.65	0.0E+00	AW470846.1	EST_HUMAN	XP5503 x1 NCI_CGAP_OX58 Homo sapiens cDNA clone IMAGE:2745245 3' similar to TR:P78335 P78335
6082	19284	32592	1.09	0.0E+00	BF165570.1	EST_HUMAN	GUANYLATE KINASE ASSOCIATED PROTEIN, 1
6082	19284	32593	1.09	0.0E+00	BF165570.1	EST_HUMAN	801559080F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
							601568060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
							h634d06 x1 NCI_CGAP_K412 Homo sapiens cDNA clone IMAGE:2875595 3' similar to TR:Q821N3
							Q821N3 MYOSIN-RHO GTPASE PROTEIN, MYR 7, 1
							QV4-HT0934-280900-399-a10 HT0984 Homo sapiens cDNA
							QV4-HT0934-280900-399-a10 HT0984 Homo sapiens cDNA



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6090	19271	32699	1.67	0.0E+00	W33069.1	EST_HUMAN	z008006.r1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
6090	19271	32600	1.67	0.0E+00	W33069.1	EST_HUMAN	z008006.r1 Soares parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:321755 5'
6091	19272		2.3	0.0E+00	AF012018.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 14
6094	19275	32604	3.37	0.0E+00	BE280197.1	EST_HUMAN	601158515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505323 5'
6100	19280	32612	2.43	0.0E+00	BE889610.1	EST_HUMAN	601312630F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3914238 5'
6102	19282	32615	0.58	0.0E+00	BE388673.1	EST_HUMAN	601286320F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613085 5'
6117	19287	32633	0.65	0.0E+00	AW782848.1	EST_HUMAN	IL3-GT0220-111189-028-E04 CT0220 Homo sapiens cDNA
6120	19289	32635	1.72	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product synaptic vesicle protein 28 homolog (KIAA0735) mRNA
6120	19289	32636	1.72	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product synaptic vesicle protein 28 homolog (KIAA0735) mRNA
6121	19300	32637	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6121	19300	32638	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6121	19300	32639	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6137	25919	32656	10.17	0.0E+00	9789889	NT	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCND2) mRNA
6140	19318	32659	1.28	0.0E+00	AA193108.1	EST_HUMAN	z40b01.r1 Soares NIH-MIPU_S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to
6140	19318	32680	1.28	0.0E+00	AA193108.1	EST_HUMAN	SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5 ;
6163	19339	32685	10.44	0.0E+00	U34825.1	NT	SW:YY05_HUMAN P42694 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5 ;
6163	19339	32686	10.44	0.0E+00	U34825.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6203	19378	32729	1.06	0.0E+00	BE258320.1	EST_HUMAN	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6213	19388	32737	1.16	0.0E+00	BE156561.1	EST_HUMAN	QVO-HT0368-09200-099-c09 HT0368 Homo sapiens cDNA
6223	19398	32747	0.66	0.0E+00	MA8107.1	NT	Human neurofibromatosis type 1 (NF-1) mRNA, 3' end of cds
6259	19433	32780	1.6	0.0E+00	BE379007.1	EST_HUMAN	601236527F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608490 5'
6265	19439	32786	1.35	0.0E+00	AU137172.1	EST_HUMAN	AU137172 PLAC1 Homo sapiens cDNA clone IMAGE:3608490 5'
6297	19460	32812	3.33	0.0E+00	U45882.1	NT	Human G protein-coupled receptor GPR-9-9 gene, complete cds
6316	19488	32844	4.34	0.0E+00	AA204740.1	EST_HUMAN	z481003.r1 Striatagene hnt neuron (8631233) Homo sapiens cDNA clone IMAGE:648005 5' similar to
6317	19489	32845	3.89	0.0E+00	11645913	NT	TR:G854195 G854195 LELUKOCYTE SURFACE PROTEIN. . .
6317	19489	32846	3.89	0.0E+00	11645913	NT	Homo sapiens xylotransferase II (XT2) mRNA
6353	19523	32880	2.23	0.0E+00	11426367	NT	Homo sapiens carboxyterminal antigen-related cell adhesion molecule 8 (CEACAM8) mRNA
6357	19527	32885	3.15	0.0E+00	BE25173.1	EST_HUMAN	601106532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350822 5'
6371	19540		0.98	0.0E+00	AI99648.1	EST_HUMAN	60111041 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2248939 3' similar to TR:Q14839 Q14839

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6375	19544	32902	1.32	0.0E+00	U35830.1	NT	Human anion exchanger (AE1) gene, exons 1-20
6383	19562	32908	0.86	0.0E+00	BE787385.1	EST_HUMAN	601687871.F1 NIH_MGC_7 Homo sapiens cDNA IMAGE:3942329 5'
6383	19562	32909	0.96	0.0E+00	BE787385.1	EST_HUMAN	601687871.F1 NIH_MGC_7 Homo sapiens cDNA IMAGE:3942329 5'
6393	19562	32922	0.71	0.0E+00	AI198025.1	EST_HUMAN	q50b11.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:1859901 3' similar to TR:Q12838 Q12836
6393	19562	32923	0.71	0.0E+00	AI198025.1	EST_HUMAN	q50b11.x1 NCI_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:1859901 3' similar to TR:Q12838 Q12836
6395	19564	32924	1.11	0.0E+00	BF357123.1	EST_HUMAN	MRQ-H10923-220800-102-b05 HT10823 Homo sapiens cDNA
6403	19572	32934	1.3	0.0E+00	U1435630	NT	Human alpha peptide transporter 3 (LOC51298), mRNA
6413	19582	32943	0.59	0.0E+00	D56646.1	NT	Human mRNA for alpha mannosidase II (Iszyme, complete cds)
6428	19587	32963	1.07	0.0E+00	AW178142.1	EST_HUMAN	IL3-HT0062-Q10939-Q14-A04 HT0062 Homo sapiens cDNA
6450	19917	32980	0.6	0.0E+00	BE674544.1	EST_HUMAN	7d02c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281302.3 similar to SW:Y176_HUMAN
6454	19921	32985	0.77	0.0E+00	7692039	NT	Q14681 HYPOTHETICAL PROTEIN KIAA0176.
6468	19935		8.28	0.0E+00	AV650020.1	EST_HUMAN	Homo sapiens KIAA0285 gene product (KIAA0285), mRNA
6477	19944	33006	3.48	0.0E+00	AW575398.1	EST_HUMAN	AV650020 GLC Homo sapiens cDNA clone GLCAD09 3'
6480	19947	33009	4.53	0.0E+00	H01255.1	EST_HUMAN	U1-HF-BL0-acc-g-12-Q-UJ.s1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3038751 3'
6488	19955	33018	0.71	0.0E+00	U1426283	NT	y27b03.r1 Scars placenta NB2HP Homo sapiens cDNA clone IMAGE:149933 5'
6492	19958	33021	1.87	0.0E+00	X15377.1	NT	Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA
6494	19960	33023	1.17	0.0E+00	AA456375.1	EST_HUMAN	Human gene for the light and heavy chains of myeloperoxidase
6495	19961	33024	1.04	0.0E+00	AI612841.1	EST_HUMAN	aa14e07.r1 Scars, NhhMPu.S1 Homo sapiens cDNA clone IMAGE:813252 5'
6501	19967	33030	4.27	0.0E+00	BE735989.1	EST_HUMAN	t257d08.x1 NCI_CGAP_Ox45 Homo sapiens cDNA clone IMAGE:2282887 3' similar to SW:NTCS_HUMAN
6501	19967	33031	4.27	0.0E+00	BE735989.1	EST_HUMAN	PS3786 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 2.
6505	19971	33037	0.86	0.0E+00	AW746596.1	EST_HUMAN	601305388.F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639616 5'
6505	19971	33038	0.86	0.0E+00	AW746596.1	EST_HUMAN	MRQ-B10264-221189-002.f11 BT0264 Homo sapiens cDNA
6507	19973	33040	52.21	0.0E+00	AU119245.1	EST_HUMAN	WFO-B10264-221189-002.f11 BT0264 Homo sapiens cDNA
6507	19973	33041	62.21	0.0E+00	AU119245.1	EST_HUMAN	WFO-B10264-221189-002.f11 BT0264 Homo sapiens cDNA
6512	19977	33047	0.8	0.0E+00	BE780453.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360 5'
6513	19978	33048	0.84	0.0E+00	X92217.1	NT	601468772.F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3877899 5'
6527	19991	33065	1.71	0.0E+00	AI999483.1	EST_HUMAN	H.sapiens germine immunoglobulin heavy chain, variable region, (13-2)
6541	19704	33076	4.08	0.0E+00	BE293163.1	EST_HUMAN	ws26c07.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2493220 5'
6541	19704	33077	4.08	0.0E+00	BE293163.1	EST_HUMAN	601105344.F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987863 5'
6573	19735	33114	1.07	0.0E+00	BE667697.1	EST_HUMAN	601105344.F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987863 5'

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6609	19769	33158	1.81	0.0E+00	AW406348.1	EST_HUMAN	UHF-BL0-acc-h-02-Q-U1.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:305931 5'
6609	19769	33158	1.81	0.0E+00	AW406348.1	EST_HUMAN	UHF-BL0-acc-h-02-Q-U1.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:305931 5'
6640	19789	33186	0.94	0.0E+00	AV719444.1	EST_HUMAN	AV719444 GLO Homo sapiens cDNA clone GLOEHC06 5'
6649	19808	33195	0.74	0.0E+00	BE888340.1	EST_HUMAN	601881150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6649	19808	33196	0.74	0.0E+00	BE888340.1	EST_HUMAN	601881150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301 5'
6652	19811	33199	2.13	0.0E+00	AF160830.1	NT	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant Cav1.1a (CACNA1G) mRNA, complete cds
6655	19814	33202	0.64	0.0E+00	L48546.1	NT	Homo sapiens tubulin (TSC2) gene, exons 38, 39, 40 and 41
6667	19816	33203	0.89	0.0E+00	11420859	NT	Homo sapiens transcription domain-associated protein (TRRAP) mRNA
6664	19823	33210	3.5	0.0E+00	AW163840.1	EST_HUMAN	au56h08 y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR-O15390 O15390 G124 [3] TR-O43840 TR-O43206 ;
6664	19823	33211	3.5	0.0E+00	AW163840.1	EST_HUMAN	au56h08 y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159 5' similar to TR-O15390 O15390 G124 [3] TR-O43840 TR-O43206 ;
6668	19827	33214	1.06	0.0E+00	W67163.1	EST_HUMAN	zb20e06.r1 Soares fetal lung NIH1.18W Homo sapiens cDNA clone IMAGE:302626 5' similar to SW:ZN45_HUMAN 002388 ZINC FINGER PROTEIN 45 ;
6668	19827	33215	1.06	0.0E+00	W67163.1	EST_HUMAN	zb20e06.r1 Soares fetal lung NIH1.18W Homo sapiens cDNA clone IMAGE:302626 5' similar to SW:ZN45_HUMAN 002388 ZINC FINGER PROTEIN 45 ;
6684	19842	33232	1.21	0.0E+00	BE764833.1	EST_HUMAN	601559371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943504 5'
6681	19849	33239	5.1	0.0E+00	BE769873.1	EST_HUMAN	601567561F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3841847 5'
6692	19850	33240	1.38	0.0E+00	BE767835.1	EST_HUMAN	QV1-GN0065-140800-318-h02 GN0065 Homo sapiens cDNA
6692	19850	33241	1.38	0.0E+00	BE767835.1	EST_HUMAN	QV1-GN0065-140800-318-h02 GN0065 Homo sapiens cDNA
6696	19854	33244	6.83	0.0E+00	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6696	19854	33245	6.83	0.0E+00	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6705	19863	33253	4.51	0.0E+00	L24493.1	NT	Human antigen CD27 gene, exons 1-2
6710	19868	33257	2.62	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6716	19874	33265	3.68	0.0E+00	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A) mRNA
6720	19877	33268	4.12	0.0E+00	AI53412.1	EST_HUMAN	1831T1.X1 NC1 CGAP GC6 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE
6722	19879	33270	1.46	0.0E+00	L32832.1	NT	P17553 WNT3 PROTO-ONCOGENE PROTEIN PRECURSOR ;
6735	19891	33283	0.82	0.0E+00	AW604350.1	EST_HUMAN	UHF-BL0-acc-h-01-Q-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081217 5'
6737	19893	33284	4.11	0.0E+00	AA434584.1	EST_HUMAN	zw52c03.r1 Soares fetal testis N12H1F8_9W Homo sapiens cDNA clone IMAGE:773668 5'
6751	19907		1.13	0.0E+00	BF217200.1	EST_HUMAN	601885317F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4103693 5'
6756	19912	33307	1.63	0.0E+00	BE826876.1	EST_HUMAN	QV3-BN0047-300900-27B-c06 BN0047 Homo sapiens cDNA

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Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6789	19944	33342	0.76	0.0E+00	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6789	19944	33343	0.76	0.0E+00	11426758	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
6760	19945	33345	0.69	0.0E+00	AW671884.1	EST_HUMAN	h962604.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952126 3'
6808	19982	33366	1.64	0.0E+00	AU126928.1	EST_HUMAN	AU126928 NT2RM4 Homo sapiens cDNA clone NT2RM4002430 5'
6810	19984	33368	0.68	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
6810	19984	33369	0.58	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-h10 NN0174 Homo sapiens cDNA
6832	19985	33393	1.27	0.0E+00	BE142383.1	EST_HUMAN	CMO-HT0143-270899-062-c08 HT0143 Homo sapiens cDNA
6854	20007	33416	2.43	0.0E+00	BE006012.1	EST_HUMAN	RCO-BN0121-260300-032-c04 BN0121 Homo sapiens cDNA
6854	20007	33417	2.43	0.0E+00	BE006012.1	EST_HUMAN	RCO-BN0121-260300-032-c04 BN0121 Homo sapiens cDNA
6976	20028	33438	7.78	0.0E+00	BE168131.1	EST_HUMAN	PM3-HT0520-260200-002-c08 HT0520 Homo sapiens cDNA
6878	20030	33440	2.04	0.0E+00	BF086637.1	EST_HUMAN	IL5-GN0032-180900-145-d07 GN0032 Homo sapiens cDNA
6915	20230	33663	3.33	0.0E+00	AA190735.1	EST_HUMAN	z98603.t1 Stratiogene Hela cell c3 937216 Homo sapiens cDNA clone IMAGE:627282 5'
6928	20241	33676	0.83	0.0E+00	U95673.1	NT	Human salivary peroxidase mRNA, complete cds
6930	20245	33678	0.76	0.0E+00	BE671687.1	EST_HUMAN	744907.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3222037 3' similar to TR:Q92285 Q92285 TEKTN.1
6940	20253	33689	5.73	0.0E+00	AI94062.1	EST_HUMAN	IL3-ST0024-230789-001-E01 ST0024 Homo sapiens cDNA
6940	20253	33690	6.73	0.0E+00	AI94062.1	EST_HUMAN	IL3-ST0024-230789-001-E01 ST0024 Homo sapiens cDNA
6951	20264	33703	2.15	0.0E+00	11435626	NT	Homo sapiens CD6 antigen (CD6), mRNA
6953	20191	33617	0.73	0.0E+00	AI042443.1	EST_HUMAN	DKFZp434D2021_t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D2021 6'
6964	20192	33618	11.05	0.0E+00	X58183.1	NT	H sapiens Intermittent bulbar T-ray chain gene, variable region
6967	20195	33621	0.92	0.0E+00	AI169270.1	EST_HUMAN	co10001.x1 Scores_NSF_F8_PV_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1565761 3' similar to TR:Q26623 Q26623 TEKTN.C1.1
6972	20200	33626	0.85	0.0E+00	BE734087.1	EST_HUMAN	801567370F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842080 5'
6981	18510	31502	1.28	0.0E+00	BE666381.1	EST_HUMAN	601339977F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682267 5'
6988	18517	31509	13.63	0.0E+00	BE807693.1	EST_HUMAN	601443667F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847897 5'
6998	18517	31510	13.63	0.0E+00	BE807693.1	EST_HUMAN	601443667F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847897 5'
7004	20140	33558	1.74	0.0E+00	BE660182.1	EST_HUMAN	764903.x1 NCI_CGAP_L024 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:CG85_HUMAN
7004	20140	33559	1.74	0.0E+00	BE660182.1	EST_HUMAN	764903.x1 NCI_CGAP_L024 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:CG85_HUMAN
7030	20168	33588	1.68	0.0E+00	BE088276.1	EST_HUMAN	Q08379 GOLGIN-95.1
7036	20172	33594	1.4	0.0E+00	AA195106.1	EST_HUMAN	CM1-HT0877-060900-397-g11 HT0877 Homo sapiens cDNA
							z734603.t1 Scores_NHMPu_S1 Homo sapiens cDNA clone IMAGE:683332 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7044	20097		11.81	0.0E+00	11034810	NT	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
7040	20089	33515	1.11	0.0E+00	11431474	NT	Homo sapiens sodium channel, nonvoltage-gated 1, beta (Liddle syndrome) (SCNN1B), mRNA
7061	20114	33529	2.69	0.0E+00	BF568905.1	EST_HUMAN	602185952F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7068	20121	33535	0.68	0.0E+00	4557364	NT	Homo sapiens Bloom syndrome (BLM) mRNA
7076	20129		2.06	0.0E+00	U03060.1	NT	Homo sapiens MYC2 gene, complete cds
7083	20177	33599	2.66	0.0E+00	AF217239.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7083	20177	33600	2.66	0.0E+00	AF217239.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
7084	20178	33601	1.07	0.0E+00	U68113.1	NT	Homo sapiens neurofibromatosis type 1 gene, exon x6
7095	18522	31515	3.59	0.0E+00	11420775	NT	Homo sapiens melanoma antigen, family B, 2 (MAGEB2), mRNA
7099	18526	31518	0.7	0.0E+00	BE568708.1	EST_HUMAN	601115515F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3356330 5'
							wf21609.x1 Soares, Dieckgraefe, colon, NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:M74297 HOMEBOX PROTEIN HOX-44 (HUMAN); contains PTR5.b1 MER22 MER22 repetitive element:
7111	18537	31483	0.62	0.0E+00	AI690911.1	EST_HUMAN	wf21609.x1 Soares, Dieckgraefe, colon, NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:M74297 HOMEBOX PROTEIN HOX-44 (HUMAN); contains PTR5.b1 MER22 MER22 repetitive element:
7111	18537	31483	0.62	0.0E+00	AI690911.1	EST_HUMAN	wf21609.x1 Soares, Dieckgraefe, colon, NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:M74297 HOMEBOX PROTEIN HOX-44 (HUMAN); contains PTR5.b1 MER22 MER22 repetitive element:
7111	18537	31483	0.62	0.0E+00	AI690911.1	EST_HUMAN	wf21609.x1 Soares, Dieckgraefe, colon, NHUC Homo sapiens cDNA clone IMAGE:2351248 3' similar to gb:M74297 HOMEBOX PROTEIN HOX-44 (HUMAN); contains PTR5.b1 MER22 MER22 repetitive element:
7120	18546	31457	1.21	0.0E+00	AU118478.1	EST_HUMAN	AU118478 HEMBA1 Homo sapiens cDNA clone HEMBA1003678 5'
7123	18549	31461	7.52	0.0E+00	BE26294.1	EST_HUMAN	601148964F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3501828 5'
7124	18550	31462	2.72	0.0E+00	Z37970.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7124	18550	31463	2.72	0.0E+00	Z37970.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7125	18551	31464	3.01	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7125	18551	31465	3.01	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7132	18558	31472	1.26	0.0E+00	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
7137	20272	33711	0.61	0.0E+00	BE762770.1	EST_HUMAN	QV3-NT0022-1-40600-223-601 NT0022 Homo sapiens cDNA
7142	20277	33717	2.56	0.0E+00	BF568905.1	EST_HUMAN	602185852F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
7144	20279	33719	0.78	0.0E+00	AJ404498.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7144	20279	33720	0.78	0.0E+00	AJ404498.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7148	20283	33725	3.26	0.0E+00	L01978.1	NT	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19
7153	20287	33728	0.72	0.0E+00	AW502862.1	EST_HUMAN	U1-HF-BR0p-ale-d-10-0-UL1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076280 5'
7153	20287	33730	0.72	0.0E+00	AW502862.1	EST_HUMAN	U1-HF-BR0p-ale-d-10-0-UL1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3076280 5'
7162	20295	33738	0.87	0.0E+00	AL039591.1	EST_HUMAN	DKFZp434D2211.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434D2211 5'
7162	20295	33739	0.87	0.0E+00	AL039591.1	EST_HUMAN	DKFZp434D2211.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434D2211 5'
7171	20304	33747	5.81	0.0E+00	BF306936.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7177	20309	33752	2.13	0.0E+00	U41302.1	NT	Human chromosome 18 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
7219	20084	33499	1.15	0.0E+00	AL049784.1	NT	Novel human gene mapping to chromosome 13
7225	20089	33506	0.84	0.0E+00	AW613069.1	EST_HUMAN	KLIA0803 PROTEIN.
7257	20340	33780	0.82	0.0E+00	AB026893.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7257	20340	33781	0.82	0.0E+00	AB026893.1	NT	Homo sapiens mRNA for vascular cadherin-2, complete cds
7262	20345	33787	0.84	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7262	20345	33788	0.84	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7268	20351	33804	1.16	0.0E+00	AW654808.1	EST_HUMAN	EST366876 MAGE resequences, MAGEC Homo sapiens cDNA
7269	20352	33805	0.72	0.0E+00	BE264703.1	EST_HUMAN	601133958F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354568 5'
7283	20366	33819	1	0.0E+00	LO1973.1	NT	Human type VI sodium channel alpha polypeptide (SCN4A) gene, exon 14
7291	20373	33829	1.03	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
7291	20373	33830	1.03	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
7297	20379	33837	1.47	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP401556 5'
7313	20385	33857	1.06	0.0E+00	11428081	NT	Homo sapiens membrane protein CH1 (CH1), mRNA
7319	20401		2.82	0.0E+00	AU143706.1	EST_HUMAN	AU143706 Y79AA1 Homo sapiens cDNA clone Y79AA1002365 5'
7320	20402	33884	0.71	0.0E+00	4758639	NT	Homo sapiens netin 1 (NTN1), mRNA
7328	20411	33872	1.25	0.0E+00	BE891283.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7329	20411	33873	1.25	0.0E+00	BE891283.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7350	18569	31436	2.43	0.0E+00	AF137288.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7350	18569	31437	2.43	0.0E+00	AF137288.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7361	20440	33901	0.87	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3629722 5'
7361	20440	33902	0.87	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3629722 5'
7371	20450	33913	4.07	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7371	20450	33914	4.07	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7385	20463	33927	0.63	0.0E+00	AF227744.1	NT	Homo sapiens voltage-dependent calcium channel alpha 1G subunit isoform aa (CA1GNA1G) mRNA, complete cds
7406	20484	33952	36.37	0.0E+00	AI128344.1	EST_HUMAN	q67a07.X1 Scores: placenta, 8tubweeks, 2NbhP8t69w Homo sapiens cDNA clone IMAGE:1714644 3' similar to SWARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR, contains element HGR
7408	20484	33963	36.37	0.0E+00	AI128344.1	EST_HUMAN	q67a07.X1 Scores: placenta, 8tubweeks, 2NbhP8t69w Homo sapiens cDNA clone IMAGE:1714644 3' similar to SWARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR, contains element HGR repetitive element:

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7408	20486	33955	0.74	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7408	20486	33956	0.74	0.0E+00	AF227135.1	NT	Homo sapiens candidate taste receptor T2R9 gene, complete cds
7410	20488	33958	5.41	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7410	20488	33959	5.41	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7413	20491		13.11	0.0E+00	BF337375.1	EST_HUMAN	602035089F.1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4182839 5'
7415	20493	33961	3.49	0.0E+00	AA128453.1	EST_HUMAN	zn6609.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562601 5' similar to TR:G806562
7420	20497	33967	0.77	0.0E+00	AL078437.1	EST_HUMAN	DKFZp434B0228.r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B0228 5'
7420	20497	33968	0.77	0.0E+00	AL078437.1	EST_HUMAN	DKFZp434B0228.r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434B0228 5'
7431	20508	33980	0.69	0.0E+00	AJ270936.1	NT	Homo sapiens partial mRNA for LTRPC5 protein (LTRPC5 gene)
7461	20536	34011	1.13	0.0E+00	BE295489.1	EST_HUMAN	601174576F.1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529794 5'
7463	20538	34012	0.91	0.0E+00	11427985	NT	Homo sapiens hypothetical protein (FLJ20261), mRNA
7466	20541		1.33	0.0E+00	AJ118607.1	EST_HUMAN	AJ118607 HEMBA1 Homo sapiens cDNA clone HEMBA1003669 5'
7467	20542	34015	1.71	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7479	20542	34016	1.71	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7479	20544	34026	0.83	0.0E+00	AF245505.1	NT	Homo sapiens adiccan mRNA, complete cds
7487	20582	34031	6.47	0.0E+00	X70172.1	NT	H. sapiens DNA for ZNGP2 pseudogene, exon 4
7489	20584	34033	5.81	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7489	20584	34034	5.81	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7502	20577	34049	0.89	0.0E+00	AW565903.1	EST_HUMAN	EST366973 IMAGE resequences, MAGD Homo sapiens cDNA
7604	20579	34051	2.31	0.0E+00	AW565916.1	EST_HUMAN	EST362586 IMAGE resequences, MAGA Homo sapiens cDNA
7631	20604	34078	1.03	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7631	20604	34079	1.03	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7631	20604	34080	1.03	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa,S.C.) Homo sapiens cDNA clone kappa_200
7652	20624		0.58	0.0E+00	M80354.1	NT	Human BTFR3 protein homologue gene, complete cds
7653	20625	34101	0.8	0.0E+00	BE408203.1	EST_HUMAN	601302679F.1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637434 5'
7660	20652		1.09	0.0E+00	R87430.1	EST_HUMAN	ym88410.r1 Soares adult brain N264H55V Homo sapiens cDNA clone IMAGE:166051 5'
7691	20653	34129	1.81	0.0E+00	AW23526.1	EST_HUMAN	kb398d5.y1 NCI_CGAP_Lu31 Homo sapiens cDNA clone IMAGE:2578640 5' similar to TR:Q08050 Q08050
7690	20670		1.5	0.0E+00	AJ117033.1	EST_HUMAN	HN93/FH TRANSCRIPTION FACTOR GENESIS :
7692	20672	34146	3.8	0.0E+00	11427135	NT	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA
7692	20692	34189	0.62	0.0E+00	AA211663.1	EST_HUMAN	zn5607.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gbX03740
7692	20698	34174	0.63	0.0E+00	BF229235.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN); MR0-AN0083-270900-004-07 AN0083 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7634	20703	34182	0.67	0.0E+00	AW405627.1	EST_HUMAN	U1-HF-BL0-abe-d-07-d-U1.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057469 5'
7641	20710	34189	0.8	0.0E+00	32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
7667	20733	34209	0.9	0.0E+00	BF306998.1	EST_HUMAN	601869823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7667	20733	34210	0.9	0.0E+00	BF306998.1	EST_HUMAN	601869823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7675	20740	34220	1.09	0.0E+00	AU18767.1	EST_HUMAN	AU18767 HEMBA1 Homo sapiens cDNA clone HEMBA1004314 5'
7733	20784	34281	4.41	0.0E+00	AI782561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH1TBC.cn17d05 random
7733	20784	34282	4.41	0.0E+00	AI782561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH1TBC.cn17d05 random
7768	20852	34344	0.8	0.0E+00	AL046347.2	EST_HUMAN	DKFZp434J087.t1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434J087 5'
7813	20868	34363	1.79	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7813	20868	34364	1.79	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7821	20876	34375	1.34	0.0E+00	U74315.1	EST_HUMAN	HSU74315 Human chromosome 14 Homo sapiens cDNA clone 1-4
7835	20890	34392	1	0.0E+00	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
7863	20917	34422	0.7	0.0E+00	AI825504.1	EST_HUMAN	wb17g05.x1 NCI_CGAP_GCS Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR:075363 075363 ABC1.1
7863	20917	34423	0.7	0.0E+00	AI825504.1	EST_HUMAN	wb17g05.x1 NCI_CGAP_GCS Homo sapiens cDNA clone IMAGE:2305976 3' similar to TR:075363 075363 ABC1.1
7871	20925	34432	1.84	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7871	20929	34435	0.88	0.0E+00	BF217806.1	EST_HUMAN	2286605.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:289456 3'
7881	20933	34438	6.1	0.0E+00	BF217806.1	EST_HUMAN	60186466F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103729 5'
7886	20938	34444	0.62	0.0E+00	BF668862.1	EST_HUMAN	802186808F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310256 5'
7891	20943	34449	3.62	0.0E+00	AU129622.1	EST_HUMAN	AU129622 NT2RP2 Homo sapiens cDNA clone NT2RP2006913 5'
7911	20955	34469	0.95	0.0E+00	AW069274.1	EST_HUMAN	ci42609.x1 Jila bone marrow stroma Homo sapiens cDNA clone HBMSC_ci42609 3'
7911	20955	34470	0.95	0.0E+00	AW069274.1	EST_HUMAN	ci42609.x1 Jila bone marrow stroma Homo sapiens cDNA clone HBMSC_ci42609 3'
7915	20968	34472	8.87	0.0E+00	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC), member 3 (ABCA3), mRNA
7922	20973	34478	0.92	0.0E+00	AV768487.1	EST_HUMAN	AV768487 BM Homo sapiens cDNA clone BMFBG305 5'
7924	20974	34480	5.78	0.0E+00	BE739670.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
7924	20974	34481	5.78	0.0E+00	BE739670.1	EST_HUMAN	601593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
7925	20975	34482	0.76	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7925	20976	34483	0.76	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; actin/b receptor interacting protein 1 (KIAA0705), mRNA
7926	20976	34484	1.05	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
7926	20978	34485	1.05	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000656 5'
7948	20998	34508	12.57	0.0E+00	BF590287.1	EST_HUMAN	nab22604.x1 Scores: NSF_f8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3263214 3' similar to contigs element TARI repetitive element;
7959	21009	34519	1.86	0.0E+00	BE187010.1	EST_HUMAN	601481713F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3894258 5'
7959	21009	34520	1.86	0.0E+00	BE187010.1	EST_HUMAN	601481713F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3894258 5'
7998	21048	34561	0.63	0.0E+00	Y18785.1	NT	Homo sapiens psbH1a pseudogene
7999	21049	34562	3.86	0.0E+00	AI348148.1	EST_HUMAN	q94305.x1 NCI_CGAP_C68 Homo sapiens cDNA clone IMAGE:1925783 3' similar to SW:EVX1_HUMAN
8001	21051	34564	0.68	0.0E+00	W52873.1	EST_HUMAN	P49940 HOMEOBOX_EVEN-SKIPPED HOMOLOG PROTEIN 1;
8002	21052	34565	0.58	0.0E+00	11426128	NT	z60070.01 Pancreatic islet Homo sapiens cDNA clone IMAGE:338443 5'
8003	21053	34566	0.59	0.0E+00	AU117333.1	EST_HUMAN	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
8004	21054		0.57	0.0E+00	BE613363.1	EST_HUMAN	AU117333 HEMBAT1 Homo sapiens cDNA clone HEMBAT1001175 5'
8018	21089	34580	0.73	0.0E+00	6995985	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8018	21089	34581	0.73	0.0E+00	6995985	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
8037	21120	34940	0.49	0.0E+00	AU133187.1	EST_HUMAN	AU133187 NT2RP4 Homo sapiens cDNA clone NT2RP4001507 5'
8038	21185		0.69	0.0E+00	BF217200.1	EST_HUMAN	601885317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103893 5'
8038	21178	34595	0.61	0.0E+00	BE313013.1	EST_HUMAN	601150347F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503050 5'
8108	21180	34710	1.36	0.0E+00	AA148781.1	EST_HUMAN	z601608.11 Stratiogene colon (R337204) Homo sapiens cDNA clone IMAGE:366410 5'
8121	21203	34724	0.72	0.0E+00	BF026828.1	EST_HUMAN	601872310F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3855131 5'
8136	21217	34738	0.55	0.0E+00	AA017021.1	EST_HUMAN	z603108.11 Soares retina N2b-4HR Homo sapiens cDNA clone IMAGE:360831 5'
8153	21235	34756	2.08	0.0E+00	BE136046.1	EST_HUMAN	601305658F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639903 5'
8170	21252	34772	3.18	0.0E+00	MS4872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
8170	21252	34773	3.18	0.0E+00	MS4872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
8200	21282	34804	0.56	0.0E+00	AW674581.1	EST_HUMAN	bs34402.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2885123 5' similar to TR:064652 064652
8200	21282	34805	0.56	0.0E+00	AW674581.1	EST_HUMAN	bs34402.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2885123 5' similar to TR:064652 064652
8207	21289	34811	2.07	0.0E+00	AA397551.1	EST_HUMAN	z615004.T1 Stratiogene schizob brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8209	21291	34812	0.86	0.0E+00	AW387131.1	EST_HUMAN	MR0-ST0031-081089-003-811 ST0031 Homo sapiens cDNA
8212	21294		0.64	0.0E+00	AB020691.1	NT	Homo sapiens mRNA for KIAA0884 protein, partial cds
8213	21295	34814	6.15	0.0E+00	AU142402.1	EST_HUMAN	AU142402 Y78A.1 Homo sapiens cDNA clone Y78A.1000277 5'
8216	21298	34818	0.86	0.0E+00	BE388421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
8216	21298	34819	0.86	0.0E+00	BE388421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
8231	21313	34833	0.59	0.0E+00	7667276	NT	Homo sapiens killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 (KIR2DS1), mRNA
8233	21315	34835	0.84	0.0E+00	W95278.1	EST_HUMAN	Z60501.1 Scores: fetal_huact_NbHH19W Homo sapiens cDNA clone IMAGE:358081 5'
8233	21315	34836	0.84	0.0E+00	W95278.1	EST_HUMAN	Z60501.1 Scores: fetal_huact_NbHH19W Homo sapiens cDNA clone IMAGE:358081 5'
8235	21317		4.11	0.0E+00	BF873098.1	EST_HUMAN	602133008F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294128 5'
8239	21321		0.83	0.0E+00	AU134114.1	EST_HUMAN	AU134114 OVARC1 Homo sapiens cDNA clone OVARC1001286 5'
8253	21335	34853	0.85	0.0E+00	BF628634.1	EST_HUMAN	602068632F1 NCJ_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4212727 5'
8253	21335	34854	0.85	0.0E+00	BF628634.1	EST_HUMAN	602068632F1 NCJ_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4212727 5'
8285	21367	34886	1.35	0.0E+00	AL120124.1	EST_HUMAN	DKFZP761P092.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZP761P092 5'
8285	21367	34887	1.35	0.0E+00	AL120124.1	EST_HUMAN	DKFZP761P092.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZP761P092 5'
8328	21410		1.16	0.0E+00	BE877693.1	EST_HUMAN	U-HF-BND-44-401-0-UJ.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077486 5'
8351	21432	34956	1.27	0.0E+00	AW500549.1	EST_HUMAN	U-HF-BND-44-401-0-UJ.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077486 5'
8359	21440	34982	14.12	0.0E+00	AW157233.1	EST_HUMAN	TR060463 O60463 TYPE 2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE, [1]:
8376	21457	34981	0.68	0.0E+00	AW072395.1	EST_HUMAN	TR060463 O60463 TYPE 2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE, [1]:
8394	21475	35002	1.11	0.0E+00	11421722	NT	element OFR repetitive element:
8397	21478	35005	0.57	0.0E+00	W01616.1	EST_HUMAN	element OFR repetitive element:
8399	21480	35007	1.3	0.0E+00	BE745597.1	EST_HUMAN	Homo sapiens centrosomal protein 2 (CEP2), mRNA
8399	21480	35008	1.3	0.0E+00	BE745597.1	EST_HUMAN	601578186F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3826988 5'
8411	21492	35022	1.13	0.0E+00	AJ271735.1	NT	601578186F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3826988 5'
8431	21512	35043	0.46	0.0E+00	D49032.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
8450	21531	35060	0.53	0.0E+00	A1367330.1	EST_HUMAN	Human DNA for centropseudin, exon 5
8462	21543	35073	2.23	0.0E+00	BE674157.1	EST_HUMAN	q985c12.x1 NCJ_CGAP_U12 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14673 KIAA0164 PROTEIN, ;
8464	21545	35075	1.96	0.0E+00	A1885871.1	EST_HUMAN	7d76804.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278862 3' similar to TR:O56783 O56783 STAUFEN PROTEIN, ;
8477	21558	35091	1.47	0.0E+00	BE68680.1	EST_HUMAN	w60b10.x1 NCJ_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2429275 3' similar to TR:O56783 O56783 STAUFEN PROTEIN, ;

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8477	21658	35092	1.47	0.0E+00	BE563650.1	EST_HUMAN	601334/790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3888655 5'
8483	21568	35102	1.72	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8485	21566	35103	1.72	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8497	21568	35105	0.84	0.0E+00	AA403192.1	EST_HUMAN	z66502.t1 Soares, total, fetus, NB2H-F9_9w Homo sapiens cDNA clone IMAGE:738619 5' similar to TR.G1304132 G1304132 TPRD. ;
8497	21568	35106	0.84	0.0E+00	AA403192.1	EST_HUMAN	z66502.t1 Soares, total, fetus, NB2H-F9_9w Homo sapiens cDNA clone IMAGE:738619 5' similar to TR.G1304132 G1304132 TPRD. ;
8528	21609		3.61	0.0E+00	AA398511.1	EST_HUMAN	z73a08.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:727958 3' similar to gb:585655
8537	21618	35165	0.5	0.0E+00	BE837533.1	EST_HUMAN	RC2-FN0094-120600-013-h07 FN0094 Homo sapiens cDNA
8538	21619	35166	1.34	0.0E+00	AW364374.1	EST_HUMAN	QV3-DT0045-221289-046-c07 DT0045 Homo sapiens cDNA
8538	21619	35167	1.34	0.0E+00	AW364374.1	EST_HUMAN	QV3-DT0045-221289-046-c07 DT0045 Homo sapiens cDNA
8557	21638	35176	1.24	0.0E+00	BE612386.1	EST_HUMAN	601452412F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3856179 5'
8557	21638	35177	1.24	0.0E+00	BE612386.1	EST_HUMAN	601452412F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3856179 5'
8572	21653	35194	1.16	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8572	21653	35195	1.16	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8581	21662	35202	0.93	0.0E+00	A1884477.1	EST_HUMAN	wnt3a11.x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE:2437724 3' similar to TR.O75457 075457
8588	21660	35208	0.71	0.0E+00	AA502294.1	EST_HUMAN	me25d10.s1 NCI CGAP_C03 Homo sapiens cDNA clone IMAGE:882269 3' similar to TR.G1139434
8601	21682	35220	0.52	0.0E+00	11446769	NT	G1139434 KIAA0187 PROTEIN. ;
8604	21685		2.08	0.0E+00	BE890797.1	EST_HUMAN	Homo sapiens proteoglycan beta 3 (PCDH3), mRNA
8630	21710	35246	0.61	0.0E+00	AW245765.1	EST_HUMAN	160411.x1 Soares, pregnant, uterus, NBHPU Homo sapiens cDNA clone IMAGE:2043117 3'
8630	21710	35247	0.61	0.0E+00	AW245765.1	EST_HUMAN	601431238F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916569 5'
8631	21711	35248	2.13	0.0E+00		EST_HUMAN	2822701.Sprintr NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
8631	21711	35249	2.13	0.0E+00		EST_HUMAN	2822701.Sprintr NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
8631	21711	35249	2.13	0.0E+00	4788895	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8635	21715	35252	0.61	0.0E+00	U88084.1	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8635	21715	35253	0.61	0.0E+00	U88084.1	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8637	21777	35308	0.48	0.0E+00	U84744.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8704	21784	35317	0.7	0.0E+00	AJ251750.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST), mRNA, complete cde
8709	21789	35323	2.81	0.0E+00	X88622.1	NT	Homo sapiens NESP55, GNA51 antisense (partial) and Xlaphas (partial) genes
8709	21789	35324	2.81	0.0E+00	X88622.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8709	21789	35325	2.81	0.0E+00	X88622.1	NT	H. sapiens mRNA for gamma-glutamyltransferase

Single Exon Probes Expressed in Placenta

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8723	21803	35339	0.76	0.0E+00	U82978.1	NT	Human immunoglobulin-like transcrip-3 mRNA, complete cds
8765	21844	35385	0.81	0.0E+00	AF022655.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8765	21844	35386	0.81	0.0E+00	AF022655.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8768	21847	35388	0.87	0.0E+00	AU131671.1	EST_HUMAN	AU131671 NT2R3 Homo sapiens cDNA clone NT2R3003016 5'
8784	21863	35406	0.64	0.0E+00	11428572	NT	Homo sapiens immunoglobulin superfamily, member 2 (IGSF2), mRNA
8788	21867		1.35	0.0E+00	AW813313.1	EST_HUMAN	cds601.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:270332 3' similar to gb:M14123_cds4
8790	21869		0.54	0.0E+00	BE783232.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN (HUMAN):
8791	21870	35409	1.62	0.0E+00	D52650.1	EST_HUMAN	HUM084C02B Clontech human fetal brain poly+ mRNA (#6535) Homo sapiens cDNA clone GEN-084C02 5'
8823	21902	35442	4.15	0.0E+00	BE378456.1	EST_HUMAN	601236488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608709 5'
8928	21908	35446	2.16	0.0E+00	AA410646.1	EST_HUMAN	232604.1 Scars ovary tumor NBH01 Homo sapiens cDNA clone IMAGE:724082 5'
8831	21910		1.35	0.0E+00	BF313948.1	EST_HUMAN	601800571F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129744 5'
8838	21917	35455	0.54	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (IL1RB3), mRNA
8843	21922	35460	1.41	0.0E+00	AW138873.1	EST_HUMAN	U14811-act-e-12-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717887 3'
8843	21922	35461	1.41	0.0E+00	AW138873.1	EST_HUMAN	U14811-act-e-12-0-U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717887 3'
8878	21958	35483	2.18	0.0E+00	BE260272.1	EST_HUMAN	601150051F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3502836 5'
8884	21963	35487	2.91	0.0E+00	BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
8884	21963	35488	2.91	0.0E+00	BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
8884	21963	35489	2.91	0.0E+00	BF700165.1	EST_HUMAN	602127664F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
8923	22002	35541	0.84	0.0E+00	AL446770.1	EST_HUMAN	AL449770 Homo sapiens fetal brain (Stanfides GS) Homo sapiens cDNA
8930	22008	35547	3.69	0.0E+00	AA86227.1	EST_HUMAN	088002.s1 NCL_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1602194 3' similar to gb:M36072 60S
8938	22015	35555	3.41	0.0E+00	10947037	NT	RIBOSOMAL PROTEIN L7A (HUMAN):
8938	22015	35556	3.41	0.0E+00	10947037	NT	Homo sapiens ankryrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
8961	22040	35583	1.63	0.0E+00	Y11107.3	NT	Homo sapiens ankryrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
8963	22042	35585	1.08	0.0E+00	BE278912.1	EST_HUMAN	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
8973	22052		2.86	0.0E+00	AV718377.1	EST_HUMAN	601156330F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139734 5'
8980	22059	35600	3.12	0.0E+00	AW337277.1	EST_HUMAN	AV718377 FHTB Homo sapiens cDNA clone FHTBA4F1 5'
8986	22065	35605	1.59	0.0E+00	AU124051.1	EST_HUMAN	kw73607.x1 NCL_CGAP_Pant Homo sapiens cDNA clone IMAGE:2833644 3' similar to gb:X53587
9063	22142	35687	0.98	0.0E+00	AU140704.1	EST_HUMAN	INTTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN):
9073	22152	35686	0.64	0.0E+00	AB007923.1	NT	AU140704 PLACE4 Homo sapiens cDNA clone PLACE4000089 5'

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6078	22157	35700	0.68	0.0E+00	R17132.1	EST_HUMAN	y009609.1 Soares infant brain 11NB Homo sapiens cDNA clone IMAGE:31674.5'
6078	22157	35701	0.68	0.0E+00	R17132.1	EST_HUMAN	y009609.1 Soares infant brain 11NB Homo sapiens cDNA clone IMAGE:31874.5'
6082	22161	35703	4.78	0.0E+00	AW692233.1	EST_HUMAN	h48a09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2935096.3'
6082	22161	35704	4.78	0.0E+00	AW692233.1	EST_HUMAN	h48a09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2936096.3'
6129	22208	35761	0.93	0.0E+00	AV174764.1	EST_HUMAN	AV174764 DCB Homo sapiens cDNA clone DCBAUA06.5'
6145	22224	35766	3.17	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1814.3'
6145	22224	35767	3.17	0.0E+00	AL040428.1	EST_HUMAN	DKFZp434C1814_s1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C1814.3'
6151	22229	36773	1.32	0.0E+00	AF133901.1	NT	Homo sapiens killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
6153	22231	35776	2.12	0.0E+00	AB040545.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
6161	22239		0.61	0.0E+00	BF056289.1	EST_HUMAN	S GAG ;
6161	22269	35808	2.79	0.0E+00	11422867	NT	Homo sapiens tumor protein p73 (TP73), mRNA
6201	22279	35818	1.59	0.0E+00	K01241.1	NT	Human Ig rearranged H-chain epsilon-3 pseudogene, constant region
6209	22287	35828	5.28	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
6209	22287	35829	5.28	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
6214	22292	35835	1.84	0.0E+00	AV680739.1	EST_HUMAN	AV680739 GIC Homo sapiens cDNA clone GICGK12.3'
6220	22298	35841	3.41	0.0E+00	7706638	NT	Homo sapiens polycystin-L (PKDL), mRNA
6226	22303	35846	0.6	0.0E+00	BE783326.1	EST_HUMAN	601688304F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942553.5'
6246	22323	35867	4.22	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740.5'
6246	22323	35868	4.22	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140740.5'
6256	22333	35883	0.6	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3850100.5'
6256	22333	35884	0.6	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3850100.5'
6259	22336		0.64	0.0E+00	M89896.1	NT	Human polymorphic loci in Xq28
6261	22338	35888	1.65	0.0E+00	X14706.1	NT	Human mRNA for GABA-A receptor, alpha 1 subunit
6279	22355	35905	0.53	0.0E+00	AU127096.1	EST_HUMAN	AU127096 NT2RP2 Homo sapiens cDNA clone NT2RP200579.5'
6283	22359	35909	0.83	0.0E+00	A061335.1	EST_HUMAN	an28a04.x1 Gassler Wilms tumor Homo sapiens cDNA clone IMAGE:2473150.3' similar to SW:MG83_HUMAN
6288	22364	35913	1.68	0.0E+00	A1954607.1	EST_HUMAN	wg34612X1 NCI CGAP_G66 Homo sapiens cDNA clone IMAGE:2473150.3' similar to SW:MG83_HUMAN
6293	22369	35919	5.69	0.0E+00	9256595	NT	O15480 MELANOMA-ASSOCIATED ANTIGEN B3 ;
6303	22379	35930	2.73	0.0E+00	AW693311.1	EST_HUMAN	Homo sapiens proteasome alpha 8 (PCDH8), mRNA
6313	22389	35940	1.32	0.0E+00	9635487	NT	EST370361 IMAGE ressequences, IMAGE Homo sapiens cDNA
6326	22404	35956	0.64	0.0E+00	AU142662.1	EST_HUMAN	Human endogenous retrovirus, complete genome
6344	22420	35974	1.04	0.0E+00	11436995	NT	AU142662 Y79AA1 Homo sapiens cDNA clone Y79AA1000678.5'
							Homo sapiens MAP-kinase activating death domain (MADD), mRNA

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8345	22421		0.78	0.0E+00	BE410738.1	EST_HUMAN	601301876F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636183 5'
8359	22434	35993	1.32	0.0E+00	BF002024.1	EST_HUMAN	797h12x1 NC1 CGAP Co18 Homo sapiens cDNA clone IMAGE:3314471 3' similar to TR:O8UH62
8373	22448	36009	1.82	0.0E+00	AB011150.1	NT	Q0UH62 HYPOTHETICAL 42.5 KD PROTEIN. ;
8374	22449	36010	3.42	0.0E+00	BE1764823.1	EST_HUMAN	Homo sapiens mRNA for KIAA0578 protein, partial cds
8376	22453	36016	0.47	0.0E+00	BE810292.1	EST_HUMAN	RC3_P10161-280600-011-c05 P10151 Homo sapiens cDNA
8378	22453	36018	0.47	0.0E+00	BE810292.1	EST_HUMAN	RC3_P10151-280600-011-c05 P10151 Homo sapiens cDNA
8381	22456	36019	0.87	0.0E+00	AU138228.1	EST_HUMAN	AU138228 PLACE1 Homo sapiens cDNA clone PLACE1003804 5'
8386	22481	36024	1.19	0.0E+00	BE883943.1	EST_HUMAN	601510247F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:3911986 5'
8403	22477	36040	1.19	0.0E+00	BE883943.1	EST_HUMAN	601510247F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:3911986 5'
8407	22481	36044	1.43	0.0E+00	AA344601.1	EST_HUMAN	Homo sapiens mRNA for KIAA0594 protein, partial cds
8407	22481	39049	1.43	0.0E+00	AA344601.1	EST_HUMAN	EST150565 Gall Bladder 1 Homo sapiens cDNA 5' end
8464	22521	36083	0.96	0.0E+00	AW673469.1	EST_HUMAN	b654d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800367 5' similar to TR:O80275 O60275
8464	22521	36084	0.96	0.0E+00	AW673469.1	EST_HUMAN	KIAA0522 PROTEIN ;
8498	22534	39116	0.99	0.0E+00	BE207063.1	EST_HUMAN	b654d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800367 5' similar to TR:O80275 O60275
8498	22534	39117	0.99	0.0E+00	BE207063.1	EST_HUMAN	KIAA0522 PROTEIN ;
8509	22716	36346	1.95	0.0E+00	BF348013.1	EST_HUMAN	b609f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb135049 Mus musculus
8545	22810	36178	3.1	0.0E+00	BE172615.1	EST_HUMAN	b609f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb135049 Mus musculus
8577	22718	36287	0.49	0.0E+00	BF034377.1	EST_HUMAN	B6-XL mRNA, complete cds (MOUSE);
8583	22725	36285	0.56	0.0E+00	AF903651.1	EST_HUMAN	B6-XL mRNA, complete cds (MOUSE);
8586	22728	36287	0.77	0.0E+00	6803068	NT	b609f05.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb135049 Mus musculus
8586	22728	36288	0.77	0.0E+00	6803069	NT	B6-XL mRNA, complete cds (MOUSE);
8586	22651	36223	0.85	0.0E+00	AL042276.1	EST_HUMAN	QV2-HT0688-250700-282-h08 H10688 Homo sapiens cDNA
8631	22886	36257	1.3	0.0E+00	AI068043.1	EST_HUMAN	601455116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859035 5'
8638	21081	34592	0.67	0.0E+00	BF309682.1	EST_HUMAN	601455116F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859035 5'

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Table 4  
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9840	21083	34595	2.32	0.0E+00	J1560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504). mRNA
9840	21083	34598	2.32	0.0E+00	J1560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504). mRNA
9842	21085	34589	6.52	0.0E+00	A1290909.1	EST_HUMAN	qim09a08.x1 NC_CGAP_L165 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW-RL2B_HUMAN
9842	21085	34600	6.52	0.0E+00	A1290909.1	EST_HUMAN	qim09a08.x1 NC_CGAP_L165 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW-RL2B_HUMAN
9843	21086	34601	2.16	0.0E+00	AW563938.1	EST_HUMAN	EST366028 MAGC resequences, MAGC Homo sapiens cDNA
9870	22632	36201	3.95	0.0E+00	AF153456.1	NT	Homo sapiens polyoma kidney disease 2 like protein (PKD2L) gene, exon 8
9873	22635	36205	0.69	0.0E+00	BE885128.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
9873	22635	36206	0.69	0.0E+00	BE885128.1	EST_HUMAN	601510882F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912165 5'
9883	22732	36305	5.87	0.0E+00	BE255829.1	EST_HUMAN	60109942F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350722 5'
9886	22735	36306	1.44	0.0E+00	BE781392.1	EST_HUMAN	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
9886	22735	36306	1.44	0.0E+00	BE781392.1	EST_HUMAN	601466828F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870007 5'
9888	22737	36307	5.46	0.0E+00	AW183779.1	EST_HUMAN	aub8c04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gb-M36072
9897	22746	36315	0.68	0.0E+00	DB7675.1	NT	60S RIBOSOMAL PROTEIN L7A (HUMAN);
9709	22758	36329	3.41	0.0E+00	BE263191.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
9727	22792	36364	4.49	0.0E+00	C08158.1	EST_HUMAN	601145064F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160477 5'
9727	22792	36365	4.46	0.0E+00	C08158.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9729	22794	36368	3.38	0.0E+00	BE746215.1	EST_HUMAN	C06158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9739	22804	36378	2.03	0.0E+00	11437282	NT	601578683F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5'
9739	22804	36379	2.03	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9). mRNA
9739	22804	36380	2.03	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9). mRNA
9759	22697	36265	1.91	0.0E+00	BE900549.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9). mRNA
9776	22816	36394	1.5	0.0E+00	AV701829.1	EST_HUMAN	601673425F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956238 5'
9788	22828	36405	2.55	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
9788	22828	36406	2.55	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
9821	22861	36442	1.13	0.0E+00	BE082977.1	EST_HUMAN	RC2-817094Z-130300-017-g01 BT0942 Homo sapiens cDNA
9841	22881	36484	1.72	0.0E+00	AW500283.1	EST_HUMAN	UI-HF-BND-46g-b-120-JU17 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9841	22881	36485	1.72	0.0E+00	AW500283.1	EST_HUMAN	UI-HF-BND-46g-b-120-JU17 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9850	22880	36470	1.87	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
9860	22890	36471	1.87	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession Id.	Top Hit Database Source	Top Hit Descriptor
9852	22892	36472	0.62	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
9852	22892	36473	0.62	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
9861	22801	36485	0.63	0.0E+00	W56626.1	EST_HUMAN	zdf661.1.1 Soares fetal heart NBH19W Homo sapiens cDNA clone IMAGE:340844 5'
9861	22801	36486	0.63	0.0E+00	W56626.1	EST_HUMAN	zdf661.1.1 Soares fetal heart NBH19W Homo sapiens cDNA clone IMAGE:340844 5'
9874	22914	36489	0.46	0.0E+00	AF208034.1	NT	Homo sapiens non-inhibitory killer-cell Ig-like receptor KIR (KIR2DS9) mRNA, complete cds
9876	22916	36500	1.04	0.0E+00	AB035356.1	NT	Homo sapiens mRNA for reusced L-alpha protein, complete cds
9878	22919	36509	0.64	0.0E+00	AU124760.1	EST_HUMAN	am56a11.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1639548 3'
9881	22921	36509	3	0.0E+00	AW500326.1	EST_HUMAN	U-HF-BND-af-c-07-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:307364 5'
9925	22965	36564	2.68	0.0E+00	AE009838.1	NT	Multiple sclerosis associated retrovirus polyprotein (ppl) mRNA, partial cds
9953	22992	36585	2.69	0.0E+00	S78468.1	NT	ALGF=androgen-induced growth factor ALGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9953	22992	36589	2.69	0.0E+00	S78468.1	NT	ALGF=androgen-induced growth factor ALGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9956	22995	36591	2.72	0.0E+00	BE563320.1	EST_HUMAN	601334603F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3686860 5'
9976	23015	36608	1.26	0.0E+00	AW363135.1	EST_HUMAN	GM2-CT0311-301189-043-h11 CT0311 Homo sapiens cDNA
9997	23035	36627	0.66	0.0E+00	11436432	NT	Homo sapiens multimerin (MMRN) mRNA
9998	23036	36628	0.62	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and TIM domain), member 3 (LILRB3) mRNA
10007	23045	36638	0.91	0.0E+00	BE206710.1	EST_HUMAN	b528c01.x1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:2984000 3'
10024	23062	36658	4.49	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10024	23062	36659	4.49	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10033	23071	36671	0.95	0.0E+00	AW500336.1	EST_HUMAN	U-HF-BF-Dp-af-c-05-0-UI.1 NIH_MGC_31 Homo sapiens cDNA clone IMAGE:3072897 5'
10039	23077	36677	13.26	0.0E+00	BE740430.1	EST_HUMAN	601508558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
10039	23077	36678	13.26	0.0E+00	BE740430.1	EST_HUMAN	601508558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
10052	23080	36682	1.56	0.0E+00	7682087	NT	Homo sapiens KIAA0345 gene product (KIAA0345) mRNA
10069	23107	36710	1.54	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434L0120 5'
10074	23112	36716	0.57	0.0E+00	AL041094.2	EST_HUMAN	DKFZp434B2416.1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434B2416 5'
10084	23122	36723	2.32	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
10085	23123	36724	2.16	0.0E+00	AF162308.1	NT	Homo sapiens protodactherin alpha 12 (PCDH-alpha12) mRNA, complete cds
10112	23150	36731	2.84	0.0E+00	AF008220.1	NT	Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds
10112	23150	36732	2.84	0.0E+00	AF008220.1	NT	Homo sapiens leucocyte immunoglobulin-like receptor-1 mRNA, complete cds
10128	23168	36765	1.13	0.0E+00	BF092888.1	EST_HUMAN	MR4-TN0114-110900-101-604 TN0114 Homo sapiens cDNA
10160	23197	36793	2.76	0.0E+00	BE280733.1	EST_HUMAN	601165227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138798 5'
10169	23206	36799	6.57	0.0E+00	BE388700.1	EST_HUMAN	601296331F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10169	23206	36800	6.57	0.0E+00	BE388730.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
10178	23215	36806	0.87	0.0E+00	AW236269.1	EST_HUMAN	xn72b01.x1 NC1_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2698977 3' similar to gb:X02152_cds1 L-
10179	23216	36807	0.84	0.0E+00	AA341305.1	EST_HUMAN	LACTATE DEHYDROGENASE M CHAIN (HUMAN);
10188	23225	36819	0.69	0.0E+00	J1427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
10208	23244	36834	0.94	0.0E+00	AW694113.1	EST_HUMAN	EST376186 MAGC resequences, MAGH Homo sapiens cDNA
10222	23258	36845	5.99	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 6'
10222	23258	36845	6.89	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
10225	23261	36849	3.31	0.0E+00	AF072428.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
10228	23263	36851	2.75	0.0E+00	J1421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
10228	23263	36852	2.76	0.0E+00	J1421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
10261	23296	36894	3.07	0.0E+00	AU136637.1	EST_HUMAN	AUT36637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
10261	23296	36895	3.07	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
10277	23312	36909	2	0.0E+00	AJ295814.1	NT	Homo sapiens partial RANBP7 gene for RANBP7limpoin7 and partial ZNF143 gene
10277	23312	36910	2	0.0E+00	AJ295814.1	NT	Homo sapiens partial RANBP7 gene for RANBP7limpoin7 and partial ZNF143 gene
10282	23317	36917	0.73	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GKCC Homo sapiens cDNA clone GKCDXA07 5'
10282	23317	36918	0.73	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GKCC Homo sapiens cDNA clone GKCDXA07 5'
10288	23323	36925	0.72	0.0E+00	AF072408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
10288	23323	36928	2.42	0.0E+00	AA1196397.1	EST_HUMAN	z997h11.1 Stratiogene muscle 837208 Homo sapiens cDNA clone IMAGE:628197 5'
10317	23352	36959	0.76	0.0E+00	AA1131248.1	EST_HUMAN	Z3101.11 Soares_pregnant. uterus_NbHPU Homo sapiens cDNA clone IMAGE:303545 5'
10317	23352	36960	0.76	0.0E+00	AA1131248.1	EST_HUMAN	Z3101.11 Soares_pregnant. uterus_NbHPU Homo sapiens cDNA clone IMAGE:303545 5'
10359	23384	37005	1.91	0.0E+00	AF178308.1	NT	Homo sapiens KIF4 (KIF4) mRNA, complete cds
10404	23439	37046	0.99	0.0E+00	BE880658.1	EST_HUMAN	601491555F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893657 5'
10417	23452	37057	5.34	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10417	23452	37058	5.34	0.0E+00	BE730772.1	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10422	23457	37062	0.8	0.0E+00	AU1212403.1	EST_HUMAN	AU127403 NT2RP2 Homo sapiens cDNA clone NT2RP2001212 5'
10432	23487	37073	0.89	0.0E+00	BE855511.1	EST_HUMAN	601645134F1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3930177 5'
10432	23487	37074	0.89	0.0E+00	BE855511.1	EST_HUMAN	601645134F1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3930177 5'
10450	23485	37084	0.48	0.0E+00	BE891497.1	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
10450	23485	37087	0.91	0.0E+00	AA311624.1	EST_HUMAN	EST182353 Jurkat T-cells VI Homo sapiens cDNA 5' end
10461	23496	37108	0.65	0.0E+00	4758927	NT	Homo sapiens neuraxn III (NRXN3) mRNA
10473	23508	37121	0.64	0.0E+00	BE891113.1	EST_HUMAN	601432228F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917598 5'
10473	23510	37123	0.77	0.0E+00	J11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10486	23521	37130	1.66	0.0E+00	AB029290.1	NT	Homo sapiens mRNA for ecclin binding protein ABP620, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10487	23522	37131	0.6	0.0E+00	BE304E22.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887918 5'
10487	23522	37132	0.6	0.0E+00	BE304E22.1	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2887918 5'
10484	23528	37137	5.8	0.0E+00	AB008E90.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10484	23528	37138	5.8	0.0E+00	AB008E90.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10502	23537	37147	0.77	0.0E+00	AA704457.1	EST_HUMAN	Z19B06.s1 Soares fetal liver spleen INFLS_S1 Homo sapiens cDNA clone IMAGE:450707 3' similar to gb:M41423_cds1 RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN);
10504	23539	37148	1.08	0.0E+00	M22921.1	NT	Human beta 1,4-galactosyl-transferase mRNA, complete cds
10506	23541	37151	4.81	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4184939 5'
10506	23541	37152	4.81	0.0E+00	BF340331.1	EST_HUMAN	602037045F1 NCI_CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4184939 5'
10530	23565	37172	0.59	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10530	23565	37173	0.59	0.0E+00	BE897149.1	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10595	23590	37237	1.07	0.0E+00	AB631818.1	EST_HUMAN	wa36903.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TRQ61204
10595	23590	37238	1.07	0.0E+00	AB631818.1	EST_HUMAN	wa36903.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TRQ61204
10595	23590	37238	1.07	0.0E+00	AB631818.1	EST_HUMAN	wa36903.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TRQ61204
10610	23544	37252	1.64	0.0E+00	T03078.1	EST_HUMAN	FB23A4 Fetal brain, Striatum Homo sapiens cDNA clone FB23A4 3' end
10638	23672	37282	0.67	0.0E+00	AU122428.1	EST_HUMAN	AU122429 MAMMA1 Homo sapiens cDNA clone MAMMA1002368 5'
10644	23678	37288	0.48	0.0E+00	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
10668	23702	37312	2.22	0.0E+00	BF436218.1	EST_HUMAN	nab46912.x1 Soares NSF_F8_9W_O1_PA_P_S1 Homo sapiens cDNA clone IMAGE:3265271 3'
10669	23703		1.71	0.0E+00	AB654786.1	EST_HUMAN	AV654765 GLO Homo sapiens cDNA clone GLOCDZ07 3'
10689	23722	37328	3.08	0.0E+00	AB571360.1	EST_HUMAN	XU74001.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2807401 3' similar to gb:U69066 MOESIN (HUMAN);
10693	23726	37332	2.88	0.0E+00	BE548213.1	EST_HUMAN	601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464703 5'
10709	23742	37348	0.82	0.0E+00	11436005	NT	Homo sapiens hypothetical protein DKFZp761p1010 (DKFZp761p1010), mRNA
10735	23768	37378	0.52	0.0E+00	X89893.1	NT	H. sapiens mRNA for NK receptor (183 Act1)
10738	23769	37379	3.36	0.0E+00	BE181742.1	EST_HUMAN	601467419F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3870700 5'
10758	23781	37409	2.32	0.0E+00	BE082720.1	EST_HUMAN	RC2-B10642-150200-012-d03 BT0642 Homo sapiens cDNA
10758	23781	37410	2.32	0.0E+00	BE082720.1	EST_HUMAN	RC2-B10642-150200-012-d03 BT0642 Homo sapiens cDNA
10784	23797	37417	0.57	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR Us and gag gene
10772	23805	37428	0.77	0.0E+00	BE143215.1	EST_HUMAN	BF54607.x1 NCI_CGAP_G66 Homo sapiens cDNA clone IMAGE:2244612 3'
10779	23812	37436	8.15	0.0E+00	BE143215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835188 5'
10784	23817	37439	0.83	0.0E+00	BE17655.1	EST_HUMAN	601441723T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3845956 3'
10784	23817	37440	0.83	0.0E+00	BE17655.1	EST_HUMAN	601441723T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3845956 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10786	23819	37442	0.46	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10786	23819	37443	0.46	0.0E+00	AB006590.1	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10809	23842	37465	0.51	0.0E+00	H39805.1	EST_HUMAN	h01a10.r1 Soares breast 3NHBst Homo sapiens cDNA IMAGE:186138 5'
10835	23859	37491	0.54	0.0E+00	DB7675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10846	23879	37499	0.69	0.0E+00	BE392276.1	EST_HUMAN	601308167r1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3928128 5'
10863	23866	37519	0.62	0.0E+00	AU126896.1	EST_HUMAN	AU125886 NT2RMA4 Homo sapiens cDNA clone NT2RMA4002536 5'
10872	23857	37588	1.84	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cl Homo sapiens cDNA clone CuAAK305 5'
10872	23857	37587	1.84	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cl Homo sapiens cDNA clone CuAAK305 5'
10874	23859	37595	2.55	0.0E+00	AW613783.1	EST_HUMAN	RC3-ST0197-120200-015-03 ST0197 Homo sapiens cDNA
10882	23866	37595	5.5	0.0E+00	AW963363.1	EST_HUMAN	EST375636 MAGE rasequences, MAGH Homo sapiens cDNA
10885	23879	37610	2.52	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10895	23879	37611	2.52	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10898	23882	37614	1.7	0.0E+00	AW057921.1	EST_HUMAN	TRQ60566 Q60566 VDX:
10906	23889	37621	8.59	0.0E+00	BE243270.1	EST_HUMAN	TCAP3D0817 Pediatric acute myelogenous leukemia cell (FAB M1) Bayle-HGSC project=TCAP
10907	23900	37622	2.72	0.0E+00	AB652239.1	EST_HUMAN	sapiens cDNA clone TCAP0917
10907	23900	37623	2.72	0.0E+00	AB652239.1	EST_HUMAN	MSR1 MSR1 repetitive element:
10912	23905	37628	1.48	0.0E+00	BE306642.1	EST_HUMAN	MSR1 MSR1 repetitive element:
10913	23906	37629	1.74	0.0E+00	BE372808.1	EST_HUMAN	601451502r1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3856289 5'
10913	23906	37630	1.74	0.0E+00	BE372808.1	EST_HUMAN	601451502r1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3856289 5'
10920	24003	37637	3.59	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10920	24003	37638	3.59	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10938	24018	37651	1.52	0.0E+00	AW404795.1	EST_HUMAN	U1-HF-BL0-acm-d-04-0-U1r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059385 5'
10940	24022	37656	2.85	0.0E+00	11424829	NT	Homo sapiens hypothetical protein FLJ20078 (FLJ20078), mRNA
10941	24023	37657	8.39	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E), mRNA
10942	24024	37659	2.68	0.0E+00	AA991827.1	EST_HUMAN	h01a10.r1 Soares breast 3NHBst Homo sapiens cDNA clone IMAGE:186138 5'
10946	24028	37665	3.22	0.0E+00	BE862109.1	EST_HUMAN	h01a10.r1 Soares breast 3NHBst Homo sapiens cDNA clone IMAGE:186138 5'
10952	24034	37668	1.55	0.0E+00	8823939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10952	24034	37669	1.55	0.0E+00	8823939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10865	24046	37680	22.14	0.0E+00	BE803304.1	EST_HUMAN	601674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957243 5'
10868	18087	32399	1.85	0.0E+00	AA169305.1	EST_HUMAN	7285b11.1 r1 Stragene muscle 837209 Homo sapiens cDNA clone IMAGE:627633 5' similar to gb:X03740
10890	24089	37703	4.49	0.0E+00	BE783498.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
10898	24077	37710	2.4	0.0E+00	BE729708.1	EST_HUMAN	601562864F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3932575 5'
10898	24077	37711	2.4	0.0E+00	BE729708.1	EST_HUMAN	601562864F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3932575 5'
10899	24078	37712	11.66	0.0E+00	AV727392.1	EST_HUMAN	AV727392 HTC Homo sapiens cDNA clone HTCAQH06 5'
10899	24078	37713	11.66	0.0E+00	AV727392.1	EST_HUMAN	AV727392 HTC Homo sapiens cDNA clone HTCAQH06 5'
11003	24082	37718	1.6	0.0E+00	R17132.1	EST_HUMAN	Y909e09.r1 Scars infant brain T1N18 Homo sapiens cDNA clone IMAGE:31674 5'
11003	24082	37719	1.6	0.0E+00	R17132.1	EST_HUMAN	Y909e09.r1 Scars infant brain T1N18 Homo sapiens cDNA clone IMAGE:31674 5'
11009	24088		2.62	0.0E+00	AW139414.1	EST_HUMAN	U1-H-B1-add-a-06-0-UI.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717674 3'
11014	24083	37732	11.81	0.0E+00	AW516058.1	EST_HUMAN	RY04g10.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2862226 3' similar to gb:M60854 40S
11020	24089	37737	4.44	0.0E+00	AU135741.1	EST_HUMAN	RIBOSOMAL PROTEIN S16 (HUMAN);
11026	24105	37741	2.66	0.0E+00	AW693833.1	EST_HUMAN	AU136741 PLAGE1 Homo sapiens cDNA clone PLAGE102764 5'
11026	24105	37742	2.66	0.0E+00	AW693833.1	EST_HUMAN	hg13402.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSRI1 repetitive element;
11026	24105	37743	2.66	0.0E+00	AW693833.1	EST_HUMAN	hg13402.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSRI1 repetitive element;
11028	24107	37744	1.87	0.0E+00	Z34897.1	EST_HUMAN	hg13402.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSRI1 repetitive element;
11029	24108	37745	2.76	0.0E+00	F13069.1	EST_HUMAN	HSC31C031 normalized infant brain cDNA Homo sapiens cDNA clone IMAGE:2736649 3'
11037	24116	37750	2.35	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
11054	24131	37767	1.71	0.0E+00	AV538094.1	EST_HUMAN	xw66b1.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832986 3' similar to gb:X17115 IG MJU
11055	24132	37768	3.75	0.0E+00	AW651230.1	EST_HUMAN	CHAIN C REGION (HUMAN);
11055	24132	37768	3.75	0.0E+00	AW651230.1	EST_HUMAN	U1-H-B18-alf-e-01-Q-UI.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
11055	24132	37769	3.75	0.0E+00	AW651230.1	EST_HUMAN	U1-H-B18-alf-e-01-Q-UI.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
11058	13443		9.52	0.0E+00	4508632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
11060	24136	37771	1.79	0.0E+00	AB014567.1	NT	Homo sapiens mRNA for KIAA0687 protein, partial cds
11073	24149	37787	1.92	0.0E+00	BE289499.1	EST_HUMAN	60118248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219 5'
11087	24161	37787	1.47	0.0E+00	AB01117.1	NT	Homo sapiens mRNA for KIAA0546 protein, partial cds
11082	24166	37803	1.39	0.0E+00	AA37505.1	EST_HUMAN	EST190347 Synovial sarcoma Homo sapiens cDNA 5' end similar to LERK-2, placenta
11106	24178	37813	3.3	0.0E+00	BE792155.1	EST_HUMAN	601582046F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936539 5'
11107	24179		76.9	0.0E+00	BF684091.1	EST_HUMAN	602141405F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302432 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit/Accession No.	Top Hit Database Source	Top Hit Descriptor
11108	24180	37814	1.45	0.0E+00	BE269238.1	EST_HUMAN	601186342F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544239 5'
11110	24182	37816	7.93	0.0E+00	AU118398.1	EST_HUMAN	AU118388 HEMBA1 Homo sapiens cDNA clone HEMBA1003486 5'
11111	24183		1.81	0.0E+00	AV236789.1	EST_HUMAN	3072B01.x1 NCI_CGAP_QAL1 Homo sapiens cDNA clone IMAGE:2699877 3' similar to gb:X02162_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN).
11118	24188	37820	6.71	0.0E+00	AU149809.1	EST_HUMAN	q43c03.x1 Soares_testis_JNHT Homo sapiens cDNA clone IMAGE:1732772 3'
11116	24188	37821	6.71	0.0E+00	AU149809.1	EST_HUMAN	q43c03.x1 Soares_testis_JNHT Homo sapiens cDNA clone IMAGE:1732772 3'
11117	24189	37822	2.63	0.0E+00	AV391837.1	EST_HUMAN	QV4-ST0234-121199-032-b08 ST0234 Homo sapiens cDNA
11127	24189		11.83	0.0E+00	AU116908.1	EST_HUMAN	AU116908 HEMBA1 Homo sapiens cDNA clone HEMBA1000255 5'
11130	24202	37827	8.67	0.0E+00	11424728	NT	Homo sapiens insulin receptor (INSR) mRNA
11132	24204	37828	2.14	0.0E+00	AB67350.1	EST_HUMAN	q95c12.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:1988334 3' similar to TRQ14673 Q14673 KIAA0164 PROTEIN.
11132	24204	37829	2.14	0.0E+00	AB67350.1	EST_HUMAN	q95c12.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:1988334 3' similar to TRQ14673 Q14673 KIAA0164 PROTEIN.
11137	24209	37835	1.63	0.0E+00	BF340308.1	EST_HUMAN	602037014F1 NCI_CGAP_Bird4 Homo sapiens cDNA clone IMAGE:4184978 5'
11139	24211	37837	13.91	0.0E+00	BE261208.1	EST_HUMAN	601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310 5'
11144	24216	37843	2.19	0.0E+00	AB028040.1	NT	Homo sapiens mRNA for KIAA1117 protein, partial cds
11147	24219	37846	1.51	0.0E+00	AB007832.1	NT	Homo sapiens mRNA for KIAA0463 protein, partial cds
11151	24222	37850	3.89	0.0E+00	U60328.1	NT	Human protein kinase C substrate 80K-41 (PRKCSH) gene, exon 15-17
11156	24226	37855	2.43	0.0E+00	BE773006.1	EST_HUMAN	RC1-F10134-170700-012407 F10134 Homo sapiens cDNA
11155	24226	37856	2.43	0.0E+00	BE773006.1	EST_HUMAN	RC1-F10134-170700-012407 F10134 Homo sapiens cDNA
11177	24246	37870	61.22	0.0E+00	AA740782.1	EST_HUMAN	0832607.81 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1326412 3' similar to contains element MSR1 repetitive element.
11186	24256	37890	2.81	0.0E+00	AB252303.1	NT	Homo sapiens signaling lymphocytic activation molecule (SLAM) gene, exon 2
11189	24268	37903	1.71	0.0E+00	BE266478.1	EST_HUMAN	601182748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535867 5'
11189	24268	37904	1.71	0.0E+00	BE266478.1	EST_HUMAN	601182748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535867 5'
11201	24270	37906	4.8	0.0E+00	CG0689.1	EST_HUMAN	CG05088 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone IMAGE:1309009 8'
11208	24277	37914	2.1	0.0E+00	AA746375.1	EST_HUMAN	0a56b01.t1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 8'
11208	24277	37915	2.1	0.0E+00	AA746375.1	EST_HUMAN	0a56b01.t1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 8'
11218	24287	37928	2.69	0.0E+00	MT8448.1	EST_HUMAN	EST100596 Fetal brain, Striatum (cat936206) Homo sapiens cDNA clone HFBCC26
11221	24290	37930	1.76	0.0E+00	BF333635.1	EST_HUMAN	QV2-H10898-020800-285-d07 H10898 Homo sapiens cDNA
11222	24291	37931	6.6	0.0E+00	AL157608.1	EST_HUMAN	DKFZp761J2116.1 761 (synonym: ham2) Homo sapiens cDNA
11234	24303	37940	1.86	0.0E+00	BE56822.1	EST_HUMAN	601336330F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3680390 5'
11236	24305	37942	6.05	0.0E+00	AU116908.1	EST_HUMAN	AU116908 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit/ Accession No.	Top Hit Database Source	Top Hit Descriptor
11250	24319	37959	1.75	0.0E+00	AV693659.1	EST_HUMAN	AV693658 GKC Homo sapiens cDNA clone GKCNC03 5'
11260	24329	37969	2.97	0.0E+00	BE386553.1	EST_HUMAN	IL3-NT0104-200500-143-A07 NT0104 Homo sapiens cDNA
11288	24354	37984	2.4	0.0E+00	BE182390.1	EST_HUMAN	PMO-HT0845-080500-002-E05 HT0845 Homo sapiens cDNA
11288	24354	37985	2.4	0.0E+00	BE182390.1	EST_HUMAN	PMO-HT0845-080500-002-E05 HT0845 Homo sapiens cDNA
11290	24358		1.51	0.0E+00	AV701132.1	EST_HUMAN	AV701132 ADA Homo sapiens cDNA clone ADAAD06 5'
11305	24370	38011	3.02	0.0E+00	BE896423.1	EST_HUMAN	607439092E1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5'
11311	24376	38019	1.83	0.0E+00	AW600307.1	EST_HUMAN	UI-HF-BND-4kg-d-02-0-UI17 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
11311	24375	38020	1.83	0.0E+00	AW600307.1	EST_HUMAN	UI-HF-BND-4kg-d-02-0-UI17 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
							UI-HF-BND-4kg-d-02-0-UI17 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
							POLYADENYLATED-BINDING PROTEIN (HUMAN), gbX65553 Musculus mRNA for poly(A) binding protein (MOUSE);
11314	24378	38023	2.49	0.0E+00	BE018293.1	EST_HUMAN	WR4-ST0118-041089-010-A12 ST0118 Homo sapiens cDNA
11346	25869	38058	1.46	0.0E+00	AW387766.1	EST_HUMAN	WR4-ST0118-041089-010-A12 ST0118 Homo sapiens cDNA
11345	25869	38059	1.45	0.0E+00	AW387766.1	EST_HUMAN	WR4-ST0118-041089-010-A12 ST0118 Homo sapiens cDNA
11353	24419	38070	3.23	0.0E+00	BE897853.1	EST_HUMAN	607440446E1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
11355	24417	38073	2.24	0.0E+00	AW69545.1	EST_HUMAN	6086611 x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
11355	24417	38074	2.24	0.0E+00	AW69545.1	EST_HUMAN	6086611 x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
11368	24430	38087	1.89	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_1 434 (synonym: hias3) Homo sapiens cDNA clone DKFZp434L0120 5'
							0u61d04.x1 NCI_CGAP_B2 Homo sapiens cDNA clone IMAGE:1632285 3' similar to SWLRP1_HUMAN
11390	24451	38112	1.37	0.0E+00	AI073917.1	EST_HUMAN	007954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR ;
							0u61d04.x1 NCI_CGAP_B2 Homo sapiens cDNA clone IMAGE:1632285 3' similar to SWLRP1_HUMAN
11390	24451	38113	1.37	0.0E+00	AI073917.1	EST_HUMAN	007954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR ;
							0u61d04.x1 NCI_CGAP_B2 Homo sapiens cDNA clone IMAGE:1632285 3' similar to SWLRP1_HUMAN
11390	24451	38114	1.37	0.0E+00	AI073917.1	EST_HUMAN	007954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR ;
11404	24465	38130	3.8	0.0E+00	14758827	NT	Homo sapiens neuron III (NRXN3) mRNA
11405	24468	38131	24.41	0.0E+00	BF206561.1	EST_HUMAN	801870902E1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4101433 5'
11411	24472	38137	11.86	0.0E+00	AW207734.1	EST_HUMAN	UI-H-B12-4kg-h-01-0-UI17 NCI_CGAP_Suid Homo sapiens cDNA clone IMAGE:2728312 3'
11418	24477	38141	3.93	0.0E+00	AB018290.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11418	24477	38142	3.93	0.0E+00	AB018290.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11418	24479	38144	2.63	0.0E+00	BE206848.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR-O76022 O76022 E18-55KDA-ASSOCIATED PROTEIN ;

Probe SEQ ID NO:	Exam SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11418	24478	38145	2.63	0.0E+00	BE208346.1	EST_HUMAN	bba04d07.yt NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B1
11428	24480	38165	2.37	0.0E+00	11582408	NT	56KDA-ASSOCIATED PROTEIN ; Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
11438	24489	38166	1.68	0.0E+00	AJ075915.1	EST_HUMAN	ov46g07.xt Soares Jeeite NIH_Homo sapiens cDNA clone IMAGE:1640412 3' similar to TR:Q14507
11445	24506	38172	1.73	0.0E+00	11024711	NT	Q14507 EPIDIDYMIS-SPECIFIC GENE PRODUCT, ALPHA. ; Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
11448	24509	38178	1.98	0.0E+00	BF093087.1	EST_HUMAN	QV0-LM0091-120800-385-612 UM0091 Homo sapiens cDNA
11448	20710	38148	1.94	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A), mRNA, complete cds
11462	24512	38178	4.61	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040300-110-104 HT0230 Homo sapiens cDNA
11462	24512	38178	4.61	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-104 HT0230 Homo sapiens cDNA
11476	24534	38204	1.66	0.0E+00	AW673469.1	EST_HUMAN	BC54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275
11476	24534	38205	1.66	0.0E+00	AW673469.1	EST_HUMAN	BC54d08.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275
11480	24549	38223	4.84	0.0E+00	BF507876.1	EST_HUMAN	KIAA0522 PROTEIN ; U1-H-B14-ack-b-10-c-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11480	24549	38224	4.84	0.0E+00	BF507876.1	EST_HUMAN	U1-H-B14-ack-b-10-c-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11486	24554	38228	4.65	0.0E+00	AU135170.1	EST_HUMAN	AU135170 PLAGE1 Homo sapiens cDNA clone PLAGE1001381 5'
11501	24559	38234	2.07	0.0E+00	BF56138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271830 5'
11501	24559	38235	2.07	0.0E+00	BF56138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271830 5'
11503	24561	38238	4.06	0.0E+00	BE878401.1	EST_HUMAN	601486828F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3889207 5'
11503	24561	38239	4.06	0.0E+00	BE878401.1	EST_HUMAN	601486828F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3889207 5'
11511	24569	38246	1.61	0.0E+00	D87932.1	NT	Human mRNA for KIAA0241 gene, partial cds
11516	24573		3.87	0.0E+00	BF240336.1	EST_HUMAN	601875830F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4093710 6'
11531	24587	38262	1.81	0.0E+00	AB03737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11531	24587	38263	1.81	0.0E+00	AB03737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11535	24591	38268	3.09	0.0E+00	11430888	NT	Homo sapiens relnoblasmalike 2 (p130) (RBL2), mRNA
11536	24601	38267	3.08	0.0E+00	11430888	NT	Homo sapiens relnoblasmalike 2 (p130) (RBL2), mRNA
11533	24608	38287	6.13	0.0E+00	4303544	NT	Homo sapiens eukaryotic translation initiation factor 6A (EIF6A) mRNA
11560	24616	38294	2.06	0.0E+00	BF676267.1	EST_HUMAN	602134132F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289502 5'
11662	24617	38297	3.53	0.0E+00	AW328173.1	EST_HUMAN	cd04g05.xt NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847177 5'
11567	24622		42.5	0.0E+00	M55083.1	NT	Human gamma actin-like pseudogene, complete cds
11571	24626	38305	1.75	0.0E+00	A1606938.1	EST_HUMAN	wf20b11.xt Soares Dickgraeef cation, NHUC Homo sapiens cDNA clone IMAGE:2351180 3' similar to
11574	24629	38307	3.37	0.0E+00	BF306998.1	EST_HUMAN	gbM87789 IG GANMA.17 HUMAN C REGION (HUMAN); 601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123848 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11574	24629	38308	3.37	0.0E+00	BF306386.1	EST_HUMAN	601689823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11681	24635	38315	47.2	0.0E+00	BF392492.1	EST_HUMAN	QV2-NN0054-230800-333-c04 NN0054 Homo sapiens cDNA
11601	24654	38336	2.52	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11601	24654	38339	2.32	0.0E+00	U36264.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11606	24656		4.33	0.0E+00	BE897051.1	EST_HUMAN	601439905F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924577 5'
11607	24660		2.37	0.0E+00	4503786	NT	Homo sapiens fyn-related kinase (FRK) mRNA
11607	24672	38361	2.34	0.0E+00	8823698	NT	Homo sapiens golgin-like protein (GLP) mRNA
11623	24674		2.07	0.0E+00	BF207692.1	EST_HUMAN	601681947F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:076022 076022 ET19
11636	24716	38407	4.53	0.0E+00	BE206946.1	EST_HUMAN	601681947F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:076022 076022 ET19
11636	24716	38408	4.53	0.0E+00	BE206946.1	EST_HUMAN	58KDA-ASSOCIATED PROTEIN. ;
11638	24718	38410	3.69	0.0E+00	AV763028.1	EST_HUMAN	QVQ-CT0225-101299-071-706 CT0225 Homo sapiens cDNA
11643	24723		3.01	0.0E+00	AA558707.1	EST_HUMAN	ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);
11644	18580	31662	2.56	0.0E+00	AIB34954.1	EST_HUMAN	wp060808.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464094 3'
11645	24724	38416	7.51	0.0E+00	AW327695.1	EST_HUMAN	wp060808.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464094 3'
11684	25870	38435	1.78	0.0E+00	AW282776.1	EST_HUMAN	U1-HBW0-6ip-4-07-0-UI.s1 NCI_CGAP_Sub0 Homo sapiens cDNA clone IMAGE:2728509 3'
11671	23889	37522	1.93	0.0E+00	4758827	NT	Homo sapiens neurxin III (NRXN3) mRNA
11677	24676	38367	1.35	0.0E+00	BE254058.1	EST_HUMAN	601113903F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354600 5'
11680	24679	38369	1.79	0.0E+00	BE865909.2	EST_HUMAN	601689088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11680	24679	38370	1.79	0.0E+00	BE865909.2	EST_HUMAN	601689088R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11681	24680	38371	3.81	0.0E+00	BE186656.1	EST_HUMAN	U1-HBW1-6ip-4-05-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071121 3'
11682	24681		1.39	0.0E+00	BF613960.1	EST_HUMAN	U1-HBW1-6ip-4-05-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071121 3'
11688	24683	38384	7.19	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G178 5'
11688	24683	38385	7.19	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G178 5'
11706	24703	38395	10.19	0.0E+00	AI923118.1	EST_HUMAN	W68g03.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2452488 5' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
11708	24749	38440	4.47	0.0E+00	AA760913.1	EST_HUMAN	nz11607.s1 NCI_CGAP_CGB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686
11708	24749	38441	4.47	0.0E+00	AA760913.1	EST_HUMAN	nz11607.s1 NCI_CGAP_CGB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686
11713	24753	38447	2.21	0.0E+00	BE810646.1	EST_HUMAN	Q13686 ALKX HOMOLOG PROTEIN. ;



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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11723	23909	37533	11.64	0.0E+00	BE676347.1	EST_HUMAN	712712.x1 NCL CGAP_CLL.1 Homo sapiens cDNA clone IMAGE:3295919 3' similar to TR:000409 000409 CHECKPOINT SUPPRESSOR 1.:
11725	23911	37535	1.47	0.0E+00	AI689358.1	EST_HUMAN	b66b09.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2274521 3' similar to gb:M55542
11727	23913	37537	3.13	0.0E+00	BE615698.1	EST_HUMAN	601278335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'
11727	23913	37538	3.13	0.0E+00	BE615698.1	EST_HUMAN	601278335F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611144 5'
11734	23920	37545	1.59	0.0E+00	AV757420.1	EST_HUMAN	AV757420 BM Homo sapiens cDNA clone BAFACH103 5'
11739	23925	37550	7.33	0.0E+00	AI037746.1	EST_HUMAN	DKFZ564C187_1 584 (synonym: hfb2) Homo sapiens cDNA clone DKFZ564C187 5'
11740	23926	37551	4.2	0.0E+00	U62769.1	NT	Human oxylchase variant 2 mRNA, complete cds
11745	23931	37557	1.33	0.0E+00	BE883398.1	EST_HUMAN	601509139F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910833 5'
11768	24759	38454	1.76	0.0E+00	Y18880.1	EST_HUMAN	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
11769	24761	38455	3.69	0.0E+00	U39997.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11769	24761	38456	3.59	0.0E+00	U39997.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11784	24774	38470	2.03	0.0E+00	AI138211.1	EST_HUMAN	601441096F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3910870 5'
11787	24787	38485	6.43	0.0E+00	BE622317.1	EST_HUMAN	601441096F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3910870 5'
11833	24822	38512	17.72	0.0E+00	BE748939.1	EST_HUMAN	601572188T1 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:3839012 3'
11833	24822	38513	17.72	0.0E+00	BE748939.1	EST_HUMAN	601572188T1 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:3839012 3'
11845	24834	38527	4.58	0.0E+00	AI141832.1	EST_HUMAN	AU141882 THYR01 Homo sapiens cDNA clone THYR01001398 5'
11845	24834	38528	4.58	0.0E+00	AI141832.1	EST_HUMAN	AU141882 THYR01 Homo sapiens cDNA clone THYR01001398 5'
11848	24837	38531	2.7	0.0E+00	AW006122.1	EST_HUMAN	w281101.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2586225 3' similar to WP.F53H10.2
11893	25971	38537	2.73	0.0E+00	BF002333.1	EST_HUMAN	CE11040 ZINC FINGER, C2H2 TYPE:
11894	24852	38548	1.32	0.0E+00	CO8264.1	EST_HUMAN	TRIO.1
11898	24858		1.66	0.0E+00	BE727811.1	EST_HUMAN	CG6284 Human pancreatic islet1 Homo sapiens cDNA similar to insulin receptor
11872	24860	38555	2.36	0.0E+00	AI472010.1	EST_HUMAN	601564180F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833730 5'
11878	24866	38563	2.84	0.0E+00	AV387776.1	EST_HUMAN	gb:MA1691 PROLACTIN RECEPTOR TYPE 2 PRECURSOR (HUMAN).
11878	24866	38564	2.84	0.0E+00	AV387776.1	EST_HUMAN	gb:MA1691 PROLACTIN RECEPTOR TYPE 2 PRECURSOR (HUMAN).
11889	24877		1.8	0.0E+00	AV663777.1	EST_HUMAN	MR4-ST018-261099-012-b03 ST0118 Homo sapiens cDNA
11901	24889	38589	3.67	0.0E+00	J1435244	NT	MR3-SN0010-310300-107-h03 SN0010 Homo sapiens cDNA
11901	24889	38589	3.67	0.0E+00	J1435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247) mRNA
11907	24894	38598	4.38	0.0E+00	U682631.1	NT	Homo sapiens KIAA0247 gene product (KIAA0247) mRNA
11911	24898	38600	28.74	0.0E+00	BE378254.1	EST_HUMAN	Human beta-2-microglobulin (BAM22) gene, exon 6

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11911	24898	38601	26.74	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:360823 5'
11917	24903	38606	4.87	0.0E+00	AW500056.1	EST_HUMAN	U1HF-BND-ak-b-03-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077332 5'
11932	24918	38621	2.05	0.0E+00	BE794758.1	EST_HUMAN	601590586F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
11934	24920	38622	65.18	0.0E+00	BE879633.1	EST_HUMAN	601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5'
11935	24921	38623	1.6	0.0E+00	MA0870.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
11941	24927	38628	1.38	0.0E+00	4799827	NT	Homo sapiens neuron III (NRXN3) mRNA
11941	24927	38630	1.38	0.0E+00	4799827	NT	Homo sapiens neuron III (NRXN3) mRNA
11946	24932	38635	1.58	0.0E+00	AF053543.1	NT	Homo sapiens glutathione transferase zeta 1 (GSTZ1) gene, exons 6 and 7
11953	24939	38642	7.28	0.0E+00	BE409893.1	EST_HUMAN	601299403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3628544 5'
11954	24940	38643	2.22	0.0E+00	BE148850.1	EST_HUMAN	MR0-HT0241-150500-01-1-02 HT0241 Homo sapiens cDNA
11955	24941	38644	2.89	0.0E+00	AF223391.1	NT	Homo sapiens cadherin channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11955	24941	38645	2.89	0.0E+00	AF223391.1	NT	Homo sapiens cadherin channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11956	18785	31831	1.48	0.0E+00	D28535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
11956	18785	31832	1.48	0.0E+00	D28535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
11958	24943	38647	11.38	0.0E+00	BF681841.1	EST_HUMAN	602155722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4298725 5'
11958	24943	38648	11.38	0.0E+00	BF681841.1	EST_HUMAN	602155722F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4298725 5'
11964	24949	38659	1.78	0.0E+00	AF132940.1	EST_HUMAN	601329340 NT2RP4 Homo sapiens cDNA clone NT2RP4.0000928 5'
11967	24952	38667	4.09	0.0E+00	BE003372.1	EST_HUMAN	601676357F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958935 5'
11983	24958	38671	1.58	0.0E+00	BF312652.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127089 5'
11983	24958	38672	1.58	0.0E+00	BF312652.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127089 5'
11986	24971	38675	3.4	0.0E+00	X51753.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11986	24971	38676	3.4	0.0E+00	X51753.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11988	24983		1.96	0.0E+00	BE08402.1	EST_HUMAN	601498553F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900398 5'
12013	24997	38700	1.46	0.0E+00	8635487	NT	Human endogenous retrovirus, complete genome
12028	25072		8.57	0.0E+00	BF309120.1	EST_HUMAN	601890534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131418 5'
12028	25072	38713	2.37	0.0E+00	BE089861.1	EST_HUMAN	RC4-NN0026-120600-018-507 NN0026 Homo sapiens cDNA
12029	25012	38714	2.37	0.0E+00	BE089861.1	EST_HUMAN	RC4-NN0026-120600-018-507 NN0026 Homo sapiens cDNA
12032	25015	38717	60.86	0.0E+00	BE29175.1	EST_HUMAN	RC4-NN0026-120600-018-507 NN0026 Homo sapiens cDNA
12046	25027	38733	1.42	0.0E+00	BE744311.1	EST_HUMAN	601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532868 5'
12046	25027	38734	1.42	0.0E+00	BE744311.1	EST_HUMAN	601576825F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837222 5'
12054	25035	38741	2.02	0.0E+00	BE267612.1	EST_HUMAN	601576825F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3837222 5'
12054	25035	38742	2.02	0.0E+00	BE267612.1	EST_HUMAN	601113009F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353378 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12084	25064	38770	2.85	0.0E+00	BE345535.1	EST_HUMAN	601070391F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456407 5'
12087	25067	38773	1.34	0.0E+00	AA999001.1	EST_HUMAN	263401.1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:729912 5' similar to SW-PM11_SCHPO
12088	25068	38774	1.55	0.0E+00	AU117874.1	EST_HUMAN	P40899 DNA METHYLTRANSFERASE PMT1 ;
12088	25068	38775	1.55	0.0E+00	AU117874.1	EST_HUMAN	AU117874 HEMBA1 Homo sapiens cDNA clone HEMBA1002612 5'
12091	25071	38778	1.72	0.0E+00	BE780453.1	EST_HUMAN	601468712F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3871899 5'
12108	25089	38792	2.15	0.0E+00	AW269390.1	EST_HUMAN	xx46h03.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:2816213 3' similar to
12118	25098	38803	1.89	0.0E+00	AU132594.1	EST_HUMAN	gbl.11706_cds1 HORMONE SENSITIVE LIPASE (HUMAN);
12131	25111	38815	1.35	0.0E+00	BE29240.1	EST_HUMAN	AU132384 NT26P3 Homo sapiens cDNA clone NT26P3004339 5'
12147	26165	31540	9.34	0.0E+00	BE312542.1	EST_HUMAN	601105652F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2588325 5'
12160	26005		3.02	0.0E+00	AL163246.2	NT	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5'
12162	26013		5.49	0.0E+00	AI190993.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C045
12172	25134		3.73	0.0E+00	AB011599.1	NT	ge1b12.x1 Soares, fetal_lung_NBHL19W Homo sapiens cDNA clone IMAGE:3739231 3'
12182	25149		6.87	0.0E+00	AL163246.2	NT	Homo sapiens gene for AF-6, complete cds
12194	25151		1.35	0.0E+00	AB016195.1	NT	Homo sapiens chromosome 21 segment HS21C046
12201	25155		3.2	0.0E+00	11417862	NT	Homo sapiens ELK1 pseudogene (ELK2) and immunoglobulin heavy chain gamma pseudogene (IGHGP)
12220	25170		4.85	0.0E+00	5802873	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12264	25973	31767	1.47	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1)
12267	25983		3.47	0.0E+00	AL041831.1	EST_HUMAN	genes, complete cds
12285	26148		3.39	0.0E+00	11418318	NT	DKFZ434K0819 J1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZ434K0819 5'
12304	25222		4.77	0.0E+00	AL046544.1	EST_HUMAN	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
12317	26017		2.82	0.0E+00	A1803487.1	EST_HUMAN	DKFZ434G218 J1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZ434G218 5'
12368	26172		1.88	0.0E+00	N54484.1	EST_HUMAN	IL-BT030-271089-001 BT030 Homo sapiens cDNA
12371	25285		4.03	0.0E+00	AF106658.1	NT	SW-POL_BAEVYM.P10222 POL.POLYPROTEIN ;
12374	14042	27106	5.36	0.0E+00	4507500	NT	SW-POL_BAEVYM.P10222 POL.POLYPROTEIN ;
12374	14042	27107	5.36	0.0E+00	4507600	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
12383	26021		3.07	0.0E+00	10082587	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
12415	13754		4.89	0.0E+00	AF003528.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
							Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
							Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions

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12450	25781	31837	3.95	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12510	25950	31765	1.64	0.0E+00	AW690082.1	EST_HUMAN	hg31606.x1 NC1_CGAP_G08 Homo sapiens cDNA clone IMAGE:2847234 3' similar to contains Ali
12542	25982		1.34	0.0E+00	L20493.1	NT	repetitive element; contains element MER22 repetitive element;
12573	26015		2.73	0.0E+00	AF088757.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
12618	25416		4.91	0.0E+00	9636487	NT	Human endogenous retrovirus, complete genome
12638	25428		1.19	0.0E+00	AV720878.1	EST_HUMAN	AV720878 GLC Homo sapiens cDNA clone G1CEP G08 5'
12680	26009		3.51	0.0E+00	AI204914.1	EST_HUMAN	an05004.x1 Stradene echizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
12694	25462		1.33	0.0E+00	AB04946.1	EST_HUMAN	an05004.x1 Stradene echizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
12702	26008		2.29	0.0E+00	BE439792.1	EST_HUMAN	HTM1-654F HTM1 Homo sapiens cDNA
12714	15187	28287	1.39	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12714	15187	28288	1.39	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12739	25490	32027	1.21	0.0E+00	AF036356.1	NT	Homo sapiens caveolin-3 (CAV3) mRNA, complete cds
12751	14889	27960	3.26	0.0E+00	H50132.1	EST_HUMAN	yo59408.1 Scores breast 3NBH81; Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:MG4099
12761	14889	27961	3.26	0.0E+00	H50132.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12765	13979	27031	1.6	0.0E+00	AB011339.1	NT	yo59408.1 Scores breast 3NBH81; Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:MG4099
12766	25509		33.13	0.0E+00	D50665.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
12771	25514	31987	5.44	0.0E+00	11418169	NT	Human gamma-cytoplasmic actin (ACTGP3), pseudogene
12771	25514	31998	5.44	0.0E+00	11418169	NT	Human gamma-cytoplasmic actin (ACTGP3), pseudogene
12776	25518		7.88	0.0E+00	AB028698.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes; complete cds)
12788	15294	28420	1.7	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
12837	25957		2.11	0.0E+00	AW684999.1	EST_HUMAN	HB6808.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878154 3'
12847	25563	31988	1.43	0.0E+00	11430460	NT	HB6808.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878154 3'
12892	14409	27471	1.74	0.0E+00	8922553	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12927	16568	28573	3.11	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
12935	18494	31532	2.3	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12938	25917		1.88	0.0E+00	AB028900.1	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12981	25639	31983	1.82	0.0E+00	9539724	NT	Homo sapiens C5T gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
13010	26107		2.93	0.0E+00	AL163246.2	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160KD subunit (CPSF1), mRNA
13017	13828	26851	2.48	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13113	25728	31943	1.17	0.0E+00	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA

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Table 4  
Single Exon Probes Expressed in Placenta

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
13116	25728		1.4	0.0E+00	AB02059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
13118	25731		3.11	0.0E+00	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
13140	25740		5.96	0.0E+00	AB026998.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
13151	28207		1.16	0.0E+00	AW505176.1	EST_HUMAN	UI-HF-BNO-aly-9-08-0-UI.1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:3081399 5'
13190	25774		1.51	0.0E+00	X57147.1	NT	Human endogenous reovirus pHE-1 (ERV8)
13208	16135	29151	1.37	0.0E+00	6908918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13208	16135	29152	1.37	0.0E+00	6908918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
13215	14345	27402	1.29	0.0E+00	896844	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA

## CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human placenta comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 13,232 or a complementary sequence, or a portion of such a sequence.

2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.

3. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.

4. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS: 13,233 - 26,232.

5. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.

6. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.

7. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 13,232 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human placenta.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 13,233 - 26,232 or a complementary sequence or a fragment thereof.

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15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human placenta which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOS.: 26,233 - 38,837, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human placenta.

16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

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20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

21. A single exon nucleic acid probe as claimed in any one



of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample derived from human placenta, comprising:  
 contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human placenta; and then measuring the label detectably bound to each probe of said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:  
 algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe, wherein said detectably labeled nucleic acids are derived from mRNA from the placenta of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

24. A method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence according to the method of claim 23; and then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 26,232 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID NOS: 1 - 26,232.

27. A peptide comprising a sequence as set out in any of SEQ ID NOS: 26,233 - 38,837.

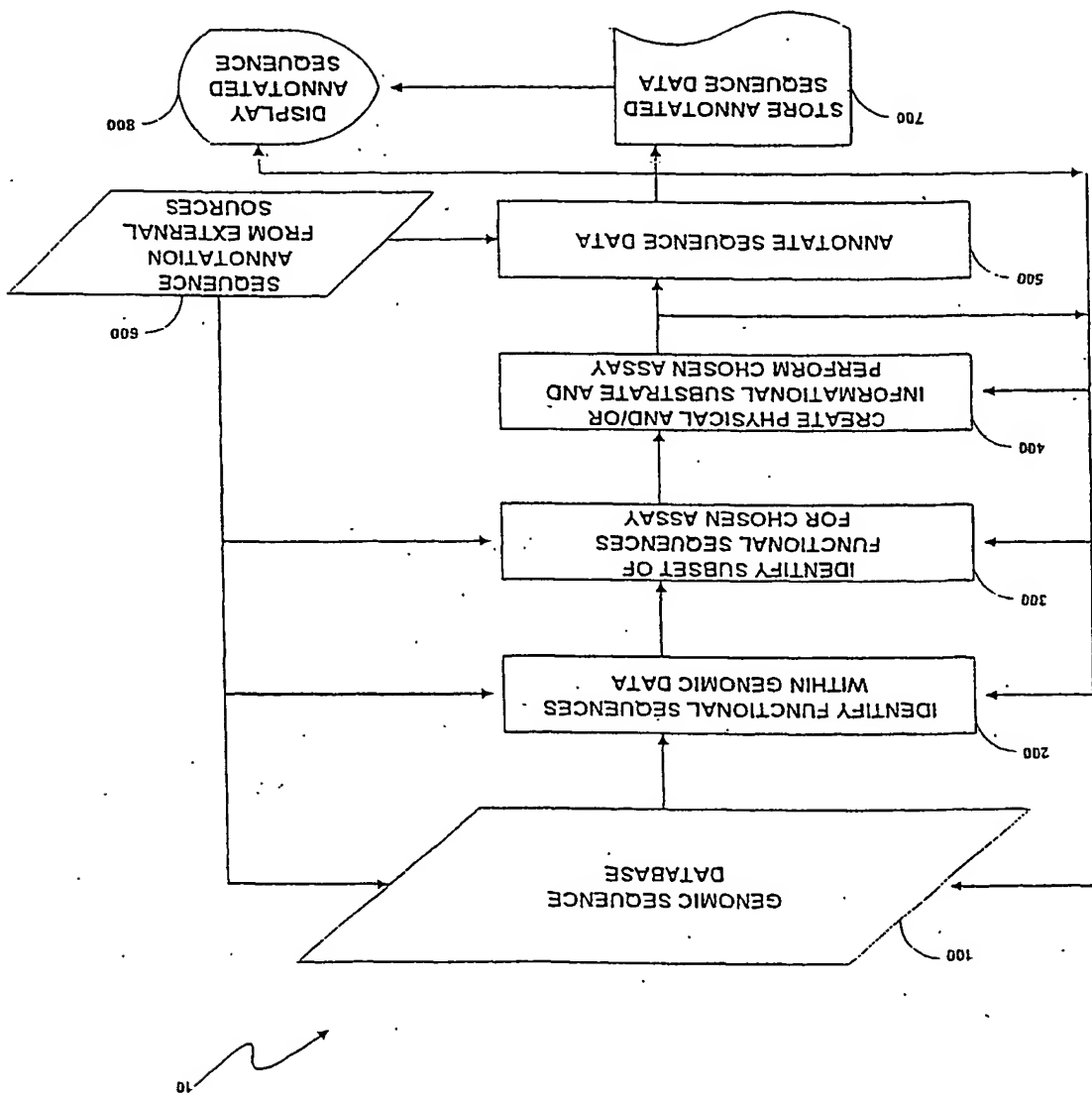


Fig. 1

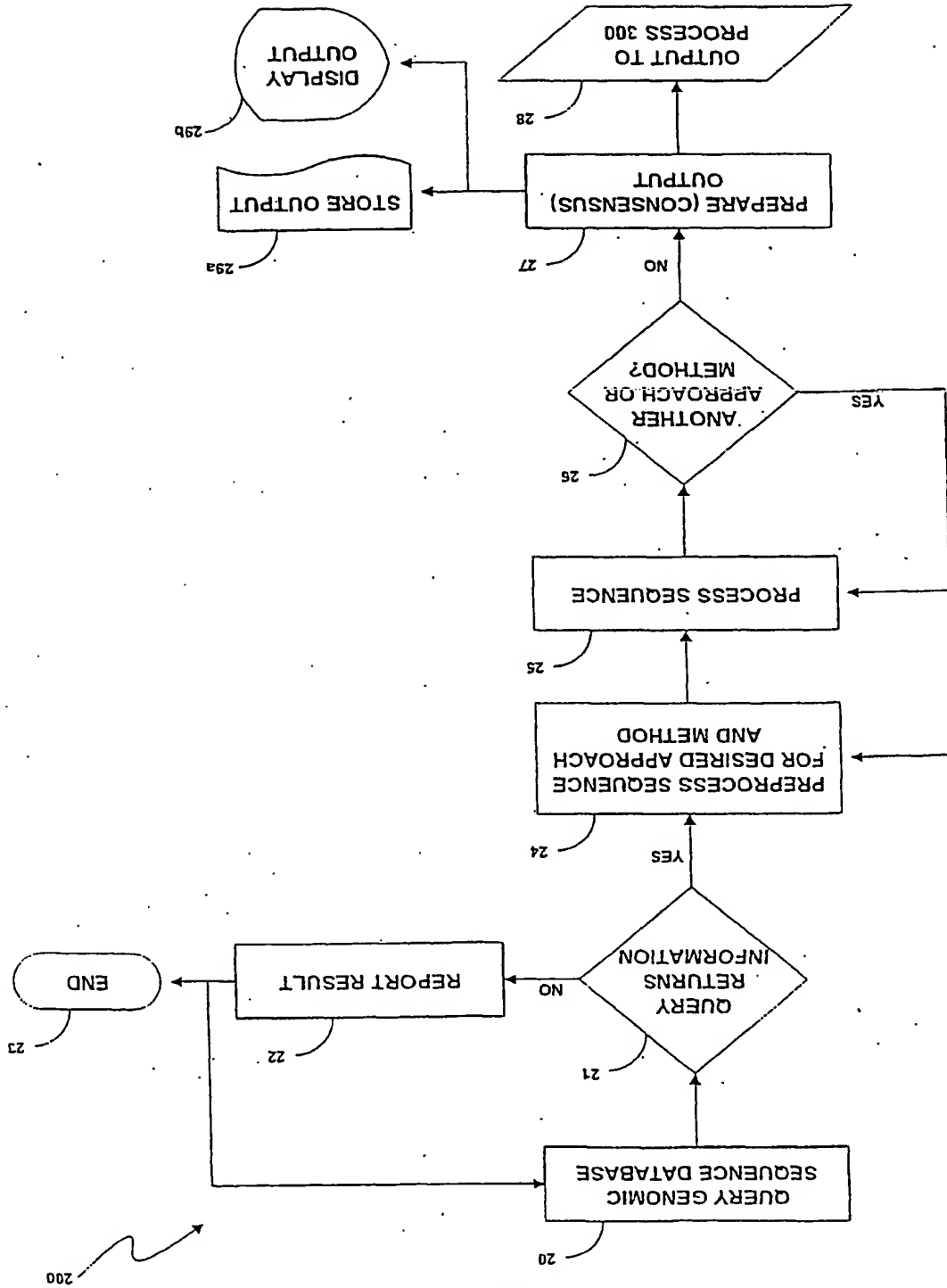


Fig. 2

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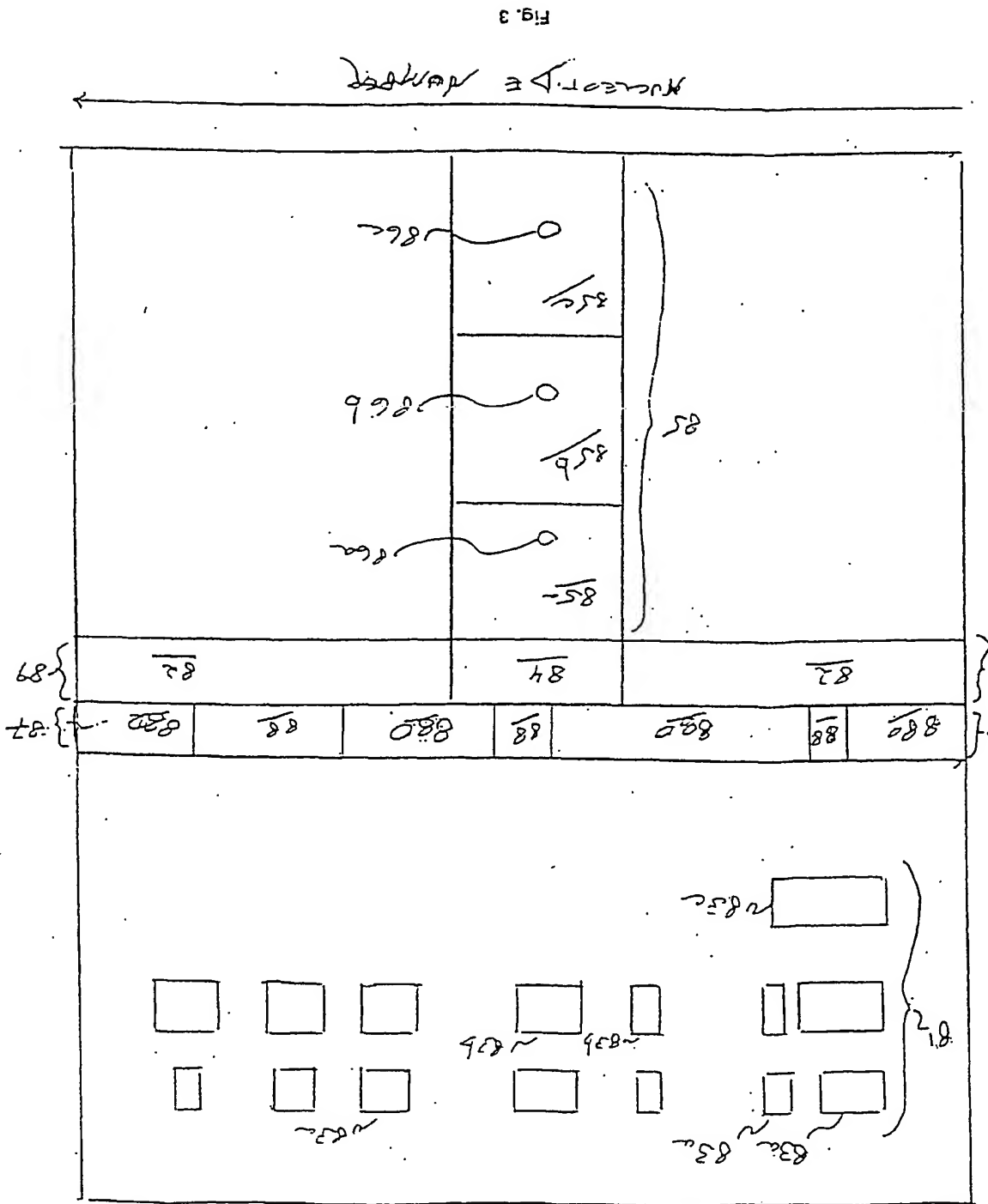


Fig. 3

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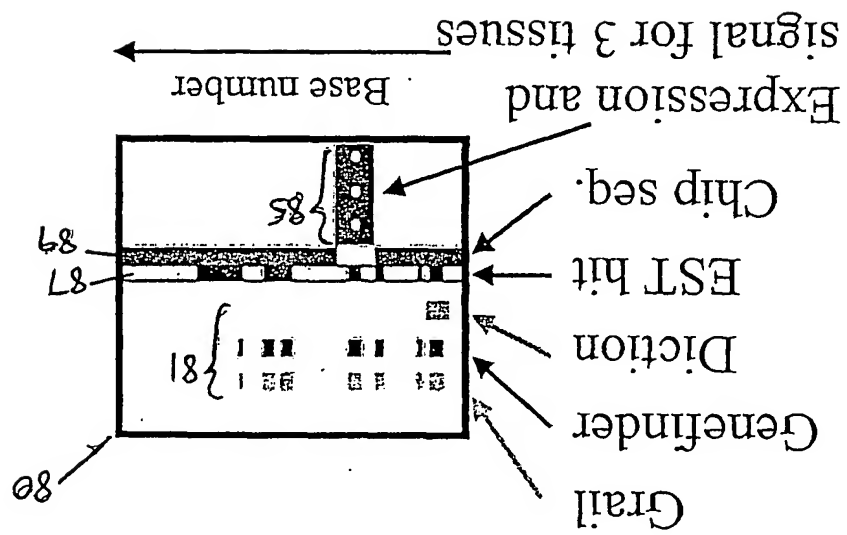


Fig. 4

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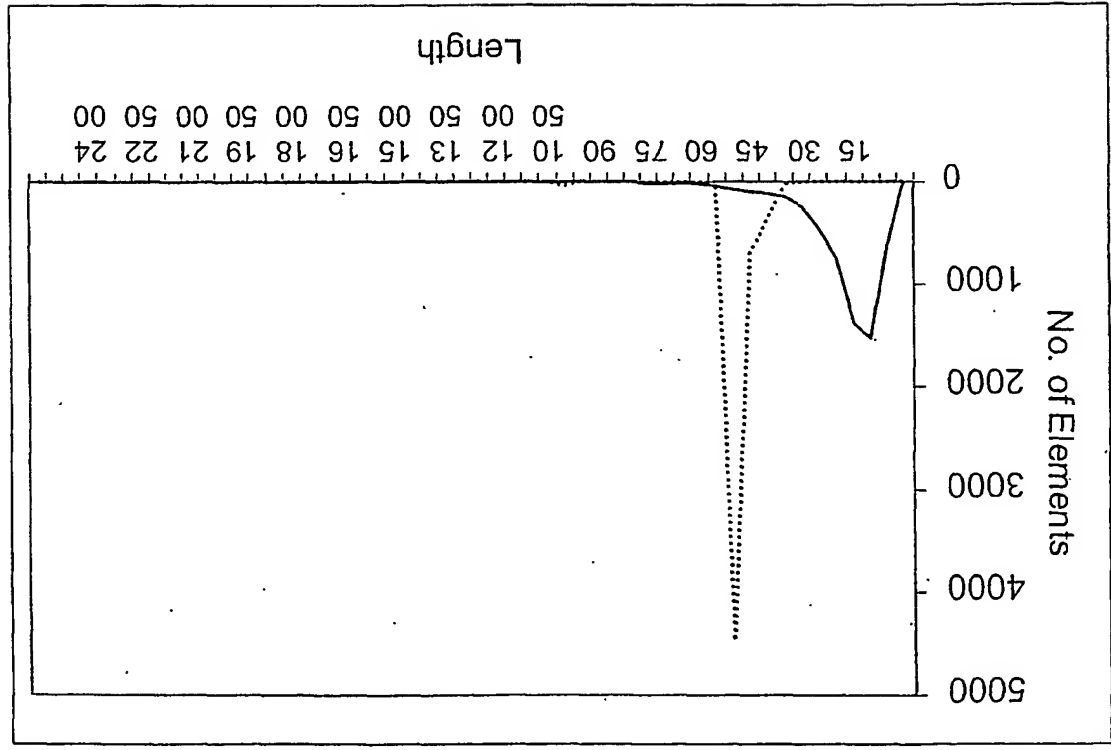


Fig. 5

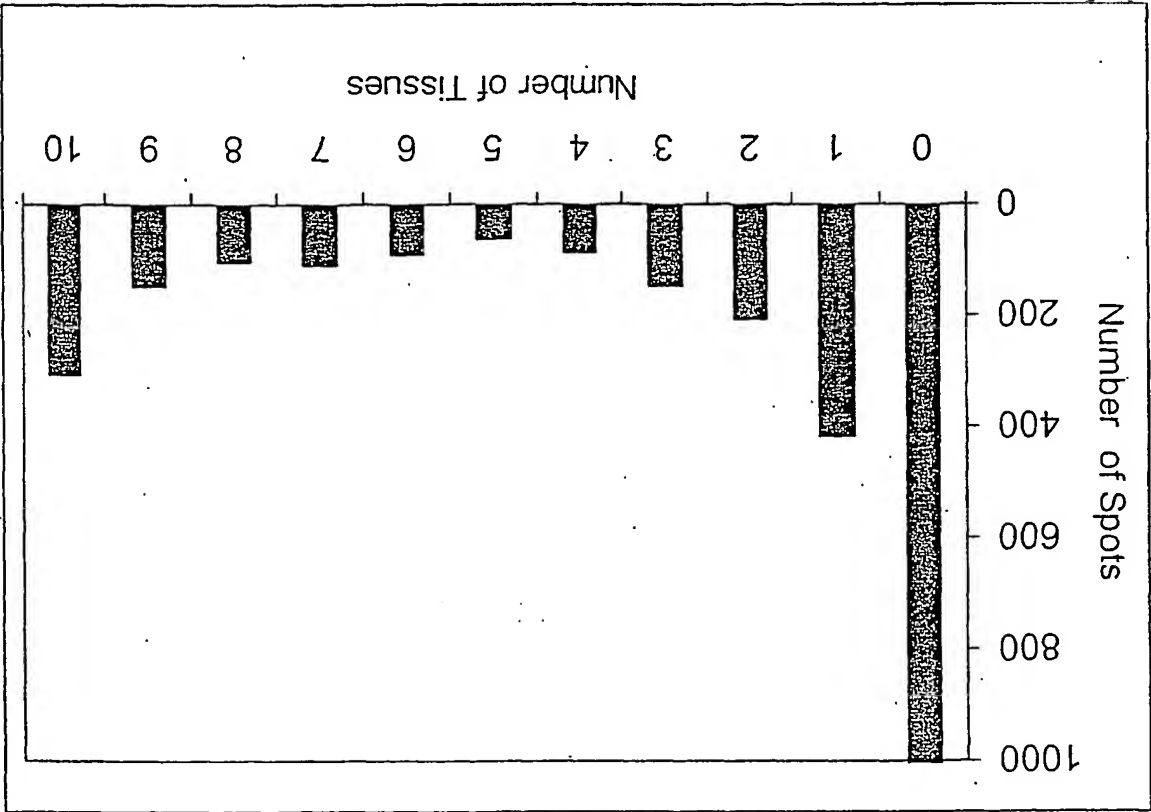


Fig. 6



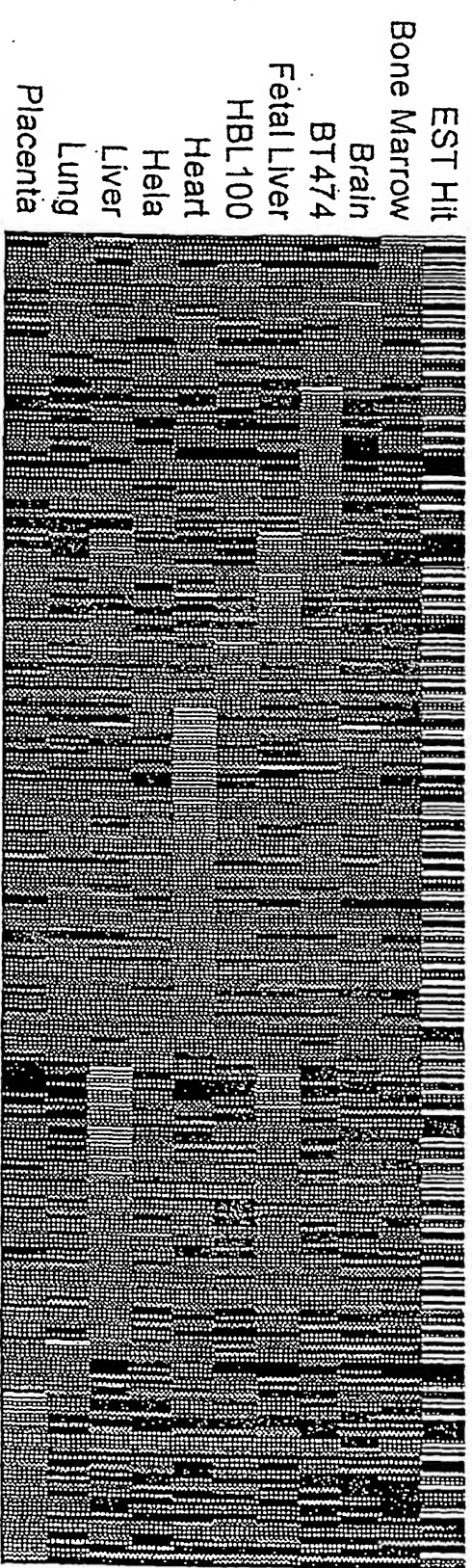


Fig. 7a

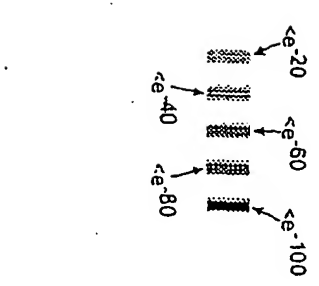


Fig. 7b

Fig. 7c

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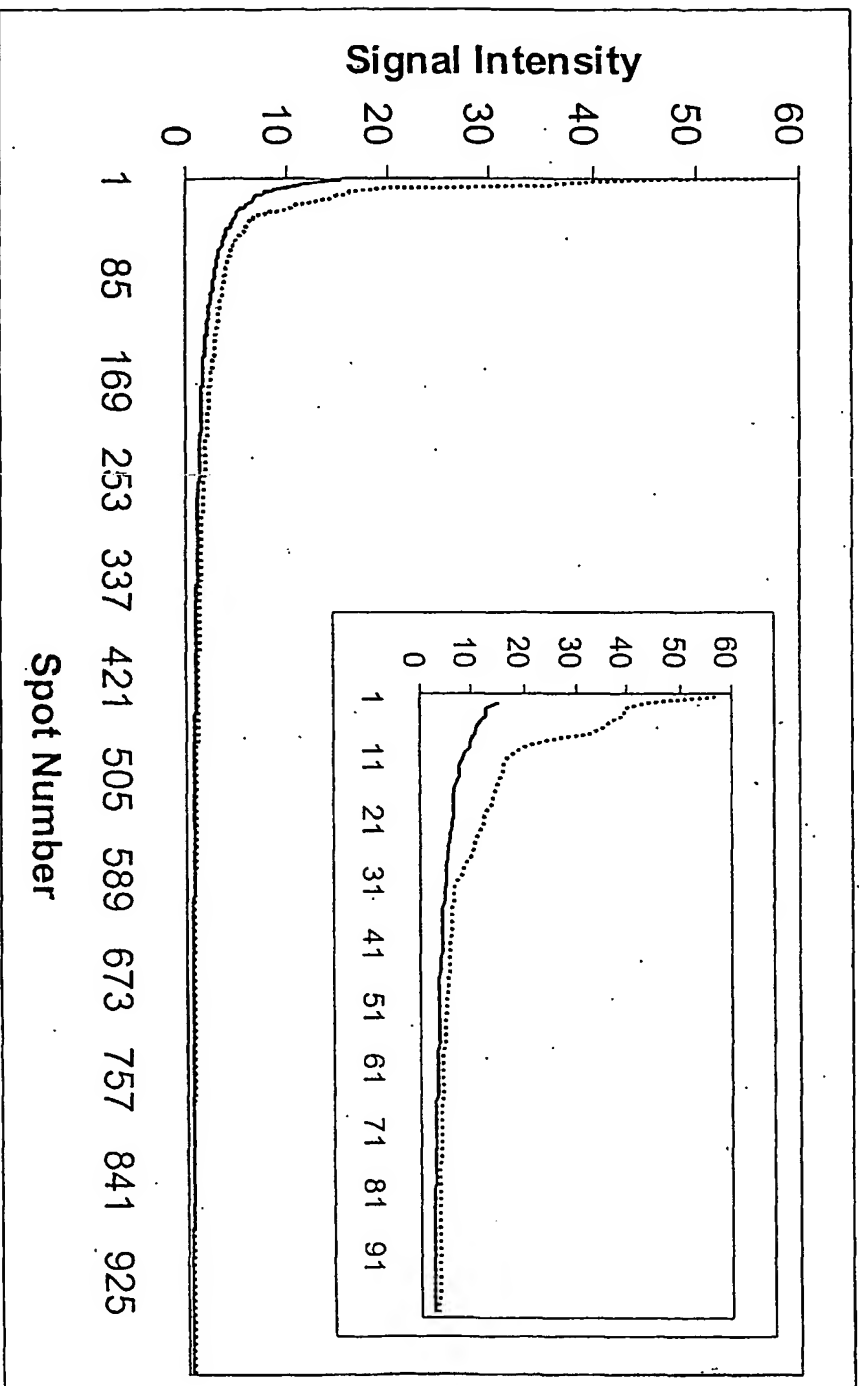
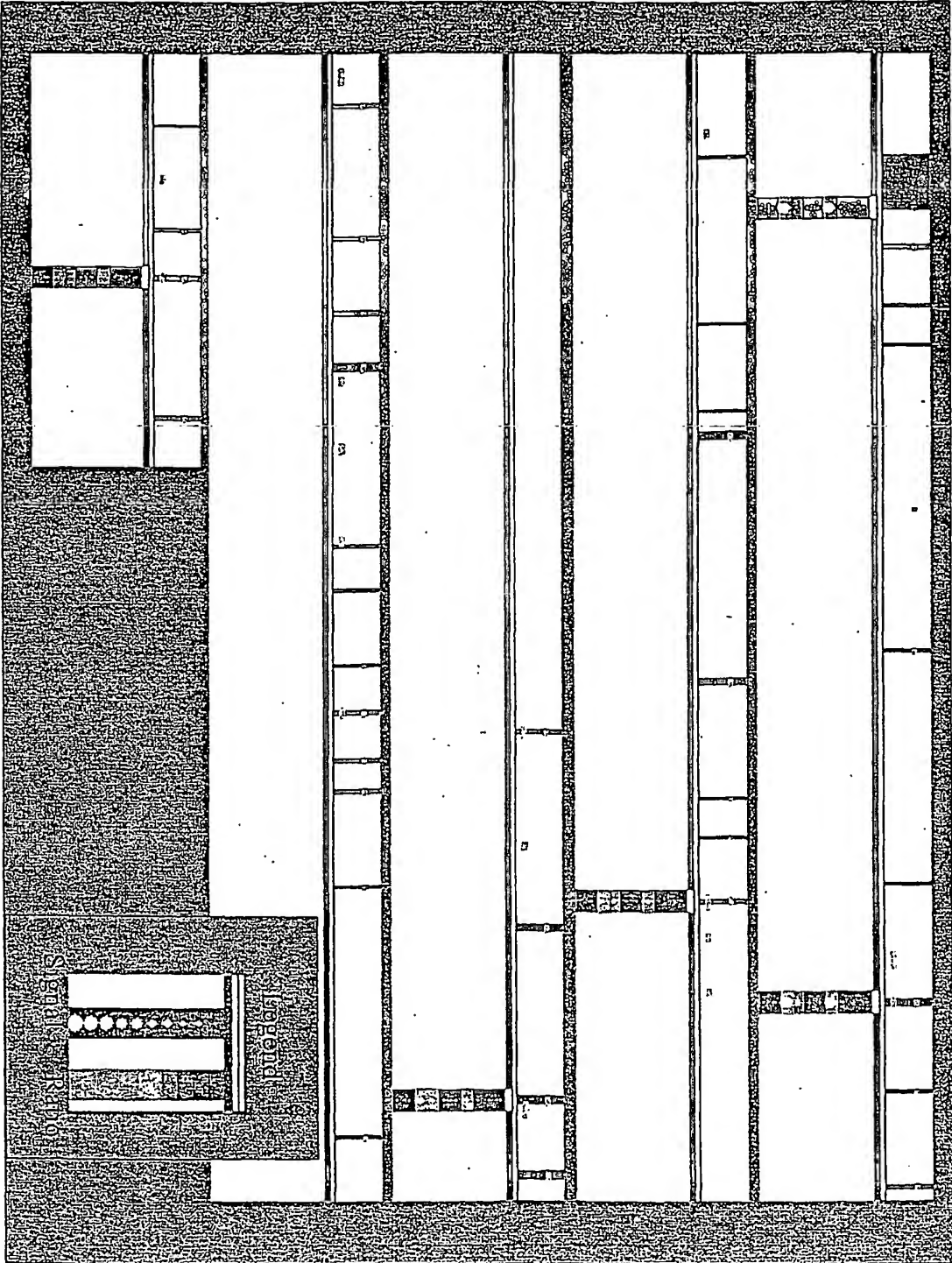


Fig. 8

Fig. 9



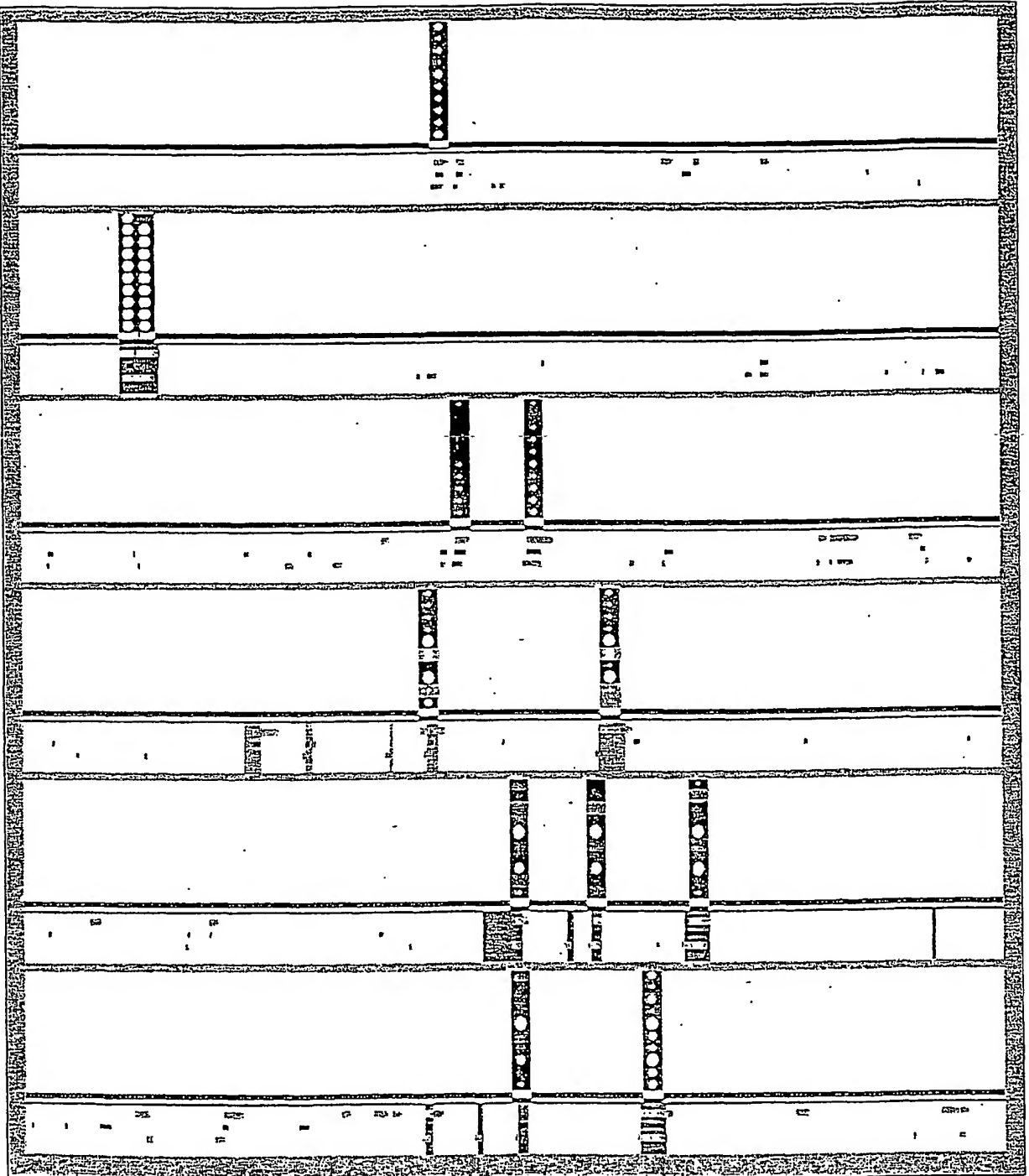


Fig. 10

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(19) World Intellectual Property Organization  
International Bureau



(10) International Publication Number  
PCT  
WO 01/057272 A3

(43) International Publication Date  
9 August 2001 (09.08.2001)

(74) Agents: RONNING, Royal, N., Jr.; Amersham Pharma-  
cia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ  
08855 et al. (US).

(21) International Application Number: PCT/US01/00663

(81) Designated States (national): AE, AG, AL, AM, AT, AU,  
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ,  
DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,  
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,  
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,  
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,  
TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(26) Publication Language: English

(25) Filing Language: English

(22) International Filing Date: 30 January 2001 (30.01.2001)

(30) Priority Data:

US	60/180,312	4 February 2000 (04.02.2000)
US	60/207,456	26 May 2000 (26.05.2000)
US	09/608,408	30 June 2000 (30.06.2000)
US	09/632,366	3 August 2000 (03.08.2000)
US	60/234,687	21 September 2000 (21.09.2000)
US	60/236,359	27 September 2000 (27.09.2000)
GB	0024263.6	4 October 2000 (04.10.2000)

Published:

— with international search report  
— with sequence listing part of description published sepa-  
rately in electronic form and available upon request from  
the International Bureau

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(88) Date of publication of the international search report:  
3 January 2003  
For two-letter codes and other abbreviations, refer to the "Guid-  
ance Notes on Codes and Abbreviations" appearing at the begin-  
ning of each regular issue of the PCT Gazette.

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE  
EXPRESSION IN HUMAN PLACENTA  
(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene  
expression in a sample derived from human placenta is described. Also described are single exon nucleic acid probes expressed in  
the placenta and their use in methods for detecting gene expression.

WO 01/057272 A3



<b>INTERNATIONAL SEARCH REPORT</b> Int. Application No. <b>PCT/US 01/00663</b>		<b>A. CLASSIFICATION OF SUBJECT MATTER</b> IPC 7 C12Q1/68 606F19/00 C07K14/47	
<b>B. FIELDS SEARCHED</b> Minimum documentation searched (classification system followed by classification symbols) IPC 7 C12Q C07K 606F		Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched	
<b>C. DOCUMENTS CONSIDERED TO BE RELEVANT</b>		Excerpted data base consulted during the international search (name of data base and, where practical, search terms used) BIOSIS, WPI Data, EPO-Internal, MEDLINE, EMBASE, CHEM ABS Data, SEQUENCE SEARCH	
According to International Patent Classification (IPC) or to both national classification and IPC		Category Creation of document, with indication, where appropriate, of the relevant passages Relevant to claim No.	
X KIRSZENBAUM ET AL: "An alternatively spliced form of HLA-G mRNA" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE, WASHINGTON, US, vol. 91, 1 May 1994 (1994-05-01), pages 4209-4213, XP002086258 ISSN: 0027-8424 abstract; figures 1,2		1-27	
Further documents are listed in the continuation of box C.		Patent family members are listed in annex.	
Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier document published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another document referring to an oral disclosure, use, exhibition or other means "O" document published prior to the international filing date but later than the priority date claimed "P" document published prior to the international filing date but later than the priority date claimed			
Date of the actual completion of the international search 2 August 2002		Date of mailing of the international search report 03.09.02	
Name and mailing address of the ISA European Patent Office, P.B. 5018 Patentkan 2 NL - 2280 HV Rijswijk Tel (+31-70) 340-2040, Tx. 31 651 epo nl Fax (+31-70) 340-3016		Authorized officer Luzzatto, E	

INTERNATIONAL SEARCH REPORT

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	STAUDER R ET AL: "Different CD44 splicing patterns define prognostic subgroups in multiple myeloma." BLOOD, (1996), VOL. 88, NO. 8, PP. 3101-8. JOURNAL CODE: A86. ISSN: 0006-4971. XP001033913 Basel Institute for Immunology, Switzerland. the whole document	1-27
X	SCREATION G R ET AL: "GENOMIC STRUCTURE OF DNA ENCODING THE LYMPHOCYTE HOMING RECEPTOR CD44 REVEALS AT LEAST 12 ALTERNATIVELY SPLICED EXONS" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE, WASHINGTON, US, vol. 89, no. 24, 15 December 1989 (1989-12-15), pages 12160-12164, XP000470187 ISSN: 0027-8424 abstract; table 1	1-27
X	WO 98 18966 A (LESCALLETT JENNIFER) 7 May 1998 (1998-05-07) page 4, line 14 - page 8, line 12; claims; table 2	1-27
X	DATABASE FBI 'online! EMBL, Heidelberg; Accession Number AA413898, 9 March 1997 (1997-03-09) MARRA M. ET AL.: "The WashU-HHMI mouse EST project" XP002184690 abstract	13
A	US 5 942 417 A (NI JIAN ET AL) 24 August 1999 (1999-08-24) column 44, line 23 - line 34; figure 3	1
A	US 5 618 671 A (LINDSTROM PER) 8 April 1997 (1997-04-08) column 1, line 60 - column 2, line 19 column 4, line 36 - column 5, line 29; claims	1-27
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# INTERNATIONAL SEARCH REPORT

Pat. No. 01/00663

International Application No.

C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category "Citation of document, where appropriate, of the relevant passages

Relevant to claim No.

A	<p>EISEN M B ET AL: "Cluster analysts and display of genome-wide expression patterns" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE, WASHINGTON, US, vol. 95, December 1998 (1998-12), pages 14863-14868, XP002140966 ISSN: 0027-8424 the whole document</p> <p>-----</p> <p>DATABASE BIOSIS 'Online! BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 1995 XU CHUN-FANG ET AL: "Distinct transcription start sites generate two forms of BRCA1 mRNA." Database accession no. PREV199698632738 XP002184501 abstract &amp; HUMAN MOLECULAR GENETICS, vol. 4, no. 12, 1995, pages 2259-2264, ISSN: 0964-6906</p> <p>-----</p> <p>SOLOVYEV V ET AL: "PREDICTING INTERNAL EXONS BY OLIGONUCLEOTIDE COMPOSITION AND DISCRIMINANT ANALYSIS OF SPLICEABLE OPEN READING FRAMES" NUCLEIC ACIDS RESEARCH, OXFORD UNIVERSITY PRESS, SURREY, GB, vol. 22, no. 24, 1994, pages 5156-5163, XP002915964 ISSN: 0305-1048 the whole document</p> <p>-----</p> <p>GUAN ET AL: "GRAIL: an integrated artificial intelligence system for gene recognition and interpretation" PROCEEDINGS OF THE CONFERENCE ON ARTIFICIAL INTELLIGENCE APPLICATIONS, MONTEREY, MAR. 2 - 6, 1992, LOS ALAMITOS, IEEE COMP. SOC. PRESS, US, vol. CONF. 8, 2 March 1992 (1992-03-02), pages 9-13, XP010027422 ISBN: 0-8186-2690-9 the whole document</p> <p>-----</p> <p>PENN SHARRON G ET AL: "Mining the human genome using microarrays of open reading frames." NATURE GENETICS, vol. 26, no. 3, November 2000 (2000-11), pages 315-318, XP002184491 ISSN: 1061-4036 the whole document</p>	<p>1, 12</p> <p>1</p> <p>1-27</p> <p>1-27</p> <p>1-27</p>
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# INTERNATIONAL SEARCH REPORT

International Application No  
 PCT/US 01/00663

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	<p>DATABASE EBI, Online!                      9 May 1997 (1997-05-09)                      MARRA M. ET AL.: "The WashU-HHMI mouse EST project; VC72C02.S1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE: 780098"                      Database accession no. AA414703                      XP002208274                      abstract</p>	13, 14, 18, 20, 21
X	<p>DATABASE EBI, Online!                      16 October 1997 (1997-10-16)                      MARRA M. ET AL.: "The WashU-HHMI Mouse EST project; V160C06.S1 Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE: 976618"                      Database accession no. AA619735                      XP002208275                      abstract</p>	13, 14, 16, 18, 20, 21
A	<p>DATABASE EBI, Online!                      27 April 1999 (1999-04-27)                      DICKHOFF R. ET AL.: "Sequencing of human chromosome 14q31 region"                      Database accession no. AC007372                      XP002208276                      abstract</p>	13, 14, 18

INTERNATIONAL SEARCH REPORT

B x I Obs vations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: -  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:  
see FURTHER INFORMATION sheet PCT/ISA/210

3. ☐ Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

1-27 (partially)

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.

☒ No protest accompanied the payment of additional search fees.

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-27 (partially)

A probe comprising the nucleotide sequence SEQ ID 1 (see claim 13), or a fragment thereof having a length of at least 15 bp (see ISA form 206), in particular comprising the sequence SEQ ID 13233(see p. 91 of the description, which indicates that this sequence corresponds to the exon comprised in SEQ ID 1), spatially addressable set of probes comprising the said sequence (claim 1), microarrays comprising said sequence (claim 12), a method for measuring gene expression (claim 22), a method for identifying exons (claim 23) and a method for assigning exons to a single gene (claim 24) comprising using the said arrays, the peptide encoded by SEQ ID 1 or 13233 (claims 26-27) having the sequence SEQ ID 26233 (see ISA form 206), which is the translation from SEQ ID 13233 (see p. 69 of the description).

2. Claims: 1-27(partially)

A probe comprising the nucleotide sequence SEQ ID 2, or a fragment thereof having a length of at least 15 bp (see ISA form 206), in particular comprising the sequence SEQ ID 13234(see p. 91 of the description, which indicates that this sequence corresponds to the exon comprised in SEQ ID 2), spatially addressable arrays comprising the said sequence, a method for measuring gene expression, a method for identifying exons and a method for assigning exons to a single gene comprising using the said arrays, a peptide encoded by SEQ ID 2 or 13234 having the sequence SEQ ID 26234, which is the translation from SEQ ID 13234 (see p. 69 of the description).

...Inventions 3-13232: similar subject-matter as above related to SEQ IDs 3-13232.

Continuation of Box I.2

The following statements concerning the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject-matter for which a search has been performed and which has been identified as inventions 1-2 in PCT form 206.

1) Claims 1-3, 5, 6, 8-15 and 18-24 relate to fragments of undisclosed length or characteristics which cannot therefore be meaningfully searched. These claims have thus been searched only insofar as related to fragments having a length of at least 15 nt (see claim 15 and description pages 10, 1. 16-23).

2) Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising SEQ ID 1 or 2 and microarrays comprising the said sets. Therefore, the claims lack clarity and conciseness (Art. 6 PCT) to such an extent as to render a meaningful search over their whole scope impossible. Consequently, with respect to the said sets and microarrays the search has been carried out only insofar as related to the SEQ ID 1 and 2 as such.

3) In view of the absence of any indication as to which other peptides could be encoded by SEQ ID 1 and 2, the search with respect to claim 26 has been limited to the peptide sequences actually disclosed in the application, i.e. 26233 and 26234 (Art. 6 PCT).

4) Claims 15-21 relate to nucleic probes, solely defined in that they code for polypeptides having the sequence SEQ ID 26233 or 26234. However, a peptide is potentially coded by an extremely large number of nucleic acid sequences. Hence, claims 15-21 lack clarity and conciseness to such an extent as to render a meaningful search over their whole scope impossible. The search has thus been limited to SEQ ID 1, 2, 13233 and 13234.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an international Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

International Application No  
PCT/US 01/00663

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